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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AACCAATCCAGAGAGCAGGGCTAAGACCTTGTGAATATGTCGAAGCAGCCAATTTCCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GAGGAAAAGAAGCCAATTCCTGGAATGAAGAÄATTTCCAGGACCTGTTGTCAACTTGTCT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

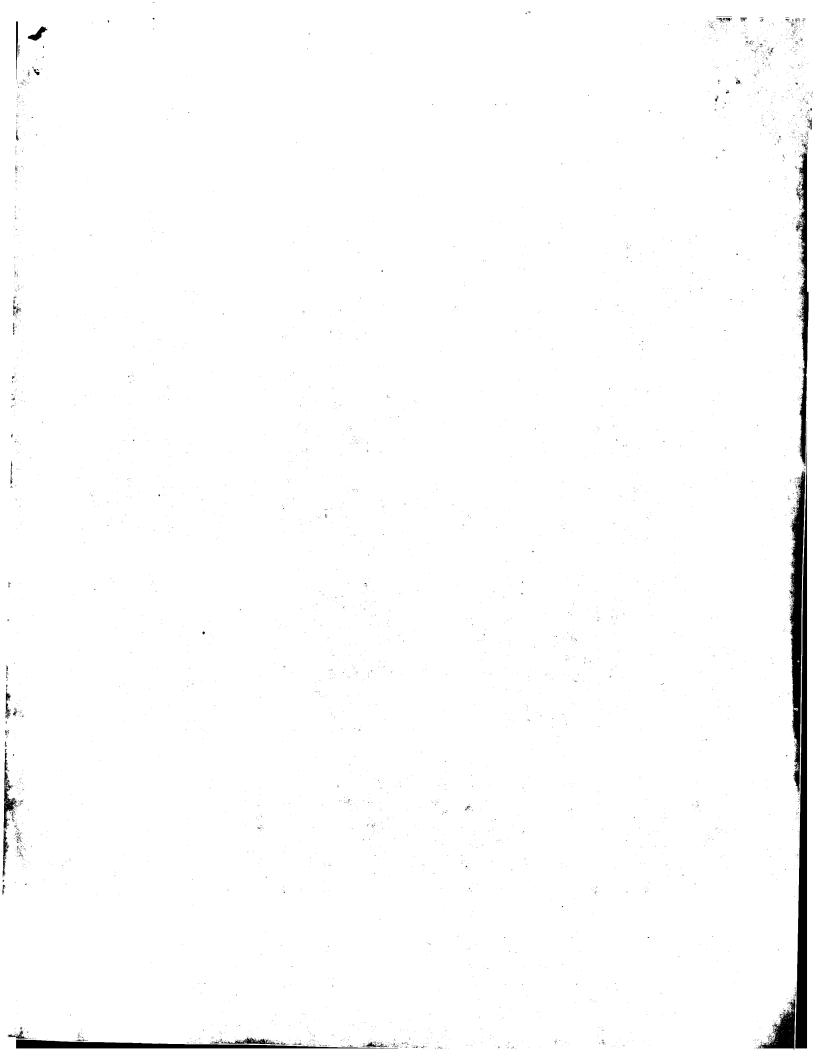
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 657)

1 (bases 1 to 657)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ176246 657 bp mRNA linear EST 30-APR-2002
UI-M-DJ2-bwg-d-13-0-UI.81 NIH BMAP_DJ2 Mus musculus cDNA clone
UI-M-DJ2-bwg-d-13-0-UI 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome: Res. ::65 (9) 7 (791 - 806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 443 1706
Fax: 301 443 9890
Email: mSTROMMAIL.nih.gov
Email: mSTROMMAIL.nih.gov
Tissue Procurement: Dr. Robin Davisson
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, M.F., Lennon, G. and Soares, M.B. Romalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ176246.1 GI:20351738
                                                                                                                                                                                                                                                         The following repetitive elements were found in this cDNA sequence: 1-40, >AT rich#Low_complexity (matched compliment) Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      louse mouse.
                                                                                                                                                                                                                                                                                                                                                          (www.resgen.com).
/organism="Mus musculus"
/strain="C57BL/6"
/db xref="taxon:10090"
/db xref="taxon:10090"
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/clone lib="NIH_BMAP_DJ2"
/clone lib="NIH_BMAP_DJ2"
/clone type="subtornical organ and postrema"
/tissue type="subtornical organ and postrema"
/dev_stage="Adult"
/dev_stage="Adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/note="Organ: brain; Vector: pT773-Pac (Pharmacia) with a
                                                                                                                                                                                                                                      Location/Qualifiers
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Query Match 63.1%; Score 491; DB 14; I Best Local Similarity 100.0%; Pred. No. 1.6e-112; Matches ,491; Conservative 0; Mismatches 0;
                                    768 TATGAAGGGGG 778
                                                                                                                       237 GCAAATCAGCACACGAATTTACAACCTGGGAAGTGTGGTTTTGAGGAGAGATGTGATTTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                      588 TGATCACAAACCTCCTGAATGCCCAAGACTCTAGCAAAAATATCCTGTTTGTACATTTAT 647
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TATGAAGGGGG 167
                                                                                                                                                                      GCAAATCAGCACACGAATTTACAACCTGGGAAGTGTGGTTTTGAGGAAGAGATGTGATTTT 767
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TISSUE-subfornical organ and postrema
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BASE COUNT ORIGIN

RESULT 7 AK009857

LOCUS DEFINITION

AK009857

S40 bp. mRNA linear HTC 19-JAN-2002 mus musculus adult male tongue cDNA, RIKEN full-length enriched hibrary, clone:2310046N05:small muscle protein, X-linked, full

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KEYWORDS SOURCE

HTC; CAP trapper.
Mus.musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:2310046N05.

Chordata; Craniata; Vertebrata; Euteleostomi;

ORGANISM

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VERSION ACCESSION

AK009857.1 GI:12844912

AK009857 nsert sequence.

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US-09-647-019-1 778

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

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Issued Patents NA:*

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Copyright (c) 1993 - 2003 Compugen Ltd.

April 15, 2003, 18:42:01 ; Search time 46.0337 Seconds (without alignments) 5183.040 Million cell updat

cell updates/sec

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BOME REMODELING GENES
FILE REFERENCE: DB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 111
LENGTH: 909
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 021
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                                                                                                                                                                                                                                                                                                       GAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGCCTTTTTGTGTT 125
GTACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTC
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                      GTACTCCTGAAACTGAGGAGGGAGGTCCTACCTC---AGAGGAAAAGAAGCCAATTC
                                                                   TCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAGAAT
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552; Conserv
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US-09-453-702B-213
US-09-455-558-39
US-08-952-170B-1
US-08-952-1017B-611
US-09-221-017B-611
US-09-302-769-28
US-08-629-001A-1
US-08-952-127-1
US-08-952-127-1
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US-08-952-136C-1
US-08-952-014C-1
US-08-952-014C-1
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US-08-952-014C-1
US-08-952-014C-1
US-08-952-014C-1
US-08-958-936A-3
US-08-41-822-1
US-08-958-936A-1
US-08-629-001A-2
US-08-629-001A-2
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Pred. No. 2.4e-103;
0; Mismatches 169;
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Score

Query Match

Length

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US-08-232-463-14
US-08-232-463-15
US-08-832-883-1
US-08-832-87-1
US-08-832-87-1
US-08-302-449-1
PCT-US94-07430-1
PCT-US95-02251-2
US-08-199-780-2
US-08-199-780-2
US-08-199-780-2
US-08-199-780-2
US-08-928-419-5
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US-09-291-283-3
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US-09-345-882-1
US-09-313-962A-15
US-09-313-962A-15
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Sequence 111, App
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Sequence 10, Appli
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Sequence 20, Appli

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US-08-232-463-14/c
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
PILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367
                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 GAATTTACAACCTGGGAAGTGTGGTTTTTGAGGAGGAGATGTGATTTTTATGA 772
                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: FALKNER, F. G.
ITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 CTGGAATGAAGAAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAAA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGGCTGTÄTTTCTTÄCTTTÄTCTTCÄTTTTTGGCACCTCACAGAACAAATTAGCCCAT
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nucleic acid
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                                                                                                           (703)683-4109
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RESULT 3
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08791849A Patent No. 5914449
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TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 3, 367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                             APPLICATION NUMBER: US/08/791,849A
FILING DATE: January 30, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1151 RRR 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1271
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                                    TELEX:
                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 805 FILL
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                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGATGCATTTCGTTGACGTGTTTTTCCAAGGGAGAAAAAACAATGGGTTGAAATAAA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCCCAAAGGTGAACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGCTTAGAATC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAACTGAAATTT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 3.6%;
11; Conservative
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3.6%; Pred. No. 0.0036;
ive 173; Mismatches 119;
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MOLECULE TYPE:

DNA (genomic)

0

TYPE: n

2885 base pairs

TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear

double

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US-08-791-849A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.4
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
Query Match
                                                                                                                                                                    TELEPAX: (215) 568-5549
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Sac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/832,883
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 ACATTTTATACATTTGTATGATGATCACAAACCTCCTGAATGCCCAAGACTCTAGCAAAA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 TTCGTTGGCTTTTTTTTCTGAATTATAAATACTCTTTGGTAACTTTTCATTTCCAAGAAC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS INVENTION: OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 ATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTTGCATTTCTCACTT 681
                                                                                              MOLECULE TYPE:
                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEB:
                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTTTTTCCAGTTATATCATGGTCCCCTTTCAAAGTTATTCTCTACTCTTTTTCATAT 809
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                                                                                                                                                          4853 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: SEIDEL, GONDA, LAVORGNA & MONACO,
Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giordano, Antonio
Baldi, Alphonso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                               70..3489
                                                                                                                                                                                                                    (215)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                              CDNA
                                                                                                                              double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%;
                                                                                                                                                                                                                         568-8383
   4.6%;
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Pred. No. 0.049;
                                                                                                                                                                                                                                                          8321-13
     Score 35.8;
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     Length 4853;
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Patent No. 5840506
GENERAL INFORMATION:
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 568-556
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4135 AAAATGCATGATTTTGTAACCCAGATTTTGCTGTATATTTGTGATAGCACTTTCTACAAT 4194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4255 TATATTTTTTAAAATGTTAAAACCCCTATAGCCACCTTTTGGGAATGTTTTAAA 4309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ME
TITLE OF INVENTION: CA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 AAAAAACAATGGGTTGAAATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MONACO, DANIEL A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593 ACAAACCTCCTGAATGCCCAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTC 652
                                4195 GTGAACTTTATTAAATACAAAACTTCCAGGCTAAACATCCCAATATTTTCTTTAATGCTTT 4254
                                                                                                   4135 AAAATGCATGATTTTGTAACCCAGATTTTGCTGTATATTTGTGATAGCACTTTCTACAAT 4194
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                            533 AAAAAACAATGGGTTGAAATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATC 592
                                                                                                                                                                                                                                                           NAME/KEY:
653 TTCCTTTTACTTGGTTGCATTTCTCACTTTAGCTACATTTTTGGCACCTTGTAGA 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEIDEL, GONDA, LA
STREET: Suite 1800 Two Penn
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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                                                                 ACAPACCTCCTGPATGCCCAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTC 652
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                                                                                                                                                                                      4.6%;
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Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antonio
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                                                                                                                                                                      ; Score 35.8; DB; Pred. No. 0.6; 0; Mismatches
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                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                            87; Indels
                                                                                                                                                                                                          Length 4853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.6%;
Best Local Similarity 49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/075,783

FILLING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/852,305

FILLING DATE: 18-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/672,183

FILLING DATE: 20-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: DESCRIPTION:
NAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 840-0712
TELEX: 425066 CURTWS
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
722 GAATTT 727
                                            801 ATCTTCCATTTTTCCTACATTATCTTTAATATTGTCTAATGGTTTTCTATATCCGAACAC 742
                                                                                                                                                                                                                                                                                                          921 TIĞĞIATAATTITITTITTICCITICATTATCIĞCATICTTATTITĞATCAATIĞITTI 862
                                                                                                                                                                                                                                                                                                                                                                        542 TGGGTTGAAATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATGACACAAACCTC 601
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Paoletti, E
APPLICANT: de Taisne,
APPLICANT: Tine, John
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                          CTTGGTTGCATTTCTCACTTTAGCTACATTTTTGGCACCTTGTAGAGCAAATCAGCACAC 721
                                                                                                                                                                           CTGAATGCCCAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTTCTTCCTTTTA 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H: 5181 base pairs
nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 0.72;
0; Mismatches 94; Indels 0
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US-08-479-722B-3
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                                                                                                                                                  Matches
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08479722B Patent No. 6074840
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (713) 934-70 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/19
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                  2413 CÁCAGCGGCTCCGATCCCTTGACAGATGATAGCCGGAGAGGCACTGACACTGGAAAGAGC 2354
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                         116 TITTIGIGITTITIGCACCIGGGCCGCCIGGGACTGTCCTCAGGCAGTAAACCAATCCA 172
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US P
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US PCT/US95/02251
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION: (713) 934-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bonadio, Jeffrey
APPLICANT: Yin, Wushan
TITLE OF INVENTION: LATENT 7
TITLE OF INVENTION: GENES, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: /CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                   56 CACTGGAATTGAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGC 115
                                                                                                                                                                                                                                                                                              LENGTH: 3759 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 77040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
CTGGTGTGTCGTGCAGATGCCATCTTGGCACACTTTCCCAGCCTCACACTCATCCA 2297
                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Williams, Morgan & Amerson
7676 Hillmont, Suite 250
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/479,722B
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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934-7011
3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/316,650
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                                                                                                                                        Score 35.4; DB 3;
Pred. No. 0.7;
0; Mismatches 51;
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AND METHODS
                                                                                                                                          51;
                                                                                                                                                                       Length 3759;
                                                                                                                                          Indels
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RESULT 8 US-08-302-449-1

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Sequence 1, Application US/08302449 Patent No. 5679635

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US-08-302-449-1
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PCT-US94-07430-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/128,020
APPLICATION NUMBER: 29-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07430
APPLICATION NUMBER: PCT/US94/07430
APPLICATION NUMBER: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SHUTT 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,449
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Balamurugan, Kuppareddi
APPLICANT: Michals-Matcalon, Kimberlee
TITLE OF INVENTION: Aspartoacylase Gene,
TITLE OF INVENTION: Methods of Screening
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          1293 CTTATTCAAAGAAGTGTTTCCTATTTCTATATAGTTTATTATACATGATACTTGGGT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
STATE: Virginia
                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                  552 TAAAÇAACTTCCTGAACATTTTATACATTTGTATGATGATCACAAACCTCCTGAATGCCC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                    APPLICANT:
                                                                                                                                                                                                                          612 AAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                  22201
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2200 Clarendon Boulevard, Suite 1400
                                                                                                        Application PC/TUS9407430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balamurugan, Kuppareddi
Michals-Matalon, Kimberlee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                        Conservative
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159..1097
Kaul, Rajinder
Cao, Guang Ping
Balamurugan, Kuppareddi
Michals-Matalon, Kimberlee
                                                                    Matalon,
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pred. No. 1.3;
0; Mismatches
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COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07/77
FILING DATE:
CLASCOTTER
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PCT-US95-02251-2/c
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APPLICATION NUMBER: US 08/128,020
APPLICATION NUMBER: 29-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SHUTT 1PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6%;
                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9502251 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: IT
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INFORMATION FOR SEQ ID NO:
COUNTAL.
ZIP: 77210
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                1293 CTTATTCAAAGAAGTGTTTCCTATTTCTATATAGTTTATTATACATGATACTTGGGT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                            552 TARACARCTTCCTGRACATTTTATACATTTGTATGATGATCACAAACCTCCTGAATGCCC 611
                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                           612 AAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                 COUNTRY: United States of America
                                                                                                                 CITY: Houston
                                                                                                                                STREET:
                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: 1435 base pairs
nucleic acid
DEDNESS: double
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2200 Clarendon Boulevard, Suite 1400
                                                                                                Texas
                                                                                                                              P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
159..1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                             Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspartoacylase Gene, Protein, and
Methods of Screening for Mutations Associated with Canavan
Disease
                                                                                                                                                                                            METHODS AND COMPOSITIONS FOR STIMULATING BONE CELLS
                                                                                                                                                                               18
                                                                                                                                                 White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۳.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.8; DB Pred. No. 1.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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RESULT 11
US-08-199-780-2/c
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08199780 Patent No. 5763416
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Goldstein, Steven A.
TITLE OF INVENTION: Gene Transfer Into Bone Cells
TITLE OF INVENTION: And Tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,780
FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   2350 CTGGTGTGTGCAGATGCCATCTTGGCACACTTTCCCAGCCTCACAGTCATCCA 2294
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2410 CACAGCGGCTCCGATCCCTTGACAGATGATAGCCGGAGAGGCACTGACACTGGAAAGAGC 2351
                                                                                                                                        COUNTRY: UC. 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TTTTTGTGTTTTTGCACCTGGCCGCCTGGGACTGTCCTCAGGCAGTAAACCAATCCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC009P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                          ADDRESSEE: Arnold, Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 CACTGGAATTGAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/199,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3753 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CONCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Conservative
                                                                                                                                                                                           Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%;
Similarity 55.6%;
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                                                                                                                                                                 USA
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CONCURRENTLY HEREWITH
                                                                                                                                                                                                                         White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS/ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.8; DB:
Pred. No. 2.2;
0; Mismatches !
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US-08-199-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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COMPUTER READABLE FORM.

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION 514
PRIOR APPLICATION NUMBER: US 08/199,780
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
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Best Local Similarity 55.6%;
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                                                                                                 APPLICATION NUMBER: US 08 FILING DATE: 30-SEP-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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                                                                                                                                                                                                                                                                                                                        STATE: Texas
COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TTTTTGTGTTTTTTGCACCTGGCCCTGGGACTGTCCTCAGGCAGTAAACCAATCCA 172
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 CACTGGAATTGAGATCCCGGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGC 115
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REFERENCE/DOCKET NUMBER: UMIC:002
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, Application US/08316650
5. 5942496
                                                                                                                                                                                                                                                                                                                                                                          Houston
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                        P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roessler, Blake J.
Goldstein, Steven A.
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                                                                                                                                                                                                                                                                                                                                                                                                 White & Durkee
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Pred. No. 2.3;
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MOLECULE TYPE: DNA (genomic) FEATURE:

TYPE: nucleic acid STRANDEDNESS: single

LENGTH:

4314 base pairs

TOPOLOGY:

linear

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; LOCATION: 157..3912
US-08-316-650-2
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                                                                       NAME/KEY:
LOCATION:
US-08-928-419-5
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Best Local Similarity 55.6%;
Matches 65; Conservative
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Query Match 4.3%; Score 33.6; DB Best Local Similarity 52.1%; Pred. No. 0.88; Matches 75; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                           LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucle
                                                                                                                                                                                                                                                        TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, RAYMOND C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185-0206P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,419
FILING DATE: 12-SEP-1997
FILING DATE: 12-SEP-1997
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APPLICANT:
APPLICANT:
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ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH,
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2509 CTGGTGTGTTCGTGCAGATGCCATCTTGGCACACTTTCCCAGCCTCACAGTCATCCA 2453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CYTOPLASMIC MALE STERILITY DNA FACTOR
TITLE OF INVENTION: AND UTILIZATION THEREOF
NUMBER OF SEQUENCES: 19
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                                                                                                                                FEATURE:
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YAMAMOTO, TOSHIYA
                                                                                       1..480
                                                                                                            CDS
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   69;
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                                    Length 480;
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   Indels
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US-09-291-283-5
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; LOCATION:
US-09-291-283-5
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                                                                                                                                                             Query Match 4.3%;
Best Local Similarity 52.1%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TENET: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/291,283
FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928,419
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CYTOPLASMIC MALE STERILITY DNA FACTOR TITLE OF INVENTION: AND UTILIZATION THEREOF NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: STEWART, RAYMOND C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 216
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APPLICANT: YAMAMOTO,
APPLICANT: OEDA, KEN
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: other nu
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                                                                                                                                                                                                                                                                                                          FEATURE:
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    166
                                      356 CAATTCCTGGAATGAAGAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATG 415
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                                                                                                                     296 GGAAAGAGAGTACTCCTGAAACTGAGGAGGGAGGTCCTACCACCTCAGAGGAAAAGAAGC 355
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                                                                              GGGATCAGCAGAATTCTAAAACTGCGGAACCAACTTCTTTCACACCAGGAGAACAACATC 165
  CGGAGCAAGGACCCCAACAGTTTGGAAGATATCTTGAGAAAAGGTTTTAGCACCGGTGTA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FALLS CHURCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703-205-8050
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                                                                                                                                                                                                                                                               CDS
1..480
                                                                                                                                                                                                                                                                                                                             other nucleic acid
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                                                                                                                                                             0; Mismatches
                                                                                                                                                                                Score 33.6; DB Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2185-0206P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
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                                                                                                                                                               69; .Indels
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Search completed: April 15, 2003, 22:41:51 Job time : 75.0337 secs
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SEQUENCE CHARACTERISTICS:
LENGTH: 651 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-928-419-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid FEATURE: NAME/KEY: CDS LOCATION: 1..651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEWART, RAYMOND C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185-0206P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22040-0747
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/928,419
FILING DATE: 12-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEB: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                      356 CAATTCCTGGAATGAAGAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATG 415
                                                                                                                                                                                                                                                 106 GGGATCAGCAGAATTCTAAAACTGCGGAACCAACTTCTTTCACACCAGGAGAACAACATC 165
                                                                                                                                                                                                                                                                                         296 GGAAAAGAGAGTACTCCTGAAACTGAGGAGGAGGGAGGCTCCTACCACCTCAGAGGAAAAAGAAGC 355
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TITLE OF INVENTION: CYTOPLASMIC MALE STERILITY DNA FACTOR
TITLE OF INVENTION: AND UTILIZATION THEREOF
                                                                                226 TCCTATATGTACTCCAGTTTATTC 249
                                                                                                                    416 TTAAAAGTGAACTGAAATTTGTCC 439
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ORGANISM AK003105 AKO03105 934 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male heart CDNA, RIKEN full-length enriched library, clone:1010001C09:small muscle protein, X-linked, full Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) HTC; CAP trapper.

Mus musculus (rain:C57BL/6J) adult male heart cDNA to clone lib:RIKEN full-length enriched mouse cDNA library clone:1010001C09. Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol: 303, 19-44 (1999) Eukaryota; Metazoa; Mammalia; Eutheria; Mus musculus AK003105.1 GI:12833554 Genome Res. 20499374 sequence. Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus mRNA, Mue.

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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakewa, T., Hara, A., Pukunishi, Y., Konno, H., Adachi, J., Pukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Yuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrinl, L.M., Staubli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshio, G., Blake, J., Boffelli, D., Bojunga, N., Pletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Lume, D. A., Kamiya, M., Lee, N.H., Lyons, P., Marchonni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Marchonni, L., Mashima, J., Mazzarelli, J., Sakamoto, N., Sasaki, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, Laboratory for Genome Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Fax:81-45-503-9216)
Fax:81-45-503-9216)
Please Visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer prepare mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase prepared by cap-trapper. cDNA went and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5']
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small muscle protein, X-linked"
/db_xref="MGD:MGI:1913356"
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/db_xref="MGD:MGI:1893249"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                            /gene="Smpx"
/note="data |
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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Score 770; DB 11 Pred. No. 2e-182; Mismatches

DB 11;

Length 934;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 890)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
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AV088480 AV088480 2 GI:16381435
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Matches 721; Conserv

Conservative

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Score 710; DB 9; Pred. No. 2.2e-167; 0; Mismatches 0;

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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
No., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jarel: 81-45-503-9222
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On Jun 25, 1999 this sequence version replaced gi:5219928.
Contact: Yoshihide Hayashizaki
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
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                    constructed a Bonaldo."
                                                T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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/dev_stage="adult"
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      Unpublished (2002)
Other ESTS: H4026C08-3
Contact: Yong Olan
Laboratory of Genetics
National Institute on Ac
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H4026C08-5 NIA Mouse 7.4K cDNA Clone Set Mus
H4026C08 5', mRNA sequence.
BQ554133 GI:21455021
                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 613)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G. and Ko, M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                               <u>AAAGGTGAACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGCTTAGAATCAGGAGA</u>
                                                                                    | CCTGAACATTTTATACATTTGTATGATGATCACAAACCTCCTGAATGCCCAAGACTCTAG
                                                                                                                                       333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Pleas.
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
plate: H4026 row: C column: 08
Seq primer: -21M13 Reverse
High quality sequence stop: 613
                               CAAAAATATC
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milarity 99.8%;
Conservative
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/strain="C578L/6"
/db_xref="niaEST:H4026C08-5"
/db_xref="niaEST:1090"
/clone="H4026C08"
/clone lib="NIA Mouse 7.4K cDNA Clone Sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pSPORT1; Site 1: Sal1; Site 2: Not1; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
140 c 138 g 144 t
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Pred. No. 6.1e-142;
0; Mismatches 1;
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163 AACCAATCCAGAGAGCAGGGCTAAGACCTTGTGAATATGTCGAAGCAGCCAATTTCCAAC
                                                                                        103
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                                                            61
                                                                                                                                                      43
                                                                                                                                                                                                 Local
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                                                    TCCTGTAAAGCGCTTTTTGTGTTTTTTGCACCT
                                                                 TCCTGTAAAGCGCTTTTTGTGTTTTTTGCACCTGGCCGCCTGGGACTGTCCTCAGGCAGTA 162
                                                                                                          GCCACATGAAAAGCACTGGAATTGAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTTCTA 60
                                                                                                                            GCCACATGAAAAGCACTGGAATTGAGATCCCCGCTCAGAGGGACACCGGGGAGTTCCTTCTA 102
                                                                                                                                                                                  504;
                                                                                                                                                                                               Similarity
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:279532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mi37cll.rl Soares mouse
clone IMAGE:465716 5', m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996
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                                                                                                                                                                                 Conservative
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Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                      M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:465716"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="unknown"
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                                                                                                                                                                                         Score 504; DB 9; L
Pred. No. 8.9e-116;
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e embryo NbME13.5 14.5 Mus musculus
mRNA sequence.
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                                               GGCCGCCTGGGACTGTCCTCAGGCAGTA 120
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                                                                                                                                                                                                      Length 504;
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REFERENCE
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                                                                                                                                                                                                                                    Genetics (www.resgen.com).

The following repetitive elements were sequence: 1-40, >AT rich#Low_complexity
                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov
Tissue Procurement: Dr. Robin Davisson
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Votact: Chin, H
Contact: Chin, H
National Institute of Mental Health
National Institute Blvd. Room 7N-7190, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                             6001 Executive Blvd.
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, M.F.,
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BQ176246.1
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="UI-M-DUZ-bwg-d-13-0-UI"
/clone_lib="NIH BMAP DJZ"
/clone_lib="NIH BMAP DJZ"
/tissue_type="subfornical organ and postrema"
/dev_stage="Adult"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                       /organism="Mus musculus'
/strain="C57BL/6"
                                                                                                                                                                             Location/Qualifiers
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Mus musculus adult male tongue cDNA, RIKEN full-length enilibrary, clone:2310046N05:small muscle protein, X-linked,
                                 AK0098571 GI:12844912
AK009857.1 GI:12844912
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA.
clone lib:RIKEN full-length enriched mouse cDNA library
clone:2310046N05.
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TAG_TISSUE-subfornical organ and postrema
TAG_SEG-GCTACATGAT
TAG_SEG-GCTACATGAT
TAG_SIG-GCTACATGAT
TAG_TISSUE-subfornical organ and postrema
                musculus
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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8 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Evkunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Pukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Indhi, Y., Itoh, M., Izawa, M., Kauskawa, T., Hara, A., Hayateu, N., Itoh, M., Izawa, M., Kauskawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Myazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, K., Sano, H., Sagaki, D., Saito, H., Saito, R., Sakai, K., Sano, H., Sagaki, D., Sohriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejama, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                   Direct Submission
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                        CCTGGAATGAAGAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Science Laboratory in RIKEN. Prepare mouse tissues. First strand cDNA was primed with a primer prepare mouse tissues. First strand cDNA was primed with a primer Prepare Mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              small muscle protein, x-linked"
/db_xref="MGD:MGI:1913356"
/db_xref="MGD:MGI:1913356"
123 c 137 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Smpx"
/note="data source:MGD, source key:MGI:1913356,
evidence:ISS
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/clone_lib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_sTage="adult"
|- .540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FANTOM_DB:2310046N05"
/db_xref="MGD:MGT:1893269"
/db_xref="taxon:10090"
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|strain="C57BL/6J"
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y Match 58.7%; Score 456.4; DB 12; Length 617; Local Similarity 96.0%; Pred. No. 7.7e-104; hes 499; Conservative 0; Mismatches 18; Indels 3; Gaps 3;	Query Match Best Local Matches 49
147 a 146 c 136 g 182 t 6 others	BASE COUNT ORIGIN
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally. Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps (Manniatis); Cloning Technique: CUA Cloning (CloneAmp, Life Technologies); Average insert size: 1.8 Kb; Insertion site: TACGTCCACTGAATTCTGAGTG>. Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar ies.httm."	
/tissue_type="Diaphragm/Hind limb muscles" /cell type="Skeletal muscle" /dev_Stage="2 months" /lab_host="DH5a"	
Seq primer: M13/pUC Reverse. Location/Qualifiers 1617	FEATURES source
Email: Jeff.Schageman@UTSouthwestern.edu cDNA library constructed by UTSW as a component of the Program for Genomic Applications (PGA) and the Reynolds Heart Disease Prevention grants for use in cDNA microarray experiments. Sequence Quality: Sequence ends were trimmed based on percentage of ambigu us base calls or 'N's in windowed segments. Sequencing: First-pass sequencing; ABI Prism 377 sequencer and analysis software	•
Contact: Schageman JJ Shohet/Garner Labs University of Texas Southwestern Medical Center 6000 Harry Hines Blvd., NA2.226, Dallas, TX 75390, USA Tel: 214 648 1674	COMMENT
UT Southwestern Medical Center, Adult Mouse Skeletal Muscle cDNA Library	TITLE JOURNAL
Rodentia; Sciurognathi; Muridae; geman,J.J., Pertsemlidis,A., Garn hohet.R.V.	REFERENCE AUTHORS
house mouse. house musculus Bukaryota, Metazoa, Chordata,	SOURCE
	ACCESSION VERSION KEYWODDS
BG794218 617 UTSW_SM1G4 UTSW Adult Mouse CDNA Clone HTSW SM1G4 FDNA	RESULT 8 BG794218/c LOCUS DEFINITION
	Db 508
	Оу 541
- CONTROL LANGUAGA GUARTICGITGA CONGRETATIT CORAGGA BADABACA 540	
	Ov 481
AGTGAACTGAAATTTGTCCCCAAAGGTGAACAGTAGTCGAAAGGACACAAAAGTTCACAT 480	

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 482)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box,8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
AA434782
AA434782.1 GI:2139696
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                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                      Seq primer: -28m13 rev2 ET from High quality sequence stop: 411 Location/Qualifiers
/organism="Mus musculus"
/strain="0578L/6J"
/db_xref="teaxon:10090"
/clone="MAGE:818976"
/clone_lib="Soares mouse NbMH"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Rodenia; Sciurognathi; Muridae; Murina 1 (bases 1 to 486)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubgeish, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                          GI:3259652
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Pred. No. 4.3e-103;
0; Mismatches 1;
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Mus musculus cDNA clone
Q93031 COSMID U228D4 ;, mRNA
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Best Local Similarity
Matches 448; Conserv
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                                                     CTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAACTGAAATTTTGTCCCCAAAG
                                                                                              GAGCTCCTACCACCTCAGAGGAAAAGGAAGCCAATTCCTGGAATGAAGAAATTTCCAGGAC
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GTGAACAGTAGTCGAAAGGACACAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
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Location/Qualifiers
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314 286 1810
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RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1381151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_mammary_gland_NbMMG'
/sex="male"
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; Pred. No. 9.7e-102;
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GATCACAAACCTCCTGAATGCCCAAGACTCTAGCAAAAATATCCTGTTTTGTACATTTATA 648
                                                                                          GGAGAAAAACAATGGGTTGAAATAAACAACTTCCTGAACATTTTATACATTTGTATGAT
                                                                                                                                 AAAAGTTCACATTGGATGCTTAGAATCAGGAGATGCATTTCGTTGACGTGTTTTTCCAAG
                                                                                                                                                            AAAAGTTCACATTGGATGCTTAGAATCAGGAGATGCATTTCGTTGACGTGTTTTTTCCAAG
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                                                                                                                                                                                                                                                                                      AAGAAGCCAATTCCTGGAATGAAGAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATC 519
                                                                                                                                                                                                                                                                                                                                                                    430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4026 row: C column: 08
Seg primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Other_ESTs: H4026C08-5
Contact: Yong Qian
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Rodentia; Sciurognathi; Mu 1 (bases 1 to 578)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatan Luo, A.G. and Ko, M.S.H.
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H4026C08-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus
H4026C08 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1;
/note="Wector: SPORT1; Site_1: Sal1; Site_2: Not1;
clone is among a rearrayed set of 7,407 clones from
than 20 cDNA libraries."
113 c 94 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6"
/db_xref="niaEST:H4026C08-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="H4026C08"
/clone_lib="NIA Mouse 7.4K cDNA Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                              Score 430; DB 14;
Pred. No. 3.2e-97;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 578;
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ni, T., Kargul, G.J.,
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     Query Match
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AA060214.1
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Zan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston
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490 bp mRNA line mj65h06.rl Soares mouse p3NMF19.5 Mus musculus IMAGE:481019 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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The WashU-HHMI Mouse EST Project
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Eukaryota; Metazoa;
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                                                                                152
                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:1553903
                                 54.7%;
                 Score 425.4; DB 9;
Pred. No. 4.5e-96;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Louis, MO
                                                 Length 490;
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCAAAATGTTAAAAGTGAACTGAAATTTGTCCCCAAAGGTGAACAGTAGTCGAAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAAAG
                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 436)

Marra, M., Hillier, L., Allen, M., Bowles, M., Detrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W36988 436 bp mRNA linear EST 1: mb65b11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone mAGE 334269 5', mRNA sequence.
                                                                                                                                                                            Fax: 314 200 2022
Email: mouseeest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                     Seq primer: ETPrimer
                                                                                                                                                                        MGI:215669
                                                                                                                     quality sequence stop:
Location/Qualifiers
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/clone_lib="Soares mouse_p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resist
                                                  organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:334269"
                                                                                                         1. .436
                                                                                                                                     436.
                                                                                                                                                                                                                                                                         St. Louis,
       resistant)"
                                                                                                                                                                                                                                                                           MO 63108
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stop: 557

Heart cDNA Library"

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48 ATGAAAAGCACTGGAATTGAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTG 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAGCGCTTTTTGTGTTTTTTGCACCTGGCCGCCTGGGACTGTCCTCAGGCAGTAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAAGCACTGGAATTGAGATCCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTG 60
                                                                                                                                                                                                                                                                                                                          L0522D07-3 NIA Mouse Newborn Heart clone L0522D07 3', mRNA sequence BMI23288
                                                                                                                       Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., I
and Ko,M.S.H.
Systematic Analyses of NIA Mouse Newborn Heart
                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, 1
                                                                                         Contact: Dawood B. Dudekula
                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 557)
                                                                                                                                                                                                                                            Mus.musculus
                                                                                                                                                                                                                                                                                                        BM123288.1
                                                                       Laboratory of Genetics
                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                  house mouse
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             cdna@lgsun.grc.nia.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
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99.8%;
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Rodentia;
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Pred. No. 5.6e-96;
0; Mismatches 0
                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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cDNA Library Mus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATTTGTCCCCAAAGGTGAACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGCTT
                                                                                                                                                                                                                                                                                                                                                  AATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATGATCACAAACCTCCTGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATTTGTCCCCAAAGGTGAACAGTAGTCGAAAAGGACAAAAGTTCACATTGGATGCTT
                                                                                                                                                                                                                                                                      CCAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                           AGAATCAGGAGATGCATTTCGTTGACGTGTTTTTCCAAGGGAGAAAAAACAATGGGTTGA
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     W13738
mb32a12.r1
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Seq primer: -21M13 Forward
High quality sequence stop: 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: heart; Vector: pSPORT1 (Invitrogen); Site 1: Sall; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xret= ..../clone="L0522D07"
/clone="L0522D07"
/clone lib="NIA Mouse Newborn
/clone rmm="Newborn Heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer [Invitrogen: 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Newborn
/dev_stage="Newborn"
/lab_host="DH10B"
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448 bp
Soares mouse p3NMF19.5
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Score 409; DB 13; Pred. No. 5.8e-92

5.8e-92;

Length 557;

RESULT 14 BM123288/c

ACCESSION

DEFINITION

VERSION

KEYWORDS

EST

ORGANISM

COMMENT

Mus musculus cDNA clone

linear

EST 10-SEP-1996

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 448)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
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High quality sequence stop: 441.
Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:212502
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ALIGNMENTS

AUTHORS	RBFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AY026524
Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,CC., Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentgen,F., Mohun,T. and Harvey,R.P.	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euterebcom.; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 787)	Mus musculus	Mus musculus.		AY026524.1 GI:14575061	AY026524	Mus musculus muscle-specific protein CSL (CSL) mRNA, complete cas.	AY026524 787 bp mRNA linear ROD 28-JUN-2001	

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J. Cell Biol. 153 (5), 985-998 (2001) 21275706
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Palmer,S., Groves,N., Schi
Sparrow,D.B., Barnett,L.,
Mohun,T. and Harvey,R.P.
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206. .463
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PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
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/chromosome="X"
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Pred. No. 4e-194;
); Mismatches 0;
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Darlinghurst, Sydney, New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, SAF Building, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 943) Kemp,T.J., Sadusky,T.J., Simon,M., Brown,R., Eastwood,M., Sassoon,D.A. and Coulton,G.R.
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Kemp, T.J.
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                 GAGAGTACTCCTGAAACTGAGGAGGAGGGAGCTCCTACCACCTCAGAGGGAAAAGAAGCCAATT
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Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel x-chromosomal human gene (SMPX) encoding a small muscular protein Hum. Genet. 105 (5), 506-512 (1999)
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/product="SMPX protein"
/protein 1da"AAKS0398.1"
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PTISEEKKPIFGMKKFPGPVNNLSEIQNVKSELKFVPKGEQ"
906._911
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/db_xref="taxon:10090"
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/evidence=experimental
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Rattus norvegicus
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
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Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein
Hum. Genet. 105 (5), 506-512 (1999)
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862. .867
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190. .447
                                                                                                                                                                 organism="Rattus norvegicus"
| db_xref="taxon:10116"
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/evidence=experimental
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Pred. No. 8.3e-135;
0; Mismatches 62;
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Homo sapiens mRNA for stretch protein (Srmx gene).
AJ250584

AJ250584.1

GI:10178976 stretch responsive

muscle

(X-chromosome)

(X-chromosome)

Eukaryota; Metazoa; Chordata; Craniata;

Vertebrata; Euteleostomi;

Homo sapiens Srmx gene;

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                                                                                         CTGAAACTGAGGAGGGAGCTCCTACCACCTC---AGAGGAAAAGAAGCCAATTCCTGGAA 367
                                                                                                                                           GCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATCAATA
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 TGAAATTTGTCCCCAAAGGTGAACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGC
                          CGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAAC
                                                  TGAAGAAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial College of Science Technology and Medicine, SAF Bldg, Level 2, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Related sequences. AC245772, U73508 to U73509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 885)
Kemp, T.J., Sadusky, T.J., Simon, M.,
Sassoon, D.A. and Coulton, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 72 (3),
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857. .862
/gene="Srmx"
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Gvppysdbekkpipgakklpgpavnlselqnikselkyvpkaeq"
451 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Srmx"
/codon_etart=1
/product-stretch responsive muscle (X-chromosome)
/protein_id="CAC08492.1"
/db_xref="GI:10178977"
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184. .450
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1. .885
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Pred. No. 7.2e-92;
0; Mismatches 152;
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TTAGAATCAGGAGATGCATTTCGTTGACGTGTTTTTCCAAGGGAGAAAAAACAATGGGTT
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Homo sapiens small muscular protein
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1 (Dases 1 to 886)

Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.

Identification, mapping, and genomic structure of a novel X-chromosomal human gene (SMPX) encoding a small muscular protein Hum., Genet. 105 (5), 506-512 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-JAN-1999) Molecular Human Genetics, Institut
Human Genetics, Fleischmannstr. 42/44, D-17487 Greifswald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                      /gene="SMPX"
/codon_start=1
/evidence=not_experimental
/product="small muscular pro
/protein_id="AAF19343.1"
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857. .862
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                                                                  /gene="SMPX"
/note="alternate
451. .>886
                                                                                                                                                   /translation="mamskopvsnvraiqaninipmgaffpgagopprrkectpevee
gvpptsdeekkpipgakklpgpavnlseiqnikselkyvpkaeq"
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<1. .>886
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BC005948
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IMAGE:4246501, u
BC005948
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FEATURES source
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Best Local
                   ACAACCTGGGAAGTGTGGTTTTTGAGGAGAGATGTGATTTTTATGA
                                                                                        TGCATTTCTCACTTTAGCTACATTTTTGGCACCTTGTAGAGCAAATCAGCACACAATTT
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AACACCTGGAGGGTGTGGTTTTTGAGGAGGGATATGATTTTATGGA
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Similarity 73.3%;
61; Conservative
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/db_xref="taxon:32644"
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GI:13543590

835 bp small muscle protein, mRNA, complete cds.

mRNA linear X-linked, clone

PRI MGC:

12-JUL-2001 :14584

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TITLE
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Matches 511; Conserv
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GAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAA
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Direct Submission
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Submitted (02-APR-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for tull length sequencing because it passed the following selection criteria: matched mRNA gi: 6625646.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Mammalia; Eutheria;
1 (bases 1 to 835)
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A.,
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a 155 c 171 g 227 t
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/lab_host="DH10B"
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/db_xref="LocusID:23676"
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/clone="MGC:14584 IMAGE:4246501"
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                                                                                                                                                                                                                                  AL732396 228031 bp DNA 228031 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced g1:22204493.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                            coverage: 8.63x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 228031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk
humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                      ATTTTTGGCACCTTGTAGAGCAAATCAGCACACGAATTTACAACCTGGGAAGTGTGGTTT
                                                                                                                                                                   ATCCTGTTTGTACATTTATATTTCTTCCTTTTÄCTTGGTTGCATTTCTCACTTTAGCTAC
                                                                                                                                                                                                                                                              ATTTTATACATTTGTATGATGATCACAAACCTCCTGAATGCCCAAGACTCTAGCAAAAAT 628
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5645 5644; gap of 100 bp
11122 11221: gap of 100 bp
1122 21310: contig of 5477 bp in length
23111 23210: gap of 100 bp
23211 42146: contig of 1889 bp in length
42147 74925: contig of 18936 bp in length
42247 74925: contig of 32679 bp in length
74926 75025: gap of 100 bp
75026 153828: contig of 78803 bp in length
153929 178635: contig of 100 bp
153929 178635: contig of 55296 bp in length
172636 172735: gap of 100 bp
172636 172735: gap of 100 bp
172636 172735: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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153929. .172635
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                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
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Rattus norvegicus clone CH230-20D15, *** SEQUENCING IN PROGRESS
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
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Pred. No. 1.2e-45;
0; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 96% of reads
Chemistry: Dye-terminator Big Dye; 3% of reads
Chemistry: Dye-terminator Big Dye; 3% of reads
Consensus quality: 235530 bases at least Q40
Consensus quality: 236735 bases at least Q30
Consensus quality: 237530 bases at least Q20
Insert size: 238467; sum-of-contigs
Insert size: 238467; sum-of-contigs
Insert size: 241670; 2.5% error; agarose-fp
Quality coverage: 7.58x in Q20 bases; sum-of-contigs Quality
coverage: 10.48x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL731811 239667 bp DNA
MUS musculus chromosome X clone RP23-60A1,
PROGRESS ***, 13 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
84329 106119: contray or 2007 106120 106219: gap of 100 bp 106220 119269: contray of 13050 bp in length 119270 119369: gap of 100 bp 119370 130432: contray of 13043 bp in length 130433 130532: gap of 100 bp 130432: contray of 87650 bp in length 218183 218282: gap of 100 bp 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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84329 10611
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39234 8422
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9233: gap of 100 bp
84228: contig of 44995 bp in length
4328: gap of 100 bp
106119: contig of 21791 bp in length
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223857 223956: gap of 100 bp
223957 2253956: contig of 2352 bp in length
226309 226408: gap of 100 bp
226409 228848: contig of 2476 bp in length
228885 228984; gap of 100 bp
228985 231639: contig of 2655 bp in length
231640 231739: gap of 100 bp
231740 236718: contig of 4979 bp in length
236719 236819: gap of 101 bp
236820 239667: contig of 2848 bp in length.
                                                                                                                                                                                                                                                                                                                                              72780
                                                                                                                                                                                                                                                           23.3%; Score 181; DB 2; 1 ilarity 100.0%; Pred. No. 6.4e-37; Conservative 0; Mismatches 0;
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236819. 239667 /
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231740. .236718
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228985. .231639
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48417 c 49370 g 67888 t 1212 others
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226409. .228884
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223957. .226308
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/note="assembly fragment:09628
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221710. .223856
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?ragment_chain:1"
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/chromosome="X"
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                                       sequence.
U73508
U73508.1 GI:1616808
                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0194629-A 2927 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 5.8e-32;
0; Mismatches 103
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                                                                                                                                                                                                                                                           This clone is from a chromosome X-specific cosmid library LLOXNCCO1
'U'. The source of the chromosomes was a human/hamster hybrid,
GM07297-F, from Robert Nussbaum at the University of Pennsylvania
School of Medicine. Please contact the Lawrence Livermore National
Laboratory at http://www-bio.llnl.gov/genome to obtain the clone.
                                                                                                                                                                                                                                                                                                                                                                                             MAPPING INFORMATION:
This clone was mapped by Grieff, M., Whyte, M. P., Thakker, and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Geno 44:227-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Direct Submission
Submitted (20-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-APR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-OCT-1996)
4 (bases 1 to 36503)
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Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restriction digest.
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db_xref="taxon:9606"
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8529. .8555
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3711. .3929
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10938. .11032
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                                                                                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 19, 2002_this sequence version replaced gi:21614755.
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 124186)
                                                                                                                                                                                                                                                                                                                                                AL772392 124186,bp DNA
Human DNA sequence from clone RP11-450P7
                                                                                                                                      Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton
                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                               AL772392.4
                   Web site: http://www.sanger.ac.uk
                                       Center code: SC
                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                             Homo sapiens.
Contact: humquery@sanger.ac.uk
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28149. .28286
/rpt_family="MIR"
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Search completed: April 15, Job time: 2269.69 secs

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Db 100555
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
ACCTGGAGGGTGTGGTTTTGAGGAGGGATATGATTTTATGGA
                                                        ACCTGGGAAGTGTGGTTTTGAGGAGAGATGTGATTTTTATGA 772
                                                                                                                                  ATTTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAATTAGCCCATAAATTCAAC 100436
                                                                                                                                                                                              ATTTCTCACTTTAGCTACATTTTTGGCACCTTGTAGAGCAAATCAGCACACGAATTTACA 730
                                                                                                                                                                                                                                                                        Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP11-450P7 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-450P7"
/clone_lib="RPCI-11.2"
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78.8%;
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Pred. No. 6.6e-28;
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Perfect score:
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1: /cgn2 6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

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17: /cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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10 US-09-960-352-5216
10 US-09-962-436-468
9 US-10-092-154-1971
10 US-09-764-847-1971
10 US-09-742-312-3
10 US-09-790-988-1
10 US-09-790-988-1
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9 US-09-796-692-8553
10 US-09-796-692-8553
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10 US-09-864-761-15062

10 US-09-822-830A-340

10 US-09-777-745-1

10 US-09-777-745-1

10 US-09-790-988-1
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Sequence 4, Appli
Sequence 468, App
Sequence 1971, Ap
Sequence 1971, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 43, Appli
Sequence 2419, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 124, App
Sequence 124, App
Sequence 12062, Ap
Sequence 15062, Ap
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ALIGNMENTS

RESULT 1 US-09-880-192-4

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Sequence 4, Application US/09880192
| Sequence 4, Application US/09880192
| Patent No. US20020077470A1
| GENERAL INFORMATION: Walker | G. APPLICANT: Walker, Michael G. APPLICANT: Walker, Michael G. APPLICANT: Walker, Tod M. APPLICANT: Klingler, Tod M. APPLICANT: Klingler, Tod M. APPLICANT: Azimzai, Yalda | TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION | FILE REFERENCE: PB-0009-1 CIP | CURRENT APPLICATION NUMBER: US/09/880,192 | CURRENT FILING DATE: 2001-06-12 | CURRENT FILING DATE: 2001-06-12 | SOPTWARE: PERL PROGRAM | SEQ ID NO 4 | LENGTH: 824 | TYPE: DNA | CRGANISM: Homo Sapiens | FEATURE: MAME/KEY: misc_feature | OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1 | US-09-880-192-4
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Best Local Similarity 73.4
Matches 565; Conservative
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                                                                           151 CTTGCATCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATA
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                                                                                                          TTTGCACCTGGCCCGGGGACTGTCCTCAGGCAGTAAACCAATCCAGAGAGCAGGCTA 185
                                                                                                                                                                              GAGATOGOAGOTOAGAGGACACOGGGCGCCCCTTCCACCTTCCAAGGAGC--TTTGTATT 150
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GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASS

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 5216

LENGTH: 4666
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                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 23-BOVMS1-014-Q1-E1-F3
US-09-960-352-5216
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US-09-960-352-5216
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Local 5
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GCTAAGACCTTGTGAATATGTCGAAGCCAGCCAATTTCCAACGTCAGAGCCATCCAGGCGA 241
                                                       TGTTCATGTACCTGACTGCCTGCGACTTTCCTCAGGCATGAAACATGTGCATATAGCACG 91
                                                                                     AATTCAACACCTGGAGGGTGTGGTTTTGAGGAGGGATATGATTTTATGGA
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                                                                                                                                        Similarity
                                                                                                                          Conservative
                                                                                                                                     29.1%;
79.8%;
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                                                                                                                     Score 226.2; DB
Pred. No. 5.4e-57
0; Mismatches 6
                                                                                                                                                 DB 10;
                                                                                                                       68;
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                                                                                                                                                 Length
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CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NO 468
LENGTH: 587
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: n=a,t,g or c
US-09-962-436-468
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US-09-962-436-468/c
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GENERAL INFORMATION:
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Best Local Similarity 66.6%;
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681 TTAGCTACATTTTTGGCACCTTGTAGAGCAAATCAGCACACGAATTTACAACCTGGGAAG
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                                                                                  GCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGATTTGCATTTCTACT
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                                                                                                                                     TCACTAAAATTTTATATATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTA
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Pred. No. 5e-38;
0; Mismatches 103;
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248 TTATCTTCATTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGG 189

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RESULT 4
US-10-092-154-1971/c
US-10-092-154-1971/c
; Sequence 1971, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
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US-09-764-847-1971/c
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                                                                                                                                                    ; LENGTH: 4672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1971
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1971
                                                                                                                                                                                                                                                                                                                                          Sequence 1971, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%;
Best Local Similarity 49.1%;
Matches 109; Conservative
                                                                                          Query Match 5.3%;
Best Local Similarity 49.1%;
                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1971
                                                                            Matches
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 TIGICAACTIGICIGAGAICCAAAATGIIAAAAGIGAACTGAAATTIGICCCCAAAGGIG 448
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                                    389 TTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAACTGAAATTTGTCCCCAAAGGTG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCAGAGTGGATATTCTAATTATCATCATATACAGTCAAGTAGTTGTCAAATACCAAGGA 2896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTTGACGTGTTTTTCCAAGGGAGAAAAAACAATGGGTTGAAATAAACAACTTCCTGAAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGCTTAGAATCAGGAGATGCATTT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTAAAAATATCCGTACTGCTTCATCATCAGGGGCACCAGGAATCTGGAAGAAATGAG 3016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGTGATGAGTAAAGGCATTTGAGATTGCATTGAATGAGTTTTCTCTTTTAAATGATTT
  TTCTANAAATATCCGTACTGCTTCATCATCAGGGGCACCAGGAATCTGGAAGAAAATGAG
                                                                            109;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 0.15;
                                                                          Score 41.2; DB 10;
Pred. No. 0.15;
0; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113;
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                                                                              Indels
                                                                                                                Length
                                                                                                                  4672;
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      3016
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US-09-742-312-3/c
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                                                                                                                                                                                                                        RESULT 7
US-09-790-988-1/c
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Patent No. US20020045166A1

GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISARAN, Ishwar et al
APPLICANT: CHANDRAMOULISARAN, Ishwar et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                   Sequence 1, Application US/09790988 Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/742,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL000838
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US/09/790,988
ENGREP FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(147309)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21129
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                                                                                                                                                                                                                                                                                                                                  739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGTAGTCGAAAGGACACAAAAGTTCACATTGGATGCTTAGAATCAGGAGATGCATTT
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                                                                                                                                                                                                                                                                                               AGTATG 20944
                                                                                                                                                                                                                                                                                                                                  AGTGTG
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Pred. No. 1
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US-09-770-445-43
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; ORGANISM: Buchnera
US-09-790-988-1
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 1200
     Matches
                                 Query Match
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Best Local Similarity
Matches 77; Conserv
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SEQ ID NO 1
                                                                                                                                                                                                                                                         APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
                                                                                                              TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                    OTHER INFORMATION: n = A,T,C or G
                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(1200)
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
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NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                        PPLICAN
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                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 CATTITATACATTTGTATGATGAT 591
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                        Davis, Keith R.
Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                   Slader,
                                                                                                                                                                                                                                                                                                                                                                                              Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matthew, Abraham V.
Ledford, Brooke L.
                                                                                                                                                                                                                                                                                                                                                                  Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                           Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu, Yang
Rameaka, Joshua G.
     Conservative
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53.5%;
              4.6%;
 ; Score 36; DB 1; Pred. No. 2.3; 0; Mismatches
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Pred. No. 60;
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                           DB 10;
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                           Length 1200;
 Indels
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APPLICANT: MANNION, JANE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP*
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
                                                                                               ; OTHER INFORMATION: n=A,T,C or US-09-796-692-8553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-796-692-8553
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Query Match
Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                              NAPULA (11)
LOCATION: (11)
OTHER INFORMATION: n
NAMEKEY: unsure
NAMEKEY: (180)
                                                                                                                                                                                                                                                                                                                                     PEATURE:
NAME/KEY: unsure
NAME/KIY: (11)
                                                                                                                                       NAME/KEY: unsure
LOCATION: (522)
OTHER INFORMATION: 1
NAME/KEY: unsure
LOCATION: (565)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
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APPLICATION NUMBER: 60/218,950

PILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/222,903 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCATATATCTAATACTACTACTACTATTAGAGTCTCTGTGTGAAGATTTATG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATTTATATTTCTTCCTTTTACTTGGTTGCATTTCTCACTTTAGCTACATTTTTG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTTCGTTGTCCAATATGCAGCTAAATCAACAATACACTAGTAATAATCTCAAATTTGG
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. US20020198362A1
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                     4.6%;
50.3%;
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Score 35.8; DB Pred. No. 1.7; 0; Mismatches
                                          DB 9;
                                          Length 597;
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533 AAAAAACAATGGGTTGAAATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATC 592

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Indels

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CURRENT APPLICATION NUMBER: US/10/084,205
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR PLILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN Ver. 3.1
SEQ ID NO 3
LENGTH: 1074
TYPE: DNA
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US-09-764-877-2419/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2419
      Best Loc
Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF JD NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2419
                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10084205
Publication No. US20030049648A1
GENERAL INFORMATION:
APPLICANT: Choi, Gil
TITLE OF INVENTION: 37 Staphylococcus aureus Genes
FILE REFERENCE: PB515P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.6%;
Best Local Similarity 50.3%;
                                          Query Match
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GENERAL INFORMATION:
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                                                                                           ORGANISM: Staphylococcus aureus
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    Local Similarity 52.4
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                    4.4%;
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                    Score 34.6;
Pred. No. 5.
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Pred. No. 17;
  Mismatches
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                                    Length 1074;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-637-3
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PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR PILLING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR PILLING DATE: 1997-01-03
PRIOR PILLING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR PILLING DATE: 1996-01-06
PRIOR PILLING DATE: 1996-01-06
PRIOR PILLING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
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US-09-925-637-3/c
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                                 APPLICANT:
APPLICANT:
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APPLICANT:
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Best Local Similarity 52.4%;
Matches 76; Conservative
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                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09925637 Patent No. US20020103338A1 GENERAL INFORMATION:
                                                                                                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2001-08-10
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 OF INVENTION:
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               NT: Wall, Daniel
NT: Trawick, John D.
NT: Carr, Grant J.
NT: Yanamoto, Robert T.
NT: Xu, H. Howard
F INVENTION: Identificati
                 Identification
Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.6; DB
Pred. No. 5.6;
0; Mismatches
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                 얁
                 Essential Genes
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FILE REFERENCE: ELITRA.011A

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US-08-781-986A-124
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; LOCATION: (1)...(1077)
US-09-815-242-8282
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 124, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/207,727
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ORGANISM: Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1077
                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                               CLASSIFICATION: 435 PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                   CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                       OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                   HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                Human Genome Sciences,
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                                                 DATA:
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                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus Polynucleotides and Sequences: 5255
                                                                                                                                                      MSDOS version 6.2
                                                                                                  US/08/781,986A
                                                                                                                                                                                       3.50 inch, 1.4Mb storage
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US-09-864-761-15062
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Best Local Similarity 52.4
76; Conservative
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                                                                                                                                                                                                                                                                                                                                       PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G.
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REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6850 GTCTCACTTAACATTTCTTCAATAT 6874
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                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                              APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                        FILING DATE:
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APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: PCT/US01/00662
                                                      FILING DATE:
                                                                      APPLICATION NUMBER: PCT/US01/00668
                                                                                                           APPLICATION NUMBER: PCT/US01/00665
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Hanzel, David K.
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Pred. No. 19;
0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2001-01-29

PRIOR FILING DATE: 2001-01-29

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 15062

LENGTH: 474

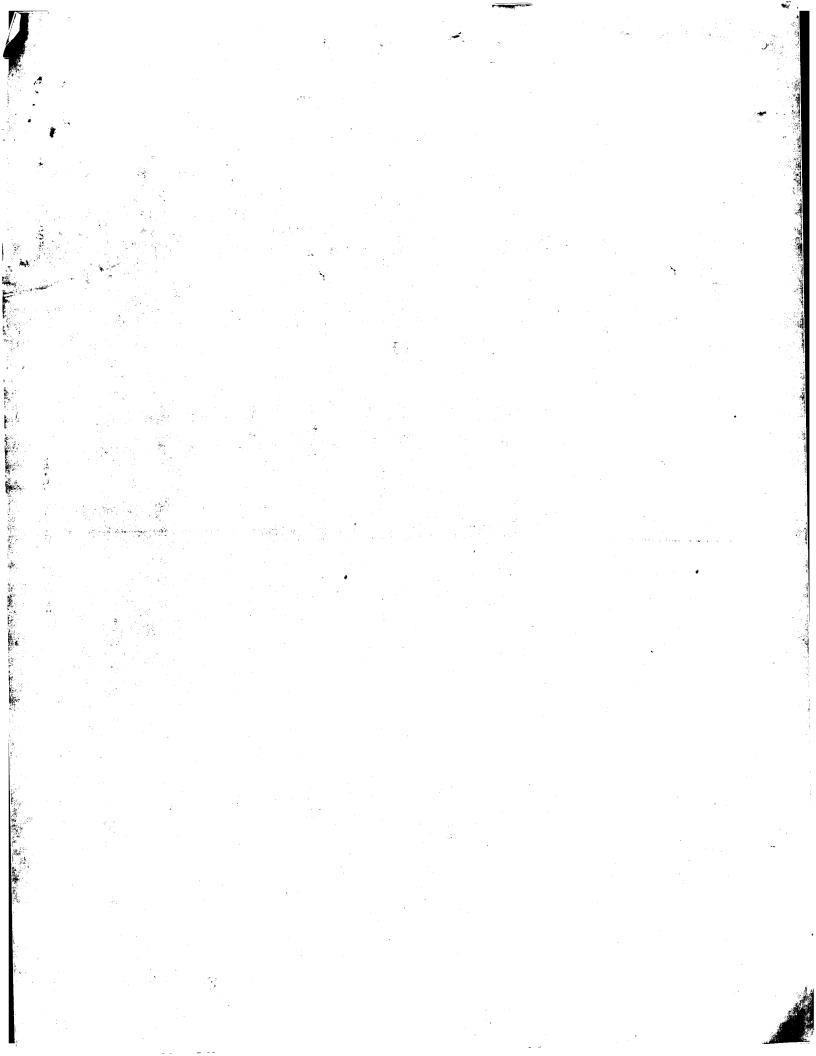
TYEE: DNA

ORGANISM: Homo sapiens

PEATURE:
OTHER INFORMATION: MAP TO AL022100.13

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

US-09-864-761-15062,
Search completed: April 16, 2003, 01:12:33 
Job time : 344.739 secs
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                                                                                       365 CTTTGTATTTCT 376
                                                                                                                                                                                                                                                                                        520 TTTTCCAAGGGAGAAAAAACAATGGGTTGAAATAAACAACTTCCTGAACATTTTATACAT 579
                                                                                                                                                                                                                                                                                                                                              185 AAAATGGAGAACCTTCCACATAATTCTTCTTGTATCAGTTGGTGGTCTTTCCCCAAGGTCA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 TCTGAGATCCAAAATGTTAAAAGTGAACTGAAATTTGTCCCCAAAGGTGAACAGTAGTCG 459
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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155.253 Million cell updates/sec
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Match Length
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Gapop 10.0 , Gapext 0.5
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   GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-757-022B-14
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US-07-757-022B-58
US-07-757-022B-104
US-07-757-022B-14
US-07-757-022B-14
US-07-757-022B-4
US-07-757-022B-4
US-07-757-022B-6
US-07-757-022B-6
US-07-757-022B-6
US-07-757-022B-6
US-07-757-022B-8
US-07-757-022B-8
US-07-757-022B-9
US-07-757-022B-9
US-07-757-022B-9
US-07-757-022B-9
US-08-887-534A-72
US-08-9461-240-2
US-08-952-92-9
US-08-952-92-9
US-08-301-162-2
US-09-461-240-18
US-09-968-297-2
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                            Sequence 14, Appl
Sequence 74, Appl
Sequence 74, Appl
Sequence 104, Appl
Sequence 142, Appl
Sequence 42, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 20, Appl
Sequence 50, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 9, Appl
Sequence 2, Appli
Sequence 3, Appli
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US-07-757-0228-14
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ALIGNMENTS

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Sequence 14, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                APPLICATION UNMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
PRIOR APPLICATION NUMBER: US 07/546,114
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBeff, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REF
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                                          TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
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CITY: Cambridge
STATE: Massachu
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: 941 amino acids
AMINO ACID
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87 CambridgePark Drive
                                                                                                                               Floppy disk
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US-07-757-022B-84
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; MOLECULE TYPE: protein
US-07-757-022B-14
                                                        Best Local Similarity 42.2
Matches 19; Conservative
                                                                                         Query Match
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Best Local S
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 32-5000
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                                                                                                                                                                                                             TELEFAX: (617)876-5851
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                     TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                             TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILLING DATE: 1991910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
25( PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STALL
COUNTRY: 02140
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                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
!: U.S.A.
                                                                                                                                                                                            1022 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CambridgePark Drive
                                                                                                                                                                                                                                           (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                      17.3%;
                                                                                                                                                                                                                             84:
                                                    Score 76; DB 4; Length 1022; Pred. No. 1.4; 2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                            GI 5190
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                    Gaps
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RESULT 4
US-07-757-022B-58
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US-07-757-022B-74
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                                                                                                                                          Query Match 17.3%;
Best Local Similarity 42.2%;
Matches 19; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
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                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)876-585
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                 322 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 0, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                   25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKPPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 382
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                     AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02140
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                                                                                                                                                                                                                                                                                 1038 amino acids
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                                                                                                                                                                                                                                                                                                                                         (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                          2;
                                                                                                                                                     Score 76; DB 4; Length 1038;
Pred. No. 1.4;
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                                                                                                                                          Mismatches
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                                                                                                                                          18;
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Sequence 58 Patent No.

58, Application US/07757022B o. 6433142

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GENERAL INFORMATION: APPLICANT: Gesner APPLICANT: Clark,

Gesner, Thomas Clark, Stephen

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MOLECULE TYPE: protein
US-07-757-022B-58
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Patent No. 6433142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                       APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CBETT, LUBIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            365 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 42.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19910
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                                                                                                                                                                                                                                                                                                                                                                                             25 PGAGQPPRRKESTPETEEGAPTTSEE-----, KKPIPGMKKPPGP 63
                                                       STREET:
                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION:
                                     Cambridge
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: U.S.A.
Massachusetts: U.S.A.
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                                                   B: Genetics Institute, Inc.
87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics Institute, Inc
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                                                                                                            Megakaryocyte Stimulating Pactors
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 4; Length 1049;
Pred. No. 1.4;
2; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)876-585
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 19910910
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                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Turner, APPLICANT: Hewick,
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                STATE:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                            4, Application US/07757022B
6433142
                                                                                                                                                             02140
                                                                                                                                                                                                               Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
                                                                                                                                                                            Massachusetts: U.S.A.
                                                                                                                                                                                                                                87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.3%;
                                                                                                                                                                                                                                                                                                                     Rodney M.
                                                                                                                                                                                                                                                                                                    Megakaryocyte Stimulating Factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels
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JS-07-757-022B-44
                                                                             PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.3%;
Best Local Similarity 42.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/07757022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -07-757-022B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No. 643314
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,0228
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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LENGTH: 1270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 29-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 366
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                                    APPLICATION NUMBER:
                                                                         FILING DATE: 29-JUN-1990
                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKPPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 08-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           02140
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87 CambridgePark Drive
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                  MBER: US 07/457,196
29-DEC-1989
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29-DEC-1989
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08-AUG-1989
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RESULT 8
US-07-757-022B-142
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                  APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
FILLING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBSTT, LUAIN
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10706-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                           APPLICATE: 18-UAL.
FILING DATE: 18-UAL.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: 29-UN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8 CITY: Cambridge CITY: Massachusetts
                                                                                                                                                           PILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 07/457,196
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
ZLECUME: (617) ET (617) E
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FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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6433142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/390,901
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Best Local Similarity 42.2%;
Matches 19; Conservative
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    Best Local Similarity 42.7
Matches 19; Conservative
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino acids
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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LENGTH: 1313 amino acids
TYPE: AMINO ACID
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/643,502
PILLING DATE: 18-JAN-1991
PRIOR APPLICATION UNMBER: US 07/546,114
PILLING DATE: 29-JUN-1990
                                                                                                                                                                                                          TOPOLOGY: 11
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T: U.S.A.
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87 CambridgePark Drive
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17.3%; Score 76; DB 4; Length 1314; 42.2%; Pred. No. 1.9; tive 2; Mismatches 18; Indels
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US-07-757-022B-46
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FILING DATE: 19910910

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

PRIOR APPLICATION DATA:
ORDER OF APPLICATION DATA:
ORDER OF APPLICATION DATA:
ORDER OF APPLICATION DATA:
ORDER OF APPLICATION DATA:
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                                                                                                                                                                                              Query Match 17.3%;
Best Local Similarity 42.2%;
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APPLICANT: Geener, Thomas G.

APPLICANT: Clark, Stephen C.

APPLICANT: Turner, Katherine

APPLICANT: Hewick, Rodney M.
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carry

NAME
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE,DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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372 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                         25 PGAGQPPRRKESTPETEEGAPTTSEE----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (617) 876-5851
(617) 876-00: 46:
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics Institute,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1989
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                                                                                                                                                  Score 76; DB 4; Length 1320; Pred. No. 1.9; 2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5190
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; Sequence 60, Application US/07757022B ; Patent No. 6433142

RESULT 11 US-07-757-0228-60

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RESULT 12
US-07-757-022B-48
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1/.3
Best Local Similarity 42.2
Matches 19; Conservative
                                                                                                                                                                                                   Sequence 48, Application US/07757022B Patent No. 6433142
                                                         APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)876-585: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gesner
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER. UT 6/07/257 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  372 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 416
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                                                                                                                                                                                                                                                                                                                                                       25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
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                        ADORESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridge
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87 CambridgePark Drive
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Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617) 876-5851
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Hewick, Rodney M.
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                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 76; DB 4; Length 1320; 42.2%; Pred. No. 1.9;
                                                                         Megakaryocyte Stimulating Factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60:
                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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Patent No. 6433142
GENERAL INPORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Conserve
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
PRIOR APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 450
                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 PGAGQPPRRKESTPETEEGAPTISEE-----KKPIPGMKKFPGGP 63
                                                                                                                                                                                             CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 199109 CLASSIFICATION: 530
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OPERATING SYSTEM:
                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                 02140
                                                                                                                                                                                             Cambridge
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1354 amino acids
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                                                                                                                                                                                                                                                                                              Megakaryocyte Stimulating Factors
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                                                                                                                                                                                                                                                                            143
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                                                                                                                                                                                                                                  Inc.
                   Version #1.25
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US-07-757-022B-52
; Sequence 52, Application US/07757022B
; Patent No. 6433142...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                           CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502

PILING DATE: 18-JAN-1991

PRIOR APPLICATION DATA:
                                                                                                                                                                           MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/07/757,022B
PILING DATE: 19910910
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MOLECULE TYPE: protein
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CITY: Cambridge
STATE: Massachu
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APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-JUN-1990 RIOR APPLICATION DATA:
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87 CambridgePark Drive
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18-JAN-1991
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acid
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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NAME: CBETT, LUARN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
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APPLICATION NUMBER: 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
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MEDIUM TYPE: Floppy disk
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87 CambridgePark Drive
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CBX4 HUMAN
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InterPro; IPR001836; Togavirin.
Pfam; PF00943; Alpha E2 glycop; 1.
Pfam; PF00944; Alpha E2 glycop; 1.
Pfam; PF01563; Alpha E3 glycop; 1.
Pfam; PF01589; Alpha E1 glycop; 1.
PRINTS; PR00798; TOGĀVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P27284;
01-AUG-1992
01-AUG-1992
16-OCT-2001
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-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

-!- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

-!- MISCELLAMEOUS: THE 6 kDa POLYPEDTIDE PROBABLY SERVES AS THE SIGN

-EQUIENCE FOR THE MEMBERANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the swibs institute. There are no restitute. The European Bioinformatics Institute. There are no restitutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this alicense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 kDa peptide; Spike glycoprotein El].

Eastern equine encephalitis virus (strain va33[ten broeck]) (Eastern equine encephalomyelitis virus).
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16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (Pl30) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91220727; PubMed=2024496;
Weaver S.C., Scott T.W., Rico-Hesse R.;
"Molecular evolution of eastern equine encephalomyelitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equine encepharomyeration ----- viruses; ssRNA positive-strand viruses, no
                                                                                                                                                                                                                                                                                                                                                                                  Coat protein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A39992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M69094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
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GLYCOPROTEIN
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SMART; SM00248; ANK; 4.

SMART; SM00252; SH2; 2.

SMART; SM00252; TYPKC; 1.

SMO215; TYPKC; 1.

PROSITE; PS50088; ANK REPEAT; 2.

PROSITE; PS500297; ANK REP REGION; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; I
InterPro; IPR000719; I
InterPro; IPR000980; S
InterPro; IPR001245; 7
                                                                                                                                                                                                                  Pfam, PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase;
ProDom; PD000093; SH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>-</del> <del>-</del> <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                                                                                                                                                                                            Pfam; PF00017; SH2; 2. Pfam; PF00023; ank; 5.
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; Euk_pkinase. ; SH2. ; Tyr_pkinase.

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Query Match
Best Local
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HT16_HY
P53356;
                                                                                                                                                                                                                                                            containing SH2 domains and Oncogene 9:1253-1259 (1994)
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01-OCT-1996
15-JUN-2002
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                           MEDLINE=94181280; Pul
Chan T.A., Chu C.A.,
                                                                                                                                                                                                                                                                                                                Steele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
EMBL; U00936; AAC27350.1;
HSSP; P08631; IAD5.
                                                           entities
                                                                                                                                                                                                                                     -!- FUNCTION: MAY BE INVOLVED IN SIGNAL
-!- CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydra attenuata (Hydra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase
                                           send an email to license@isb-sib.ch).
                                                                                                                                                            TYSOSINE PHOSPHATE.
TISSUE SPECIFICITY: EPITHELIAL CELI
SIMILARITY: BELONGS TO THE TYR FAMI
SIMILARITY: CONTAINS 2 SH2 DOMAINS
SIMILARITY: CONTAINS 5 ANK REPEATS
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A., Rauen K.A.,
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90192810; PubMed-2156268;
Banerji J., Sands J., Strominger J.L., Spies T.;
"A gene pair from the human major histocompatibility complarge proline-rich proteins with multiple repeated motifs single ubiquitin-like domain.";
Broc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                   "Dense Alu clustering and a family within a 90 kilobase Nat. Genet. 3:137-145(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93272029; PubMed=8499947;
Iris F.J.M., Bougueleret L., Prieur
Perrot V., Jurka J., Rodriguez-Tome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-1860 FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen D.
                                                             or send an email to license@isb-sib.ch).
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       M33509;
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BAT2 (HLA-B-associated transcript 2).
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Pred. No. 6.6;
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                                                                                                                                                                        There are no restri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caterina D., Pr. Claverie J.-M.,
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EMBL; M33512; AAA35586.1; J
EMBL; Z15025; CAA78744.1; -
PIR; B35098; B35098
PIR; S36152; S36152.
Genew; HGNC:13918; BATZ.
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MIM; 142580; -.
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STANDARD;
PRT; 1239 AA.

PO8768;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
(Capsid protein (Pla0) (Contains: Coat protein C (EC 3.

(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein
6 kDa peptide; Spike glycoprotein E1.
6 kDa peptide; Spike glycoprotein E1.
6 kDa peptide; Spike glycoprotein E1.
Viruses; ssRNA positive-strand viruses, Alphavirus. NCBI_TaxID=11021;
                                                                                                                                                            875
                        virus)
                                                                                                                               932
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                                                                                                                                PRRAGPIKKPPPPTKVEEL 950
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> PPHRGPAGNWGPP
> K (IN REF. 2).
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                                 (Eastern equine encephalomyelitis
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                   no DNA stage; Togaviridae;
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Matches 19
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InterPro; IPR00936; Alpha E2-glycop.
InterPro; IPR00936; Alpha E2-glycop.
InterPro; IPR001836; Alpha core.
InterPro; IPR001836; Alpha core.
InterPro; IPR001836; Alpha core.
IPR00943; Alpha E2-glycop; 1.
Pfam; PF00943; Alpha E2-glycop; 1.
Pfam; PF01583; Alpha E3-glycop; 1.
Pfam; PF01583; Alpha E3-glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
Coat protein; POlyprotein; Transmembran
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SEQUENCE
100
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-i- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
-i- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-i- MISCELLANEOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
--- PROTECT PROTECT PRICNES TO PEPTIDASE FAMILY S3.
                                                                                                                                                                                                                                                                                                                                                             Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X05816; CAA29261.1;
PIR; A26816; VHWVEE.
HSSP; P03315; 1VCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of the genome region encoding the eastern equine encephalomyelitis virus and the deduced sequence of the viral structural proteins.";

J. Gen. Virol. 68:2129-2142(1987)
                      59 K 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-82V-2137;
MEDLINE-87282265; PubMed-2886548;
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Ø
                                                           ISNVRAIQANINIPMGAFRPGAGQPPRRKESTP----ETEE---GAPTTSEEKKPIPGMK 58
                                   IEDLŔRSIANLTLKORÁPNÞÞÁGÞÞAKRKKÞÁÞSLSLÉTKKKRÞÞÞÞAKKOKRKÞKÞGKR 99
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ilarity 31.1%;
Conservative 1:
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                                                                                             13;
                                                                                        Score 75.5; DI
Pred. No. 17;
13; Mismatches
                                                                                                                                                  COAT PROTEIN C.
SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
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                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Hydrolase;
                                                                                                                                           MW;
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                                                                                                                                                                                                                                                                                              NATURE 364:304:308(1991).

-i- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS:
SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
MEMBRANE POTENTIAL STRABILIZATION, SIGNAL TRANSDUCTION AND
TRANSEPTHELLAL TRANSPORT.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN SKELETAL MUSC
-i- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.

-i- SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                           use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 350-467 FROM N.A.
MEDLINE=92065955; PubMed=1659665;
Steinmeyer K., Klocke R., Ortland
Gruender S., Jentsch T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Inactivation of muscle chloride channel by transposon insertion myotonic mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The mouse Clc1/myotonia gene: ETn insertion, a variable AATC repeat, and ECR diagnosis of alleles."; Mamm. Genome 8:718-725(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97468267; PubMed=9321463;
Schnuelle V., Antropova O., Grone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
STRAIN=C57BL/6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gronemeier M., Wedemeyer N., Jockusch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 C.,
                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gronemeier M., Jockusch H.,
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                                                                                                                                                                                                                      EMBL outstation
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MBL outstation -
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L; Z95131; CAB08359.1; J

L; Z95132; CAB08359.1; J

L; Z95133; CAB08359.1; J

L; Z95134; CAB08359.1; J

L; Z95135; CAB08359.1; J

L; Z95136; CAB08359.1; J

L; Z95137; CAB08359.1; J

L; Z95139; CAB08359.1; J

L; Z95140; CAB08359.1; J

L; Z95140; CAB08359.1; J

L; Z95142; CAB08359.1; J

L; Z95143; CAB08359.1; J

L; Z95144; CAB08359.1; J

L; Z95146; CAB08359.1; J

L; Z95147; CAB08359.1; J

L; Z95148; CAB08359.1; J

L; Z95149; CAB08359.1; J

L; Z62895; CAA44686.1; L

L; X62895; CAA44686.1; L
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RESULT 6. CLC1_MOUSE

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SMART; SM00116; CBS; 1.
Ionic channel; Ion transport;
CBS domain; Repeat.
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Pfam; PF00654; voltage
                                                                                                  DOMAIN
SEQUENCE
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TISSUE=Skeletal muscle;
MEDLINE=9265954; PubMed=1659664;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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15-JUN-2002 (Rel.
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This SWISS-PROT entry is copyright. It is produced through a cobvergen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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IPR001807; Cl-channel_volt.
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Last annotation update)
ein, skeletal muscle (Chloride
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CYTOPLASMIC (POTENTIAL).
13 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CBS 1.
CBS 2.
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Pred. No. 17;
7; Mismatches
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ng as its content is in no
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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) [Contains: Coat
(Capsid protein C); Spike glycoprotein E3; Spi
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DOMAIN
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Pfam; PF00654; voltage_CLC; 1.
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PIR; S19595; S
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InterPro; IPR001807; C1-channel_volt.
between
the Euro
                                                                             MEDLINE=88320369; PubMed=3413072;
Hahn C.S., Lustig S., Strauss E.G., Strauss J.H.;
Hahn C.S., Lustig S., Strauss E.G., Strauss J.H.;
"Western equine encephalitis virus is a recombinant virus.";
Proc. Natl. Acad. Sci. U.S.A. 85:5997-6001(1988).
-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
-!- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGN SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                              6 kDa peptide; Spike glycoprotein Western equine encephalitis virus.
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NCBI_TaxID=11039;
                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Everopean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                         HEMAGGLUTININ. SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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Q88696; Q88697;
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Pred. No. 17;
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            restrictions
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INTERPRO; S03.001; -..

INTERPRO; IPR002548; Alpha E1_glycop.

INTERPRO; IPR00936; Alpha E2_glycop.

R INTERPRO; IPR00933; Alpha E3_glycop.

R INTERPRO; IPR001836; Alpha core.

IR INTERPO; IPR000930; Togavirin.

Pfam; PP00943; Alpha E2_glycop; 1.

PFam; PP00944; Alpha E2_glycop; 1.

DR Pfam; PP01563; Alpha E3_glycop; 1.

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Matches 16
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SEQUENCE FROM N.A. STRAIN-Bristol N2;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                     Development
[2]
                                                                                                     Mueller
                                                                                                                                   MEDLINE=20530482;
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03854; AAA42999.1; PIR; A35587; VHWVWE.
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                                                                                                                 Zelewsky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
16; Conser
                                                elegans Mi-2 chromatin-remodelling
te determination.";
ment 127:5277-5284(2000).
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320
743
798
136
142
210
684
719
758
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                                                                                                                   T., Palladino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                          PubMed=11076750;
Palladino F., Brunschwig K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 N-LINKED
N-LINKED
136082 MW; 07561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%;
26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB:
Pred. No. 29;
14; Mismatches
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KE GIÆCOPROTEIN E1.
RGE RELAY SYSTEM (BY
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GLYCOPROTEIN
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                                                                            proteins
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                                                                                                            Tobler H.,
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M (BY SIMILARITY).
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TONB SALTY
ID TONB SALTY
ID TONB SALTY
AC P25945;
DT 01-MAY-1992
DT 01-UU1-1993
DT 15-UUN-2002

STANDARD;

242 B

TonB protein.

(Rel. (Rel. (Rel.

. 22, Created) . 26, Last sequ. . 41, Last anno

annotation update)

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Best Local S
Matches 20
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Pfam; PF00176; SNP2_N; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00385; Chromo; T.
Pfam; PF00385; Chromo; T.
Pfam; PF00628; PHD; 2.
SMART; SM00290; PHD; 2.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 2.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000953; Chromo.
InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; HeliCase C.
InterPro; IPR001305; SNP2 N.
InterPro; IPR001955; Znf PHD.
InterPro; IPR001841; Znf_ring.
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NP BIND
SITE
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PROSITE; PS50013; CHROMO 2; 1.
PROSITE; PS50013; CHROMO 2; 1.
PROSITE; PS00159; DEAH ATP HELICASE; 1.
PROSITE; PS01159; ZF PHD 1; 2.
PROSITE; PS50016; ZF PHD 2; 2.
Chromatin regulator; Nuclear protein; Recommendation of the comment of th
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
ZN FING
ZN FING
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
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EMBL; Z67881; CAA91810.1;
EMBL; Z67881; CAA91798.1;
EMBL; Z67884; CAA91798.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthews P., McMurray A.;
Submitted (NOV-1995) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; T14G8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF308444; AAG29837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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SUBCELLULAR LOCATION: Nuclear (Potential).

SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.

SIMILARITY: CONTAINS 2 PHO-TYPE ZINC FINGERS.

SIMILARITY: CONTAINS 2 CHROMO DOMAINS.
EEEVETEESQGVPTTSEKKKPPPKKKKGGKKSSKKKNNCDYPDPYKSTS
                              Similarity
                                                                                                                                                                                                                                              59
265
328
373
373
501
1287
641
                                                                                                   Conservative
                                                                                                                                                                                                                       Zinc-finger.
59 62
265 312
328 375
373 476
373 583
501 583
287 1291
641 648
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40.8%;
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                                                                                                ; Score 72.5; DI
; Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                  PHD-TYPE 1.
PHD-TYPE 2.
CHROMO 1.
CHROMO 2.
POLY-ARG.
ATP (POTENTIAL).
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; Repeat; Helicase; DNA-binding;
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                                                                                                                                                DB
                                                                                                11;
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                                                                                                                                              Length 1787;
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     84
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                                                                                           Gaps
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Bacteria, Proteobacteria; Salmonella.

gamma subdivision;

Enterobacteriaceae;

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Salmonella typhimurium.

STM1737.

NCBI_TaxID=602;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES SUCH AS COBALAMIN, AND VARIOUS IRON COMPOUNDS (SUCH AS IRON DICITRATE, ENTERCHELIN, AEROBACTIN, ETC.). IN THE ABSENCE OF TONB THESE RECEPTORS BIND THEIR SUBSTRATES BUT DO NOT CARRY OUT ACTIVE TRANSPORT. TONB ALSO INTERACTS WITH SOME COLICINS AND JS INVOLVED IN THE ENERGY—DEPENDENT, IRREVERSIBLE STEPS OF BACTERIOPHAGES PHI-80 AND TI INFECTION. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER MEMBRANE PROTEINS.

-I- SUBUNIT: HOMODIMER. FORMS A COMPLEX WITH THE ACCESSORY PROTEINS EXHB AND EXED (By SIMILIARILY).

-I- SUBCELLULAR LOCATION: PERIPLASMIC. ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille F.
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Forea L., Miller W., Sconeking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDILINE=91094049; PubMed=2266561;

Hannavy K., Barr G.C., Dorman C.J., Adamson J., Mazengera L.R.,

Gallagher M.P., Evans J.S., Levine B.A., Trayer I.P., Higgins C.F.;

"Tons protein of Salmonella typhimurium. A model for signal transduction between membranes.";
                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A sequence-spec
of the TonB prof
Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karlsson M., Hannavy K., Higgins C.F.; "A sequence-specific function for the of the TonB protein.";
                                                                                                                                                                                                     EMBL; X56434; CAA39818.1; -. EMBL; AE008777; AAL20655.1; -. PIR; 813257; 813257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 42; 58-60 AND 168 MEDLINE-93302513; PubMed-831608
                                                                                                            InterPro; IPR003538; TonB. Pfam; PF03544; TonB; 1. PRINTS; PR01374; TONBPROTEIN.
                                                                                                                                                                  HSSP; P94739; 11HR.
StyGene; SG10391; tonB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol.
                                                                           Periplasmic;
                                                                                            Transport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                        proteome.
                                                                           Transmembrane;
       33
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216:897-910(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8:379-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8316087;
 32
242
83
                                                                         Signal-anchor; Repeat; Phage recognition
SIGNAL-ANCHOR (BY SIMILARITY).
PERIPLASMIC (BY SIMILARITY).
7 X 2 AA TANDEM REPEATS OF E-P
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Best Local
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(29Y618; Q9Y500; Q13354; O00613; O15416;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Nuclear receptor co-repressor 2 (N-CoR2) (Silencing mediator retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Tretinoic-acid-receptor-associated co-repressor) (TAAC) (CTG26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross ("CDNAs with long CAG trinucleotide repeats from human brain Hum. Genet. 100:114-122(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Cervical adenocarcinoma;
MEDLINE=96008552; PubMed=7566127;
Chen J.D. Evans R.M.;
"A transcriptional co-repressor the company of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.; "SMRTe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                 "Identification of TRACs (T3 receptor-associating cofactors), a family of cofactors that associate with, and modulate the activity of, nuclear hormone receptors ", mol. Endocrinol. 10:813-825(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor corepressor.";
Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Park E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Unique forms of human and mouse nuclear receptor corepressor Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99178941; PubMed=10077563;
Ordentlich P., Downes M., Xie W., Genin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                              TISSUE=Brain cortex;
MEDLINE=97369492; PubMed=9225980;
                                                                                                                        TISSUE-Brain
                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                               MEDLINE=96408715; PubMed=8813722;
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM TRAC-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Cervical adenocarcinoma;
MEDLINE=99199215; PubMed=10097068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 377:454-457(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     łomo sapiens (Human)
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Eutheria;
                                                                                                                                                                                                                                                                                                     Privalsky M.L.;
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Primates;
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Pred. No. 6.2;
8; Mismatches
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EMBL; U37146; AAC50236.1; --
EMBL; S83390; AAB50847.1; --
EMBL; U80750; AAB51446.1; --
TRANSPAC; T04689; --
Genew; HGNC:7673; NCOR2.
MIM; 600848; --
                                             CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00395; SANT; 2.
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ANTIREPRESSOR.

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INSUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION AFTISCUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION AFTISCHED IN LUNG, SPLEEN AND BRAIN.

INDUCTION: REGULATED DURING CELL CYCLE PROGRESSION.

DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTURE AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTURE AND RD3.

INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTIONS.
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SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SINJA/B AND HISTONE DEACETYLASES HARC1 AND HARC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (REAR) IN THE ABSENCE OF LIGAND, AND MAY STABILIZE THEIR INTERACTION WITH TRIB. SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; SMRT/TRAC-2 (SHOWN HERE) AND TRAC-1; ARE PRODUCED BY ALTERNATIVE SPLICING. TRAC-1 CONTAINS ONLY THE C-TERMINAL RECEPTOR-INTERACTING DOMAIN AND ACTS AS AN ANTITERBRACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY: CONTAINS 1 SANT-A DOMAIN.
SIMILARITY: CONTAINS 1 SANT-A DOMAIN.
SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 CORNR BOXES.
SIMILARITY: BELONGS TO THE N-COR NUCLEAN
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAINS (ID1 AND ID2).

DOMAIN: THE TWO INVERTICAL DOMAINS (ID) CONTAIN A CONSERVED DOMAIN: THE TWO INVERTICAL TO SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED SUPFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUIFICANCING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
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COILED COIL (POTENTIAL).
INTERACTION WITH SINJA/B
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THE N-COR NUCLEAR RECEPTOR COREPRESSORS
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POLY-GLY.
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MISSING (IN ISOFORM T
L -> P (IN REF. 2).
K -> E (IN REF. 2).
L -> W (IN REF. 2).
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                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                               SEQUENCE FROM N
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                                                                                                             PATHWAY: Thiamine biosynthesis. SUBCELLULAR LOCATION: Cytoplasm
                                                                                                      SIMILARITY: BELONGS TO THE THII FAMILY.
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A -> S (IN REF. 2).
G -> R (IN REF. 2).
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IPR004114; THUMP_dom

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Best Local S
Matches 15
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Pfam; PF02926; THUMP; 1.
TIGRFAMs; TIGR0342; ThII; 1.
Thiamine biosynthesis; Complete
SEQUENCE 381 AA; 43436 MW; 0
                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatist the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commentations as institutions as long as its content is not removed.
                                                                                                                                                                                                                                                                                                                                                                   region. , (4:44-50(2000).

Genomics 64:44-50(2000).

-!- TISSUE SPECIFICITY: Expressed at moderate levels
-!- TISSUE SPECIFICITY: Appeal and pancreas, and at l
                                                                                                                                                                                                                                                                                                                                                                                                                                Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U., Portier B.P., Ueki K., Billings S., Ramaswamy S., Mohrenweiser H.W., Scheithauer B.W., Louis D.N., Jenkins R.B.; "A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003720;
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MEDLINE=20175430; PubMed=10708517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                             SEQUENCE
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S84 LPLGLQQPQAQQPPQ----APTPQAAAPPQATTPQPSPGLASSPEKIV
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                        18 IPMGAFRPGAGOPPRRKÉSTPETEEGAPTTSÉEKKPIPGMKKFPGPVV
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                                                                                                                                                                                                                                                                                                                                                             placenta, skeletal muscle, and lung, liver, and kidney.
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884
1214
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
r suppressor candidate region gene
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                                                                                                           POLY-PROMW; 7C514
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Pred. No. 12;
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                                                                  Score 71;
Pred. No.
                                                                                                                                    POLY-GLY.
POLY-PRO.
POLY-SER.
POLY-PRO.
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                                                                                                             7C5144F443CE6821 CRC64;
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CBS2 HUMAN STANDARD; PRT; 1484 AA (9BEXF3; Q9CGC3; Q9GEF5 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last amotation update) 15-JUN-2002 (Rel. 41, Last amotation update)
                                                                                                                                                                         and B/CECR2B; are produced by alternative splicing.

-! TISSUE SPECIFICITY: Highly expressed in skelatal muscle, thymus, placenta and lung. Expressed at lower level in brain, heart, colon, spleen, kidney.

-!- MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a developmental disorder associated with the duplication of a 2 Mb region of 22q11.2. Duplication usually takes in the form of a surpernumerary bisatellited isodicentric chromosome, resulting in four copies of the region (represents an inv dup(22)(q11)). CES is characterized clinically by the combination of coloboma of the iris and anal atresia with fistula, downslanting palphral fissures, presuricular tags and/or pits, frequent occurrence of heart and renal malformations, and normal or near-normal mental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of LRPPRC and its SEC1 domain interaction partners suggests roles in cytoskeletal organization, vesicular trafficking, nucleocytosolic shuttling, and chromosome activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O., Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which coding tor large proteins in vitro.";

DNA Res. 7:347-355(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McDermid H.E.;

**Rhalysis of the cat eye syndrome critical region in region of conserved synteny in mice: a search for can or near the human chromosome 22 pericentromere.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=21275466; PubMed=11381032;
FOOTE T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Broote T.K., Brinkman-Mills P., Banting G.S., Shinizu l Bridgland L.J., Hu S., Blirren B., Minoshima S., Shinizu l Bruyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S., Phan Nguyen T., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21082932; PubMed=11214970;
Nagase T., Kikuno R., Hattori A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 11:1053-1070(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 79:124-136(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21686162; PubMed=11827465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 168-1484 FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: May be involved through its interaction with the integration of cytoskeletal network with vesicular trafficking, nucleocytosolic shuttling, transcription, remodeling and cytokinesis.
SUBUNIT: Interacts with IRPPRC.
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Interacts with LRPPRC.
ALTERNATIVE PRODUCTS: 2 isoforms; A (shown
                                                                                                                                             SIMILARITY: CONTAINS 1 BROMODOMAIN.
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l S., Phan S.,
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Yao
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MACS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16527;
01-AUG-1990
EMBL; M31650; AAA48946.1; --
PIR; A41400; A41400.
Interpro; IPR002101; MARCES.
Pfam; PP02063; MARCKS; 1.
                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           -!- FUNCTION: MARCKS IS THE MOST PROMINENT CELLULAR SUBSTRATE FOR PROTEIN KINASE C. THIS PROTEIN BINDS CALMODULIN, ACTIN, AND SYNAPSIN. MARCKS IS A FILAMENTOUS (F) ACTIN CROSS-LINKING PROTEIN.
-!- PTM: PHOSPHORYLATION BY PKC DISPLACES MARCKS FROM THE MEMBRANE. IT ALSO INHIBITS THE P-ACTIN CROSS-LINKING ACTIVITY.
-!- SIMILARITY: BELONGS TO THE MARCKS FAMILY.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90114197; PubMed=2608063;
MEDLINE=90114197; PubMed=2608063;
Graff J.M., Stumpo D.J., Blackshear P.J.;
"Molecular cloning, sequence, and expression of a cDNA encoding the "Molecular cloning, sequence, and expression of a cDNA encoding the chicken myristoylated alanine-rich C kinase substrate (MARCKS).";
Mol. Endocrinol. 3:1903-1906(1989).

-1- FUNCTION: MARCKS IS THE MOST PROMINENT CELLULAR SUBSTRATE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Myristoylated alanine-rich C-kinase substrate (MARCKS).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00503; BROMODO
SMART; SM00297; BROMO; 1
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EMBL; AB05157; BAB51831.1; -.
EMBL; AF411609; AAL07393.1; -.
HSSP; Q92831; 1B91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 INIPMGAFRPGAGOPPRRKESTPETEEGAPTTSEEKKPIPGMKKFPGPVVNLSE 69
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PR00503; BROMODOMAIN.
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333 337
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1250 1253
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ilarity 29.6%;
Conservative 13
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614 POLY-SER.
1253 POLY-SER.
1253 POLY-PRO.
318 MISSING (IN ISOFORM B).
526 EYTKMSDN -> GKQGRSLC (IN ISOFORM B).
1484 MISSING (IN REFC 2).
1899 MISSING (IN REFC 2).
1045 R -> W (IN REFC 2).
1045 R -> W (IN REFC 2).
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13; Mismatches
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Phosphorylation; MyristaTe; Calmodulin-binding; Actin-binding;
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Search completed: April 9, 2003, 12:36:11 Job time: 14.6532 secs

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structural polyprotein - eastern equine encephalomyelitis virus
N,Contains: 6K protein; capsid protein; E1 protein; E2 potein; E3 protein
C,Species: eastern equine encephalomyelitis virus
C,Species: eastern equine encephalomyelitis virus
C,Pacession: S72350
C,Accession: S72350
R,Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.W.
R,Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.W.
Virology 197, 375-390, 1993
A,Title: A comparison of the nucleotide sequences of eastern and western equine encephal
A,Reference number: S72349; MUID:94025587; PMID:8105605

Apaccession: S72350

RESULT S72350

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RESULT 1

ALIGNMENTS

	QY 6 ISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETBEGAPTTSEEKKPIPGMKK 59
Gaps 1;	Query Match 17.8%; Score 78.5; DB 1; Length 1240; Best Local Similarity 33.3%; Pred. No. 12; Matches 18; Conservative 12; Mismatches 21; Indels 3;
#status predicted	F;259-276/Domain: transmembrane #status predicted <tm1> F;259-276/Domain: transmembrane glycoprotein E3 #status predicted <eg3> F;361-332/Product: membrane glycoprotein E2 #status predicted <eg2> F;324-743/Product: membrane glycoprotein E2 #status predicted <tm2> F;695-712/Domain: transmembrane #status predicted <tm3> F;722-738/Domain: transmembrane #status predicted <tm3> F;744-799/Product: 6K protein #status predicted <kp6> F;781-799/Domain: transmembrane #status predicted <tm3> F;800-1240/Product: membrane glycoprotein E1 #status predicted <eg1> F;1212-1236/Domain: transmembrane #status predicted <tm5> F;449,271,625,638,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted</tm5></eg1></tm3></kp6></tm3></tm3></tm2></eg2></eg3></tm1>
3697 and GUU for residue rotein	A?Molecule type: genomic RNA A.Residues: 1-1240 <wea> A.Residues: 1-1240 <wea> A.Cross-references: GB:M69094; NID:g323696; PIDN:AAA42980.1; PID:g323697 A.Cross-references: GB:M69094; NID:g323696; PIDN:AAA42980.1; PID:g323697 A.Note: the authors translated the codon AGC for residue 036 as Arg and GUU for residue C.Superfamily: togavirus structural polyprotein C.Koywords: coat protein; glycoprotein; polyprotein; transmembrane protein C.Koywords: coat protein C #scatus predicted <cpc></cpc></wea></wea>
лв in North America	C;Accession: A3392 R;Weaver, S.C.; Scott, T.W.; Rico-Hesse, R. R;Weaver, S.C.; Scott, T.W.; Rico-Hesse, R. Virology 182, 774-784, 1991 A;Title: Molecular evolution of eastern equine encephalomyelitis virus in North America A;Reference number: A39992; MUID:91220727; PMID:2024496 A;Accession: A39992
nin VA33 (Ten Broeck brane glycoprotein 11-1999	VHWVEV Structural polyprotein - eastern equine encephalomyelitis virus (strain VA33[Ten Broeck structural polyprotein; coat protein C; membrane glycoprotein E1; membrane glycoprotein N;Contains: 6K protein; coat protein C; membrane glycoprotein C;Species: eastern equine encephalomyelltis virus A;Note: host Equus caballus (domestic horse) A;Note: host Equus caballus (domestic horse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999

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submitted to the EMBL Data Library, August 1992
A;Reference number: S37671
A;Accession: S37671
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A;Introns: 38/2; 97/2; 129/3; 154/1; 202/1; 252/3;
C;Superfamily: collagen alpha 1(IV) chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Virol. 127, 305-314, 1992
A;Title: Genetic characterization of an antigenic subtype of eastern equine encephalomye
A;Reference number: A56605; MUID:93090093; PMID:1280945
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A;Molecule type: genomic RNA
A;Residues: 1-1242 <WEBA>
A;Cross-references: EMBL:U01034; NID:g393006; PIDN:AAC53735.1; PID:g393008
C;Superfamily: togavirus structural polyprotein
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                                                                                                                                17.5%; Score 77; DB 30.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%;
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33.3%; Pred. No. 12;
tive 12; Mismatches
                   70
                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78.5; DI
Pred. No. 12;
12; Mismatches
                                                                                                              Mismatches
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12;
                                                                                                                                            DB 2;
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                                                                                                             31;
                                                                                                                                                                                      279/2; 327/1; 357/2; 429/3; 588/1;
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                                                                                                                                              Length 1870
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                                                                                                             Indels
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R;Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T. Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A;Title: A gene pair from the human major histocompatibility complex encodes A;Reference number: A35098; MUID:90192810; PMID:2156268
A;Accession: B35098
                                                                                                                C;Species: Homo sapiens (man)
C;Date: 10-Aug-1990 #sequence
C;Accession: B35098
                                                                                                                                                         B35098
MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues, A;Residues, A;Cross-references: EMBL:Z15025
A;Note: in the authors' translation residues 32-34 are shown after residue
A;Note: in the authors' translated the codon AAT for residue 1000 as His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1872 <IRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S36152
MHC class III histocompatibility antigen HLA-B-associated protein 2 [similarity]
C;Species: Homo sapiens (man)
C;Date: 06-Jun-1995 #sequence_revision 17-Nov-1995 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within A;Reference number: S36152; MUID:83272029; PMID:8499947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot,
Nature Genet. 3, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S36152
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Best Local
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                                                                                                                                                                                                                                                                                              944
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                                                                                                                                                                                                                                                                                                                                                                KEETAQLTGPEAGRKLP--ASRSGAGPPPPRRESRTETRWG-PRPGSSRRGIPPEEPGAP 943
                                                                                                                                                                                                                                                                                                                                                                                         KQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETBEGAPTTSEEKKPIP-----
                                                                                                                                                                                                                                                                                          PRRAGPIKKPPPPTKVEEL
                                                                                                                                                                                                                                                                                                                                ----GMKKFPGPVVNLSEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; 97/2; 129/3; 154/1; 202/1; 252/3; 279/2; 327/1; 357/2; 429/3; 588/1; collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                            #sequence_revision 06-Nov-1992 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 77; 30.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                70
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A53273
MHC class II histocompatibility antigen DR alpha chain -
C;Species: Equus caballus (domestic horse)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_
                                                                                      RESULT 7
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-2142 <BAN>
A;Cross-references: GB:M33509; NID:g179338; PIDN:AAA35585.1; PID:g179339; GB:M31293
A;Note: the authors translated the codon AGT for residue 97 as Gly
C;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                            875
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                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                               KEETAQLTGPEAGRKLP--ASRSGAGPPPPRRESRTETRWG-PRPGSSRRGIPPEEPGAP 931
                                                                                                                                                                                                                            KQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGAPTTSEEKKPIP-----
                                                                                                                                    PRRAGPIKKPPPPTKVEEL
                                                                                                                                                                     ----GMKKFPGPVVNLSEI
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                                                                                                                                                                                                                                                                                         17.5%;
30.4%;
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                                                                                                                                                                                                                                                                      Score 77; DB:
Pred. No. 30;
10; Mismatches
                                                                                                                                                                                                                                                                                                       2;
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12-May-1994 #text_change

21-Jan-2000

horse

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R.Chang, G.J.J.; Trent, D.W.
J. Gen. Virol. 68, 2129-2142,
A;Title: Nucleotide sequence of the genome
A;Reference number: A26816; MUID:87282265;
A;Accession: A26816...
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C;Superfamily: class II histocompatibility antigen; immunoglobulin
F;97-162/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M60100; NID:g164236; PIDN:AAA30956.1; PID:g164237
C;Genetics:
A;Gene: DRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Albright, D.; Bailey, E.; Woodward, J.G.
Immunogenetics 34, 136-138, 1991
A;Title: Nucleotide sequence of a CDNA clone of the horse (Equus caballus) DRA gene.
A;Reference number: A53273; MUID:91331619; PMID:1869308
RESULT 9
S19595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-1239 <CHA>
A; Residues: 1-1239 <CHA>
A; Cross-references: EMBL.X05816; NID: 962074; PIDN: CAA29261.1;
C; Superfamily: togavirus structural polyprotein
C; Keywords: cost protein; glycoprotein; transmembrane protein
C; Keywords: cost protein; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
N;Contains: 6K protein; coat protein C; membrane glycoprotein El; membrane glycop
C;Species: eastern equine encephalomyelitis virus
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A; Residues: 1-226 < AL
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A;Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                                                      Reywords: cost protein; glycoprotein; transmembrane protein; 1-259/Product: cost protein C #status predicted <CPC>
7;1-259/Product: membrane glycoprotein E3 #status predicted <MG3>
7;261-277/Domain: transmembrane #status predicted <TN1>
7;261-277/Domain: transmembrane #status predicted <TN2>
7;323-742/Product: membrane glycoprotein E2 #status predicted <MG2>
7;684-701/Domain: transmembrane #status predicted <TN2>
7;727-737/Domain: transmembrane #status predicted <TN2>
7;727-798/Product: 6K protein #status predicted <TN4>
7;777-798/Domain: transmembrane #status predicted <TN4>
7;777-798/Domain: transmembrane #status predicted <TN5>
7;1211-1235/Domain: transmembrane #status predicted <TN5>
7;1211-1235/Domain: transmembrane #status predicted <TN5>
7;49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted <TN5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                      100 Q 100
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                                                                                                                                                                                                               IEDLRRSIANLTLKORAPNPPAGPPAKRKKPAPSLSLETKKKRPPPPAKKOKRKPKPGKR 99
                                                                                                                                                                                                                                                    ISNVRAIQANINIPMGAFRPGAGQPPRRKESTP----ETEE---GAPTTSEEKKPIPGMK 58
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31.1%;
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                                                                                                                                                                                                                                                                                                                     Score 75.5; DI
Pred. No. 23;
L3; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-994 <STE>
A;Cross-references: GB:K62894; NID:g57744; PIDN:CAA44683.1; PID:g57745
C;Superfamily: CBS homology
C;Keywords: transmembrane protein
F;830-877/Domain: CBS homology <CBS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S19595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: G86168
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C Chin. C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
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A;Accession: S19595
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  R;Hahn, C.S.,
Proc. Natl. Acad.
                                       structural polyprotein - western equine encephalomyelitis virus (strain BFS1703) N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glyco C;Species: western equine encephalomyelitis virus C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: A35587 R;Hahn, C.S.; Lustig, S.; Strauss, E.G.; Strauss, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1-222 <STO>
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Best Local :
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Lustig, S.; Strauss, E
cad. Sci. U.S.A. 85, 59!
ern equine encephalitis
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Pred. No. 23;
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Pred. No.
                        E.G.; Strauss, J.H. 5997-6001, 1988
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                                                                                                                                         membrane glycoprotein
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Maiti, R.; Marziali
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; Dewar, K.;
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virus 18

recombinant virus

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R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V. Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A;Title: Complete nucleotide sequence of the eastern equine A;Reference number: S26369; MUID:91375524; PMID:1896061
                                                                                                                                                                                                                                     genome polyprotein - eastern equine encephalomyelitis virus
N;Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein
C;Species: eastern equine encephalomyelitis virus
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A;Title: Cloning of four cyclins from maize indicates that higher plants have A;Reference number: A57742; MUID:94316698; PMID:8041798
A;Accession: B57742
                                A;Molécule type: mRNA
A;Residues: 1-1241 <V
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R; Volchkov, V.E.; Vo
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A;Residues: 1-1236 <HAH>
A;Residues: 1-1236 <HAH>
A;Cross-ferences: GB:J03854; NID:g323728; PIDN:AAA42999.1; PID:g323730
C;Superfamily: togavirus structural polyprotein
C;Superfamily: togavirus structural polyprotein transmembrane protein
                                                                            A; Accession: S26373
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A; Residues: 1-445 < REN>
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F;719-737/Domain: transmembrane #status predicted <TN2>
F;743-797/Product: 6K protein #status predicted <K6P>
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Cross-references: EMBL:X63135; NID:g59185; PIDN:CAA44845.1; PID:g59186
                                                                                                                                                                                                                    ;Date: 06-Jan-1994 #sequence_revision
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Best Local
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Best Local
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                             1-1241 <VOL>
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Pred. No. 1
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Feb-1997
C;Accession: S04497
                                  A; Title: Homology between surface protein antigen genes A; Reference number: S04497; MUID: 89290018; PMID: 2661267
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FEBS Lett. R;Takahashi,

i, I.; Okahashi, N.; Sasakawa, C.; Yoshikawa, M.; Hamada, S.; 249, 383-388, 1989

of.

Streptococcus sobrinus

and တ္ Koga,

Н

N;Alternate names: surface

surface antigen PAg - Streptococcus sobrinus

antigen SpaA

(fragment)

A; Accession: S04497

compared with conceptual translation

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• B
RESULT 15
S04497
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A;Residues: 1-1787 <WI2>
A;Cross-references: EMBL:Z67884; PIDN:CAA91810.1; GSPDB:GN00028; CESP:T14G8.1
                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1995 A;Reference number: Z19955
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A; Residues: 1-1787 <
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A;Reference number: Z19231
A;Accession: T20160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T14G8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20160; T24924
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F;324-743/Product: envelope protein E2 #status predicted <EP2>
F;744-800/Product: 6K protein #status predicted <6KP>
F;801-1241/Product: envelope protein E1 #status predicted <EP1:
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ALIGNMENTS

RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC STRAIN=C57BL/6; RX MEDLINE=21275706; PubMed=11381084; RA Palmer S., Groves N., Schindeler A., Yeoh T., Biben C.,	 SEQUENCE FROM N.A. MEDLINE=20065879; PubMed=10598820; Patzak D., Zhuchenko O., Lee C.C., Wehnert M.; Patzak D., Zhuchenko and genomic structure of a "Identification, mapping, and genomic structure of a chromosomal human gene (SMPX) encoding a small muscul Hum. Genet. 105:506-512(1999).	RC STRAIN=C57BL/10; TISSUB-SKELEFAL MUSCLE; RX MEDLINE=21295047; PubMed=11401441; RA Kemp T.J., Sadusky T.J., Simon M., Brown R., Eastwood R., RA Sassoon D.A., Coulton G.R.; RT "Identification of a Novel Stretch-Responsive Skeletal M. RT (Smpx)."; RL Genomics 72:260-271(2001).	(Muscle-specific protein CSL). SMPX OR SRMX OR CSL. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae NCBI_TaxID=10090; [1] SEQUENCE_FROM N.A.	RESULT 1 Q9ER98 ID Q9ER98 PRELIMINARY; PRT; 85 AA. AC Q9ER98; DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-DT-C2001 (TrEMBLrel. 19, Last annotation update) DE Stretch responsive muscle (X-chromosome) (SMPX protein)
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EMBL; AF364071; AAK50399.1;
SEQUENCE 85 AA; 9120 MW;
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MEDILINE=20065879; PubMed=10598820;

Patzak D., Zhuchenko O., Lee C.C., Wehnert M.;

"Identification, mapping, and genomic structure of a novel X-
chromosomal human gene (SMPX) encoding a small muscular prote:

hum. Genet. 105:506-512(1999).
                                                        Q90Z58
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Mammalia; Eutheria; Rodentia;
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01-DEC-2001 (TrEMBLrel. 19,
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EMBL; AF364070; AAK50398.1; -.
EMBL; AY056524; AAK07682.1; -.
MGD; MGI:1913356; Smpx.
SEQUENCE 85 AA; 9253 MW; 4:
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Last annotation update)
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0
                                                                                                                                                                                                     Score 410; DB 11;
Pred. No. 2.2e-37;
3; Mismatches 4;
                                                                                                                                                                                                                                                    52654F8C790C932C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 440; DB 11;
Pred. No. 1.2e-40;
; Mismatches 0;
                                                                                                              85
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        sequence update) annotation updat
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                                                                                                                                                                                                      4.
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RESULT 4
Q9MZT1
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ACCOMMENTATION
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Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                 Rhodes T.H., VILE ....
Rhodes T.H., Jr.;
George A.L. Jr.;
"A missense mutation in canine CIC-1 car
T congenita in the dog.";
TERS Lett. 456:54-58(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                  Rogers C.S., George A.L. Jr., Rhodes T.H.;
Submitted (UTL-2000) to the EMBL/GenBank/DDBJ
EMBL; AF162445; AAF82606.1; -.
InterPro; IPR000644; CBS domain.
InterPro; IPR001807; Cl-channel_volt.
InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                PRINTS; PR00762; CLCHANNEL.

PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
                                                                                                                                                 Pfam; PF00571; CBS; 2.

Pfam; PF00654; voltage CLC; 1.

PRINTS; PR00762; CLCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLCN1.
Canis familiaris (Dog).
Canis familiaris (Dog).
Chordata; Craniata; Ver
                                                                                                                                                                                                                                                                                                                    STRAIN-BREED MINIATURE SCHNAUZER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manner.";
J. Cell B
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BREED MINIATURE MEDLINE=99379598; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSI.
Kenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Ratrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MZT1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mohun T.J., Harvey R.P.;
"The Small Muscle-specific Protein Csl Modifies
Promotes Myocyte Fusion in an Insulin-like Growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF343894; AAK71068.1; -
SEQUENCE 91 AA; 10006 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmer S., Groves N., Schindeler /
Sparrow D.B., Barnett L., Jenkins
Mohun T.J., Harvey R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21275706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMKKFPGPVVNLSEIQNVKSELKFVPKGEQ
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                                                                                  976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
scle chloride channel ClC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINIATURE SCHNAUZER;
9598; PubMed=10452529;
Vite C.H., Giger U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                  AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11381084;
N., Schindeler A., Yeoh T., Bir
                                                                                  108053 MW;
                    18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.2%;
72.2%;
                 Score 81.5; D
Pred. No. 2.3;
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Pred. No. 3e-28;
6; Mismatches
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                                                                                  8F85593E7C858F6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patterson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
ia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    recessive myotonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                  databases
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and N.G., F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell
                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahlke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Canis.
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Similarity

Conservative

7;

Mismatches

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Indels

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Gaps

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Q9PZX6
  RRRRRROCCOSSTT
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001836; Alpha_E1_glycop.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR0002548; Alpha_E2_glycop.
InterPro; IPR000253; Alpha_E2_glycop.
InterPro; IPR000253; Alpha_E3_glycop.
InterPro; IPR000930; TogavIrin.
Pfam; PF00944; Alpha_core; 1.
Pfam; PF01984; Alpha_E2_glycop; 1.
Pfam; PF01989; Alpha_E2_glycop; 1.
Pfam; PF01963; Alpha_E2_glycop; 1.
Pfam; PF01963; Alpha_E3_glycop; 1.
PRINTS; PR00798; TOGĀVIĶIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MA38-MASS;
Brault A.C., Powers A.M., Kang W., Tesh R.B.,
"Genetic and Antigenic Diversity among Eastern
viruses fron North, Central and South America.
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
EMBL, AF159550; AAF04792.1; -..."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PZX7
STRAIN-LASO-ARTH167;
Brault A.C., Powers A.M., Kang W.,
"Genetic and Antigenic Diversity an
viruses from North, Central and So
                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virue)
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                                                                                                                                                                                           Q9PZX6
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                                                                      Alphavirus.
NCBI_TaxID=11021;
                                                                                             Viruses; seRNA positive-strand
                                                                                                           Virue)
                                                                                                                                  Structural polyprotein
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                                                SEQUENCE FROM N.A.
                                                                                                                     Eastern equine encephalitis
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                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                    l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyprotein
                                                                                                                                                                                                                                                                                                                                                 1242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  137667 MW;
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                                                                                                                                                                                                                                                                                                            18.1%;
33.3%;
                                                                                                                                                                                                                                                                                                    12;
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Last sequence update)
Last annotation updat
                                                                                                                                             Last
Last
                                                                                                                                                                                                                                                                                                  Score 79.5; DE
Pred. No. 5;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus
                                                                                                                     virus (Eastern equine encephalomyelitis
                                                                                                                                                                     Created)
                                                                                                                                                                                            PRT;
                                                                                               viruses,
  y among
South A
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                                                                                                                                             sequence update) annotation update)
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             Tesh R.B., Shope R. mong Eastern Equine
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   America.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA stage; Togaviridae;
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                                                                                               DNA stage; Togaviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encephalomyelitis
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                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .E., Weaver S. encephalitis
             .E., Weaver S.C.; encephalitis
                                                                                                                                                                                                                                                                                                                            1242;
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                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                    Gaps
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RESULT Q9PZX4 ID Q9 AC Q9

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Q9PZX4 Q9PZX4;

PRELIMINARY;

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Q9PZX5
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Best Local Similarity
Matches 18; Conserv
                                                                                       Matches
                                                                                                         Query Match
Best Local S
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Q9PZX5;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00944; Alpha_core; 1.
Pfam; PF01589; Alpha_E1_glycop;
Pfam; PF00943; Alpha_E2_glycop;
Pfam; PF01563; Alpha_E3_glycop;
PRINTS; PR00798; TOGĀVIRIN.
                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1999) to the EMBL; AF159552; AAF04794.1; HSSP; P03315; IVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brault A.C., Powers A.M., Kang W., Tesh R.B., S
"Genetic and Antigenic Diversity among Bastern
viruses fron North, Central and South America."
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, Structural polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein.
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA
Alphavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eastern equine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001836; Alpha_core.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR0002533; Alpha_E2_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MS83-4789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus).
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Pfam; PF001589; Alpha_E1_glycop;
Pfam; PF00943; Alpha_E2_glycop;
Pfam; PF01563; Alpha_E3_glycop;
PRINTS; PR00798; TOGĀVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro;
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P03315; 1V
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IEDLRRSIANLTLKORAPNPPÄGPPAKKKKPAPKPK---PAQAKKKRPPPPPAKK
                                           ISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGAPTTSEEKKPIPGMKK
                                                                                       18;
                                                                                                         Similarity
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IPR002548; Alpha_E2_glycop.
IPR000936; Alpha_E2_glycop.
IPR002533; Alpha_E3_glycop.
IPR000930; Togavirin.
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                                                                                       Conservative
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33.3%;
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Pred. No. 6.5;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                          MW;
                                                                                     Score 78.5; D
Pred. No. 6.5;
12; Mismatches
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Last annotation updat
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n Equine
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                                                                                                                              Length
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ADD DATE OF THE PROPERTY OF TH
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Q9PZX3
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Best Local (
                               InterPro; IPRO01836; Alpha core.
InterPro; IPRO02548; Alpha E1 glycop.
InterPro; IPR002548; Alpha E2 glycop.
InterPro; IPR000936; Alpha E2 glycop.
InterPro; IPR000936; Togavīrin.
Pfam; PF00544; Alpha E1 glycop; 1.
Pfam; PF00549; Alpha E1 glycop; 1.
Pfam; PF00543; Alpha E2 glycop; 1.
Pfam; PF00543; Alpha E2 glycop; 1.
Pfam; PF00543; Alpha E3 glycop; 1.
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InterPro; IPR002548; Alpha E1 glycop.
InterPro; IPR002548; Alpha E2 glycop.
InterPro; IPR002533; Alpha E2 glycop.
InterPro; IPR00936; TogavIrin.
Pfam; PF00944; Alpha E1 glycop; 1.
Pfam; PF00543; Alpha E1 glycop; 1.
Pfam; PF00543; Alpha E2 glycop; 1.
Pfam; PF01563; Alpha E2 glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=FL93-939;
Brault A.C., Powers A.M., Kang W., Tesh R.B., Shope
"Genetic and Antigenic Diversity among Eastern Equin
viruses from North, Central and South America.";
Submitted (JUN 1999) to the EMBL/GenBank/DDBJ databa
EMBL; AF159554; AAF04796.1; -.
HSSP; P03315; IVCP.
Pfam; PF
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structural polyprotein.
Eastern equine encephalitis
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Brault A.C., Powers A.M., Kang W.
"Genetic and Antigenic Diversity
viruses from North, Central and S
Submitted (JUN-1999) to the EMBL/
EMBL; AF15953; AAF04795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Structural polyprotein.
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SEQUENCE :
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                    PR00798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus
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Last sequence update)
Last annotation updat
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and South America."
EMBL/GenBank/DDBJ di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78.5;
Pred. No. 6.
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annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Eastern equine encephalomyelitis
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                                                                                                                                                                                                                                                                                                             Eastern Equine
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encephalitis
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encephalitis
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RA, Braul

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DR HSSP;

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DR Pfam;

DR Pfam;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
                                                                                                                   Q9PZX1
Q9PZX1;
Q1-MAY-2000 (TrEMBLrel. 1
Q1-MAY-2000 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
Structural polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=TX95-PV5-2547;
Brault A.C., Powers A.M.
"Genetic and Antigenic I
viruses fron North, Cent
Submitted (JUN 1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9PZX2 PRELIMINARY;
O9PZX2;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, I
O1-DEC-2001 (TrEMBLrel. 19, I
Structural polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00944; Alpha core; 1.
Pfam; PF01589; Alpha El glycop;
Pfam; PF01583; Alpha E2-glycop;
Pfam; PF0153; Alpha E3-glycop;
PRINTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VITUSES from North, Central and South America."; Submitted (JUN-1999) to the EMBL; AF15955; AAF04797.1; -. HSSP; P03315; 1VCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S03.001; ...
InterPro; IPR001836; Alpha_E1_glycop.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR000936; Alpha_E3_glycop.
InterPro; IPR0002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
SEQUENCE FROM N.A.
STRAIN=FL96-14834;
                                        Alphavirus.
NCBI_TaxID=11021;
                                                                         Viruses; ssRNA
                                                                                            virus).
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                                                                                                         Eastern
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NCBI_TaxID=11021;
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SEQUENCE 1242 AA;
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18; Conserv
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33.3%;
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Last annotation updat
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L Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF159556; AAF04798.1; -.

R HSSP; P03315; 1VCP.

R InterPro; IPR001836; Alpha_core.

R InterPro; IPR001836; Alpha_E1_glycop.

R InterPro; IPR0002548; Alpha_E2_glycop.

R InterPro; IPR0002548; Alpha_E2_glycop.

R InterPro; IPR000253; Alpha_E2_glycop.

R InterPro; IPR000330; TogavIin.

R Pfam; PF01869; Alpha_E2_glycop; 1.

Pfam; PF0189; Alpha_E2_glycop; 1.

R Pfam; PF0189; Alpha_E3_glycop; 1.
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InterPro; IPR002548; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR002533; Alpha_E1_glycop; 1.
Pfam; PF00944; Alpha_E2_glycop; 1.
Pfam; PF001589; Alpha_E2_glycop; 1.
Pfam; PF00943; Alpha_E2_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
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Brault A.C., Powers A.M., Kang W., Tesh R.B., Shope R.E.
"Genetic and Antigenic Diversity among Eastern Equine en
viruses fron North, Central and South America.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF159557; AAF04799.1; -.
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01-DEC-2001 (TrEMBLrel. 19,
Structural polyprotein.
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                                            ISNVRAIQANINI PMGAFRPGAGOPPRRKESTPETEEGAPTTSEEKKPIPGMKK
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l Similarity 33.3%;
18; Conservative 1
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; Pred. No. 6.5;
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InterPro; IPR002548; Alpha E1_glycop.
InterPro; IPR0002548; Alpha E2_glycop.
InterPro; IPR000936; Alpha E2_glycop.
InterPro; IPR000930; TogavIrin.
Pfam; PF00944; Alpha E0_glycop; 1.
Pfam; PF001589; Alpha E1_glycop; 1.
Pfam; PF00943; Alpha E2_glycop; 1.
Pfam; PF00943; Alpha E2_glycop; 1.
Pfam; PF001563; Alpha E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
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Q9PZW9;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
Structural polyprotein.
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01-NOV-1996
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Structural po
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Q88790;
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                                                       equine encephalomyelitis viruses related RNA viruses "; related RNA viruses "; virology 197:375-390(1993). EMBL; U01034; AAC53735.1; -. HSSP; P03315; 1VCP.
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                                                                                                                                                                                                                                                                    MEDLINE=94025587; PubMed=8105605; Weaver S.C., Hagenbaugh A., Belle Chang G.J., Clarke D.K., Gousset
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=NORTH AMERICAN ANTIGENIC VARIETY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alphavirus.
NCBI_TaxID=11021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eastern equine
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                                                                                                                                                                                                                                           Chang G.J., Clarke Holland J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses,
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                                  nterPro;
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Alpha_core.
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Trent D.W.,
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alphaviruses
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InterPro; IPR002548; Alpha E1 glycop.
InterPro; IPR002548; Alpha E2 glycop.
InterPro; IPR002533; Alpha E2 glycop.
InterPro; IPR002533; Alpha E3 glycop.
InterPro; IPR000930; TogavIrin.
Pfam; PF00944; Alpha E1 glycop; 1.
Pfam; PF001589; Alpha E2 glycop; 1.
Pfam; PF00943; Alpha E2 glycop; 1.
Pfam; PF01563; Alpha E3 glycop; 1.
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Q88792;
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SEQUENCE
J. Virol. 68:158-169(1994).
EMBL; U01552; AAC53755.1; -.
HSSP; P03315; IVCP.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Structural polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94076404; PubMed=8254725;
Weaver S.C., Hagenbaugh A., Bellew L.A., Gousset L., Mallampalli V.,
Holland J.J., Scott T.W.;
"Evolution of alphaviruses in the eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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InterPro; IPR002533; Alpha_B3_glycop.
InterPro; IPR00253; TogavIrin.
Pfam; PF00944; Alpha_Core; 1.
Pfam; PF01569; Alpha_B1_glycop; 1.
Pfam; PF01563; Alpha_B2_glycop; 1.
Pfam; PF01563; Alpha_B3_glycop; 1.
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NCBI_TaxID=11021;
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262 324 E3.
325 744 E2.
745 801 6K.
802 1242 E1.
1242 AA; 137627 MW; BCA1B498B4AABD27 CRC64;
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·2 AA;
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321
744
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33.3%;
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21 E3.
44 E2.
72 6K.
42 E1.
137523 MW; 0B8C5FF55D9940DE CRC64;
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33.3%; Pred. No. 6.5;
tive 12; Mismatches
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12; Mismatches
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Db 41 IEDLRRSIANLTLKQRAPNPPAGPPAKKKKPAPKPK---PAQAKKKRPPPPAKK 91

Search completed: April 9, 2003, 12:38:25 Job time : 46.5282 secs

Title: Perfect score:

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US-09-647-019-2

Run on:

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Scoring table: Sequence:

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Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

248812 seqs, 61136040 residues

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275.668 Million cell updates/sec
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2 US-10-124-557-62
US-08-781-986A-5237
US-09-764-868-705
2 US-10-081-281-115
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US-10-124-557-104

US-10-124-557-42

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US-10-124-557-60

US-10-124-557-52
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  Sequence 14, Appl
Sequence 84, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 46, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 48, Appl
Sequence 40, Appl
Sequence 62, Appl
Sequence 50, Appl
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US-10-124-557-14
; Sequence 14, Application US/10124557
; Patent No. US20020137894A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION NUMBER: US/07/643,502
FILING DATE: 16-Apr-1091
APPLICATION NUMBER: US 07/643,502
FILING DATE: 19-JUN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-JUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-JUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: OB-JUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: OB-JUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSEAT, LUANN
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Turner, Katherine Clark, Stephen C.
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A.
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STREET: 87 CambridgePark Drive
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10 US-09-935-658-42
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Sequence 5, Appli
Sequence 5, Appli
Sequence 52, Appli
Sequence 12, Appli
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Sequence 1411, Ap
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Sequence 6084, Appli
Sequence 6084, Appli
Sequence 8, Appli
Sequence 42, Appli
Sequence 2, Appli
Sequence 117, App
Sequence 117, Appli
Sequence 91, Appli
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Sequence 93, Appli
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Sequence 50, Appli
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Regult No.

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Query

Length

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SUMMARIES

US-10-124-557-14 US-10-124-557-84 US-10-124-557-74 US-10-124-557-58

1029 1028 1029 11049 11270 1311 1313 1320 1320 1354 1361 1363

score greater than or equal

Pred. No.

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; SEQUENCE DESCRIPTION: US-10-124-557-84
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US-10-124-557-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                        INFORMATION FOR SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TBLEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 941 amino acids
TYPE: amino acid
                                                                                                                                                             ELEFAX:
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Hewick, Rodney M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turner, Katherine Clark, Stephen C.
                                                                                                                                                        E: (617)876-1170
(617)876-5851
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                SEQ ID NO:
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TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-124-557-74
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US-10-124-557-74
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                                                                                                      Query Match
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Patent No. US200201378
GENERAL INFORMATION:
                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino a
322 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 366
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECONMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 382
                               25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                       19;
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                              TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10124557
                                                                     Conservative
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                                                                                   17.3%;
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                                                               Score 76; DB 12; Length 1038; Pred. No. 11; Indels 2; Mismatches 18; Indels
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RESULT 4 US-10-124-557-58

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US-10-124-557-104

/ Sequence 104, Application US/10124557

/ Patent No. US20020137894A1

/ GENERAL INFORMATION:
/ APPLICANT: Turner, Katherine
/ Clark, Stephen C.
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HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
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Best Local Similarity
Matches 19; Conserv
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APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989
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APPLICATION NUMBER: US/10/124,557
APPLICATION APPLICATION
PILING DATE: 16-APPLICATION
PI
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LENGTH: 1049 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
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Clark, Stephen C.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
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STREET: 87 CambridgePark Drive
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                                                                                                                    Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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Hewick, Rodney M.
Gesner, Thomas G.
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US-10-124-557-44
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: Massachusetts CITY: Cambridge COUNTRY: U.S.A.

STREET: 87 CambridgePark Drive

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: Genetics Institute, Inc.

APPLICANT:

Turner, Katherine

Jacobs, Kenneth Hewick, Rodney M. Gesner, Thomas G. Clark, Stephen C. Application US/10124557

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MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-124-557-104
                                                                                        Matches
                                                                                                          Query Match
Best Local S
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TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
456 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APTTORNEY/AGENT INFORMATION:
                                         25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                        19;
                                                                                                        h 17.3%;
Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cserr, Luann
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
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STATE: Massachusetts
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                          LENGTH: 1140 amino acids
                                                                                        Conservative
                                                                                     2
                                                                                 Score 76; DB 12; Length 1140;
Pred. No. 12;
2; Mismatches 18; Indels
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RESULT 7
US-10-124-557-42
; Sequence 42, Application US/10124557
; Patent No. US20020137894A1
; GENERAL INFORMATION:
: APPLICANT: Turner, Katherine
: APPLICANT: Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
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Best Local Similarity
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APPLICATION NUMBER: US 07/643,502
FILLING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILLING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILLING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                           FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
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LENGTH: 1270 amino acids
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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STATE: Massachusetts
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FILING DATE: 16-Apr-2002
                                                                                  APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
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Hewick, Rodney M.
Gesner, Thomas G.
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42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luann
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US-10-124-557-142
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Matches
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Patent No. US20020137894A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 42:
                 INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AND THE CREET, LUAND NAME: CREET, LUAND REGISTRATION NUMBER: 31,822 REGISTRATION NUMBER: GI 5190 TELECOMMUNICATION INFORMATION: (617)876-1170
                               CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                 TELEFAX: (617)876-5851
N FOR SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1311 amino acids
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TOPOLOGY: linear

H MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-50
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US-10-124-557-50
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              Query Match
Best Local Similarity 42.3
Matches 19; Conservative
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Best Local Similarity
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                                                                                                                                                                                                           TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US(10/124,557
PILING DATE: 16-Apr-2002
CLASSIFICATION INUMBER: US 07/643,502
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/357,196
FILING DATE: 29-DEC-1999
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-ANG-1999
APPLICATON NUMBER: US 07/390,901
PILING DATE: 08-ANG-1999
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                          NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1313 amino acids TYPE: amino acid
                                                                                                                                                                                       LENGTH: 1314 amino acids
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                                17.3%;
42.2%;
2; Mismatches
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                                  Score 76; DB
Pred. No. 15;
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                                                    12; Length 1314;
                Indels
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            Gaps
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RESULT 11
US-10-124-557-60
; Sequence 60, Application US/10124557
; *Patent No. US20020137894A1
; GENERAL INFORMATION:
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HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-124-557-46
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US-10-124-557-46
); Sequence 46, Application U;
); Patent No. US20020137894A1
); GENERAL INFORMATION:
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Matches
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SEQUENCE CHARACTERISTICS:
                                                                                                                                        372 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Appr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                25 PGAGOPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                           Local Similarity
les 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CBerr, Luann
NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                               OMMUNAL
TELEPHONE: (617)876-5851
TELEPHONE: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1320 amino acids
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                                                                                                                                                                                                                      17.3%; Score 76; DB 42.2%; Pred. No. 15; cive 2; Mismatches
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                                                                                                                                                                                                                        Indels
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APPLICANT: Turner, Katherine

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RESULT 12
US-10-124-557-48
; Sequence 48, Application US/10124557
; Patent No. US20020137894A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.3%;
Best Local Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              372 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                    25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                      APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                    TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
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                                    STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Cambridge
: Massachusetts
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                                                                                                                                          Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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87 CambridgePark Drive
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                                                           Genetics Institute, Inc.
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RESULT 13
US-10-124-557-40
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-124-557-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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RESULT 14
US-10-124-557-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/10124557
Patent No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 457
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mes 19; Conservative
                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/6,43,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: Unknown>
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein. SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                            APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                        APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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Hewick, Rodney M.
Gesner, Thomas G.
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// MOLECULE TYPE: protein
// SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-124-557-52

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                             INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                              NAME: CGERT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE,DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION IMPORMATION:
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LENGTH: 1404 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CUNknown>
                                                                                            TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
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TOPOLOGY: linear
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Clark, Stephen C.
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Query Match

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Minimum I
Maximum I
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seq length: 2000000000
A_Geneseq_101002:*

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6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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AMOUTOSO	AAW19395	AAU04136	AA002197	ABB69750	ABB68168	ABG03920	ABB71759	AAU99253	AAE01154	ABB61187	ABG20365	ABB63753	AAB29778	AA006906 .	AAY36096	AAY53666	AAU56185	AA012898	ABG00985	ABB70137	AAU17140	AAU87594	AAU87304	AAW89789	AAU75492	AAW97714	ABB65388	AAU32495	AAB40574	ABG27048	AAG49497	AA004777	4	ABB58529
Human porypeptice		Tomato REV protein	Human polypeptide		Drosophila melanog	Novel human diagno	Drosophila melanog	Human lipase, horm	Testicular isoform	Drosophila melanog	Novel human diagno	Drosophila melanog	Human MSF-derived	Human polypeptide	Extended human sec	Sequence gi/101742			Novel human diagno	ophila me		central	Novel central nerv	Staphylococcus aur	S. aureus antigeni	Staphylococcus aur	Drosophila melanog	Novel human secret	Human ORFX ORF338	Novel human diagno	Arabidopsis thalia	Human polypeptide	Herbicidally activ	Drosophila melanog

ALIGNMENTS

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17-JAN-2000
                                                      Murine chisel (Csl) protein.
                                                                    AAY28650 standard; Protein; 85
                                                          (first entry)
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Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Decker's myotonic dystrophy; beart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain.

Mus sp.

WO9950410-A1

07-OCT-1999.

26-MAR-1999; 99WO-AU00220

27-MAR-1998; 98AU-0002634.

(CHAN-) CHANG CARDIAC RES INST VICTOR. (GEHO) GEN HOSPITAL CORP. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

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The present sequence is the murine chisel protein (Cs1), that is a CC member of the EF-Hand protein super family and is involved in signalling pathways. Csl protein is localised to the nucleus and does not show C significant homology to any known protein. Structural homology between CC csl and scallop regulatory myosin light chain is however detected. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle of disferentiation or adaptive processes that maintain muscle components. This sequence can be used in the detection, diagnosis, CC prophylactic and therapeutic treatment of diseases such as those CC involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, compositive such as Duchenne muscular dystrophy, and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, cmyofiber atrophy, etc. The Csl gene sequence can also be used in gene therapy, for the production of transgenic animals and for drug screening.
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Best Local
                                                                                                                                                                                                                              skeletal myopathy; Becker's myotonic dystrophy; heart failure; transgenic animal; drug screening; gene therapy; homology; scallop regulatory myosin light chain.
                                                                                                                                                                                                                                                                                  Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; regulation; Xq21.3-q22; adaptive process; muscle homeostasis; cardiac hypertrophy; detection; diagnosis; prophylaxis; treatment; differentiation; nucleus; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy;
                                      27-MAR-1998;
                                                                            26-MAR-1999;
                                                                                                                                                           WO9950410-A1
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Human chisel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28651 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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(CHAN-) CHANG CARDIAC RES INST VICTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                           (Csl) protein.
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Pred. No. 3.4e-40;
Mismatches 0;
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                                                                                                                                                             Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; yene therapy; syncope; transgenic animal; expressed sequence tag; EST; 66214 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the human chisel protein (Cs1), that is a member of the EF-Hand protein super family and is involved in signalling pathways. Csl protein is localised to the nucleus and has 86% homology to the mouse Csl. Structural homology between Csl and scallop regulatory myosin light chain is also detected. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, keletal myopathies such as Duchenne muscular dystrophy and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, myofiber atrophy, etc. The Csl gene sequence can also be used in gene therapy, for the production of
                                                                                                                                                                                                                                                                                                     Human 66214
                                                                                                                                                                                                                                                                                                                                    09-APR-2002
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                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    AAE16632 standard; Protein;
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(HALL-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPGPAVNLSEIQNIKSELKYVPKAEQ
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HALL INST MEDICAL RES WALTER &
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30-MAY-2000; 2000US-207400P 30-MAY-2001; 2001WO-EP06165.

WO200192567-A2

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RESULT 4
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Best Local
                                                                                                                                                                                                     Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; xenopus; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; buchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat disease of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary heart disease, valvular heart disease, congenital heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicament for the treatments of the stream of the process of the invention are useful for the development for medicaments for the treatments of the stream of the stre
26-MAR-1999;
                                                    07-OCT-1999.
                                                                                                                                                         Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus chisel (Csl) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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  99WO-AU00220
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Pred. No. 6e-34;
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RESULT 5
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Best Local (
18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                     Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                                                                                                                                                                                                                        Novel human secreted
                                                                                                                                                                                                                                                                                                                                        AAU33195 standard; Protein; 2153 AA.
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                                                16-APR-2001; 2001WO-US08656
                                                                                                                WO200179449-A2
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treating cardiomyopathy, cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harvey
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                        18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHAN-) CHANG CARDIAC RES INST VICTOR.
(CEHO) GEN HOSPITAL CORP.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGAPT----TSEEKKPIP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSKQPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESBEKSEBKKPIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                        GAVKLPGPAFNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMKKFPGPVVNLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 262.5; DB
Pred. No. 4.9e-21
5; Mismatches 1
                                                                                                                                                                                                                                          #3686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chisel, used to develop products for chypertrophy, heart failure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosenthal NA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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RESULT 6
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                                       THE PRINCIPLE OF A CONTROL OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptide and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                          25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics;
biodiversity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM24322 standard; Protein; 1299
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded protein SEQ ID NO: 1847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2153 AA;
                                                               ; 2000US-0491404.
; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic test;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sic test; gene mapping; therapy; nutrition.
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<u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RRESULT 7
AAR26049
ID AAR26049
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, set, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
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N-PSDB; AAH98981.
                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                            Megakaryocyte colony stimulating stability; proteolytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for antibodies and research
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                                                                                                                                                                                                                                                                                                      Synthetic
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            Region
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Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                         /label= Exon_III
                                                                                                                                                                                                                                                                                 Location/Qualifiers
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vA, Zhang
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                                                                                                                                         'label≈
                                                                                                                                                                                                                                                         label= Exon_I
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                                                            . 1331
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                                                                                                                                                           Exon_V
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                                                                                                                                       Exon_VI
Exon_XII
                                           Exon_X
                                                                  Exon_IX
                                                                                          Exon_VIII
                                                                                                                Exon_VII
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JJ, W
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Pred. No. 20;
2; Mismatches
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Werhman
                                                                                                                                                                                                                                                                                                                             factor; secretion signal; meg-CSF;
adhesion; alternative splicing.
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nan T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                 27-APR-2001
                                                                                                                                                                                                       AAB60568 standard, Protein; 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human mega-karyocyte stimulating factors - immune deficiencies, cancer, exposure to radiat bacterial and viral infections, etc.
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10-SEP-1991;
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                                                                                                                                                                                                                                                                                                     456 PKEPTPTTPKEPAPTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 500
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                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                  PGAGQPERRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
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                                                                                   megakaryocyte stimulating
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1404 AA
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                            (first
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91US-0757022.
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                                                                                                                                                                                                                                                                                                                                                                                                         17.3%;
                                                                                                                            entry
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                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB
Pred. No. 22;
                                                                                   factor (MSF,
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            BG
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                                                                                                                                                                                                                                                                                                                                                                                                                        13; Length 1404;
                                                                                     CACP).
                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating :ion or drugs,
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                   CC The invention relates to a method of treating osteoarthritis via the Cadministration of a composition comprising the camptodactyly-arthropathy-CC coxa vara-pericarditis (CACP) protein, or portions of the CACP protein. The composition may further comprise a local anaesthetic. The composition of the invention may be administered via intra-articular or intravenous conjection. The human CACP protein is identified in the invention as conjection. The human CACP protein is identified in the invention as conjection. The human CACP protein is identified in the invention as conjection. The gene encoding conjection (MSF) is located on chromosome 1q25-31, and mutations in this gene are responsible for the heritable disorder camptodactyly-cathy-coxa vara-pericarditis, in which patients have symovial conjections of inflammation. CACP protein (MSF) contain (MSF) contain a symovium lubricant, and can be used to lubricate tissue and conjoints in the treatment of osteoarthritis. The composition may be caplied to reduce the symptoms of osteoarthritis (e.g., joint pain, conjoint damage). The present sequence conjoint damage). The present sequence is not given in its entirety in figure 4 of the composition, although a GenBank accession number was given. This sequence obtained from GenBank (U70316).
                                                                       Matches
                                                                                                          Query Match
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising the camptodactyly-arthropathy-coxavara-pericarditis protein in combination with an anesthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1999; 99US-0145328
19-JUL-2000; 2000US-0145328
   456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page -; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-182721/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Warman ML
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                                 25 PGAGOPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP
                                                                                        Local
PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP
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                                                                     l Similarity
19; Conserv
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                                                                   Conservative
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                                                                                    17.3%;
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                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as lubricants of tissue and joints
                                                                                    Score 76;
Pred. No.
                                                                  Mismatches
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                                                                                                     22;
                                                                   18;
                                                                                                     Length 1404;
                                                                   Indels
                                 63
                                                                  6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
                                                                  Gaps
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AAB29773
                                 AAB29773 standard; Protein; 1404
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Human megakaryocyte stimulating
                                              AAB29773;
                         28-FEB-2001
                        (first entry)
factor
  (MSF),
 SEQ
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Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic. gene therapy; ij NO:1

Homo sapiens

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                                                                                                                                                                                                                                                                                          AAU32262
                                                                                                                                                                                                                                                                                                                RESULT 10
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Crepeats of a motif having at least 50% identity to the sequence KEPAPTT
C(AAB29774). The invention also relates to a nucleic acid encoding a
thuman MST-derived tribonectin; a biocompatible composition comprising a
Chuman MST-derived tribonectin; a biocompatible composition comprising a
CC human MST-derived tribonectin; a biocompatible composition comprising a
CC human tribonectin for inhibiting tissue adhesion formation; and a method
CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by
CC measuring the amount of MSF or its fragment in a biological sample of a
CC indicates the presence of or predisposition to developing
CC indicates the presence of or predisposition to developing
CC creatment of osteoarthritis, where they may be used for lubricating
CC mammalian joints, such as articulating joints of humans, dogs or horses.
CC The tribonectin, when formulated as a membrane, foam, gel or fibre, is
CC useful for inhibiting adhesion between two surfaces such as the injured
CC tissues of a mammal, where the injury is caused by a surgical insertion
CC or trauma, or an artificial device e.g., an orthopaedic implant. In
CC particular, one of the surfaces is pericardial tissue. DNA encoding a
CC tribonectin may be used in gene therapy. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety
                                                                                   Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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               WO200179449-A2
                                                  Homo sapiens.
                                                                                                                                                            Novel human secreted protein #2753.
                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                           AAU32262 standard;
                                                                                                                                                                                                                                                                                                                                                                    456 PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP 500
                                                                                                                                                                                                                                                                                                                                                                                         25 PGAGQPPRRKESTPETEEGAPTTSEE-----KKPIPGMKKFPGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 7; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3%;
                                                                                                                                                                                                                                                                         1415
                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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Pred. No. 22;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc polypeptides and antibodies to the polypeptides are useful for condensity of the presence of or predisposition to a disease associated condensity of the presence of or predisposition to a disease associated condensity of the presence of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells carpressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptides and cells genetically the mucleic acids encoding the polypeptides and cells genetically considered to express them are also useful for producing the proteins. They may be used to therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in the construction of the construction and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid or sequences of novel human secreted proteins of the invention.
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2001
                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                     ABB58529 standard; Protein; 771 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel
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                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                            27-SEP-2001.
                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 2379.
                                                                                                                                                                                                                                                                                                                                          ABB58529;
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                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human secreted polypeptides.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invent of discloses genomic DNA sequences (ABLJ6176-ABLJ0511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid ramino acid sequences from pwith nucleic acid or amino acid sequences from non-plant organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention capable of det
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                                                                                                                                                                                                                                                                                                                        Herbicidal;
                                                                                                                                                                                                                                                                                                                                              Herbicidally active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic
                                                         Claim
                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                       WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                             WO200210210-A2
                                                                                                                                                                                    (FARB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ention relates to an isolated nucleic acid detection of detecting 1000 or more genes from Drosophila. The
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                                                                                                                                                                                    BAYER
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                                                                                                                                                                                                                                                                                                 thaliana
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                                                                                                                                                            Weidler
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                                                                                                                                                                                                                                                                                                                        agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                            polypeptide
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                                                      261pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                   411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.5;
Pred. No. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers
                                                                                                                                                                                                                                                                                                                         herbicide
                                                                                                                                                                                                                                                                                                                                               di bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                      Sequence Listing;
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                                                       English
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The invention i
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 Query Match
Best Local S
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                                              cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines competite therapy. The polypeptides have various cytokine-like activities e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity instructions and/or activity in the diagnosis and/or
                                                                                                                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suitable search parameters, where plant sequences having an greater by a factor of 3 than the Evalue of most similar no sequences are selected. The polypeptides or nucleic acids er are "useful for identifying modulators. The identified modulators are the sequence are modulators.
                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; peptide therapy; stem cell growth factor; tissue growth factor; immunomodulatory; cancer; le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                              Claim
                                                                                                                                                                                                      disorders
                                                                                                                                                                                                               diagnosing
                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA004777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO04777 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous
                       inflammation.
                                     treatment of cancer, leukaemia, nervous
                                                                                                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
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                                                                                                                                                                                                                                                                                            ΥT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGENAEPVFPNIPGLKKFTGPVVHTS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKOLFISYVESYAARFNI-----KPVFNOTVEKAEFDDASGLWNVKTQDGVYTSTWLVVA 140
                                                                                                                                                                                                                                                        2001-514838/56
)B; AAI84708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine;
                                                                                                                                                                                                                                                                                                                    HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system
                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herbicides.
                                                                                                                                                                                                                                                                                           Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                             ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                                                                                                                                                             Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
              data
                                                                                                                                                                           18669; 1399pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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              for this
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Pred. No.
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           patent did not
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                                      system
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                                                                                                                                                                             Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                      disorders,
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              form
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directly
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             of the printed
                                      arthritis
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                                                                                     activities,
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      25-FEB 1999
05-MAR 1999
05-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
26-APR 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 62625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIGKPTRMGKGEKPPPPRGKK---KKKGGPPTLGKNKNPVPGWPGAFLPPLEEKKKPFPG 83
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      99US-0123548
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99US-01206714
99US-0130449
99US-0130891
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34.4%; Pred. No. 1.8;
tive 7; Mismatches
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07-JUN-1999;
 99US-0137782
99US-0137782
99US-0137528
99US-0137528
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99US-0139452
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PR 05-AUG-1999 99US-0147920.
PR 105-AUG-1999 99US-014726.
PR 105-AUG-1999 99US-014726.
PR 105-AUG-1999 99US-014726.
PR 105-AUG-1999 99US-014736.
PR 11-AUG-1999 99US-014739.
PR 11-AUG-1999 99US-014819.
PR 21-AUG-1999 99US-015819.
PR 21-AUG-1999 99US-01581
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) may be therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC Mote: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at figure in the printed produce other traits patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at figure in the printed produce and produce the sequence of the lovention of the printed CC specification, but was obtained in electronic format directly from WIPO CC at figure in the printed produce and produce the sequence of the lovention of the printed content of the printed produce of the printed printed printed printed produce the printed pri
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Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS91235.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #27039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001
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21; Conservative
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AUTHORS
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ORGANISM
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7cl: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue.Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                          (denome Res: 46(4)); 794; 806; (1996): 3 4
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1 (bases 1 to 719)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
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BG224246 1M0030E01
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BP126275 601650456
BF073866 220906 MA
BG224245 1M0004805
BF7961282 1M0004805
BF7961282 1M0004805
BF796136 600250354
F36800 HSPD34697 H
A1355905 3055-10R-
AA38947 M104 Peta
BG224307 1M0033A12
A1355904 BH11-F1-C
BG358790 BOVMS1-01
F26916 HSPD14595 H
AA214155 2875810.r
W07478 2896610.r
BG222652 1M00010F0
BG222652 1M00010F0
BG223652 1M00010F0
BG225652 1M00010F0
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A1035961 ub50b12.r
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AA211521 zn55b01.r

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AI190689 qd50d01.x
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BF672126 602152580
BF575112 602134792
AA211443 zn55b01.9
BM717052 UI-B-EJO-
BM674432 UI-B-EJO-
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Clone Distribution: Researchers may obtain clones from Research

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                                                                                                                              TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="HORB" (Life Technologies) (TI phage resistant)"
//lab_host="NOrgan: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-NXO is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 trail. The
sequence tag for this library is AGANTCAAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="fetal eyes"
/dev_stage="fetal"
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/clone_lib="UI-E-DXO"
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/db_xref="taxon:9606"
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99.2%;
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                            CGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGT 319
CGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGT 565
                                                                                                                                                                                                       681;
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1 (bases 1 to 683)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE856875 683 bp mRNA linear EST 29-SEP 7f70c03.xl Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:3300004 3' similar to TR:Q9UHP9 Q9UHP9 SMALL MUSCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE856875.1 GI:10370341
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                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSP pool 1: 309384-310919, 323208-325895 Soares NBHSP pool 1: 309384-310919, 323208-325895 Soares NBHP pool 1: 150407, 151176-152327 Soares NBHF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 733720-726407, 739080-74099 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
db_xref="taxon:9606"
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99.7%;
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Pred. No. 6.7e-141;
0; Mismatches 1;
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   seq length: 0
seq length: 2000000000
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1: /cgm2_6/ptodata/1

2: /cgm2_6/ptodata/1

3: /cgm2_6/ptodata/1

4: /cgm2_6/ptodata/1

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Maximum Match 100%
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Sequence 111, App
Sequence 14, Appl
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Sequence 11, Appl
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ALIGNMENTS	PCT-US96-00419-1	US-09-133-962A-15 US-08-368-776A-1	US-09-134-001C-795	5256558-7	US-08-687-080-105	US-09-098-219B-6	US-09-098-219B-5	US-09-182-117-4	US-09-182-117-5	US-09-182-117-1	PCT-US96-04294-3	PCT-US96-04294-1	US-08-930-188-3	US-08-930-188-1	US-09-154-344-1	US-08-557-146-1	US-09-502-600-30
	۲.	Sequence 1, Appli	795,	Patent No. 5256558	Sequence 105, A	Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 3, Appl:	Sequence 1, Appl	Sequence 3, Appli	Sequence 1, Appl:	Sequence 1, App	Sequence 1, Appli	Sequence 30, App
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Sequence 111, Application US/0948
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Mayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODE
FILE REFERENCE: PB-0014 US ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
US-09-484-970B-111 CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 111
LENGTH: 909
TYPE: DNA US/09484970B REMODELING No. 6426186 021656.2CB1 GENES

121. GCATCT-GGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAG 179 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA ACTGCATG-AATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATC GATCGCAGCTCAGAGGACACC-GGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA 95 ACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCA ACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGAAGCCAATTCCA 358 AATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAAGAATGT **ACTIGCATIGAAAAATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATC** GCATCTGGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAG GATCGCAGCTCAGAGGACACCGGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT AATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGT Score 836.4; I Pred. No. 3.4e 0; Mismatches <u>;</u> Indels ښ --Gaps 155 395 335 298 275 238 215 120 2

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Patent No. 5670367
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENTY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                    ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
                                                                                                                                                                                                                                                                                                                                        STREET: 1000
CTTY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCAC 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCCAAGCTACTTCCT 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATATATTTGTATGATG
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                                                                                                                                                                                                                                                                                                                                                                          1800 Diagonal Road,
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      30472/114 IMMU
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RESULT 3
US-08-961-527-111/c
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 111, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICATION NUMBER: UPFILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCIL Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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6.8%; Score 60; DB 1; Length 7218;
Local Similarity 2.4%; Pred. No. 2.6e-07;
nes 9; Conservative 222; Mismatches 137; Indels
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTCACT 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maryland
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                                                                                                                                                                                                                                                                                                                                           Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunsch
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FILING DATE: ATTORNEY/AGENT INFORMATION:

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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1047
LENGTH: 1755
TYPE: DNA
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US-09-134-001C-1047
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PACENT NO. 6380370 S
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
ELIC DEFENDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 111
SEQUENCE CHARACTERISTICS:
LENGTH: 14672 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                           Query Match 4.4%;
Best Local Similarity 46.1%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                        1373 AAACAGTTGTATGTTTTGTAGGAGATGGCGGTTTTCAAATGACGAACCAAGAAATGGCTT 1432
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                                                                                                                                                      1433 TACTTCCAGAATATGGACTTAACGTCAAAATÁGTACTTATTAATAACGGAACTTTAGGTA 1492
703 AGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTT
                                                                                                                                                                                                                                                                          523 ATATATTTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 AAATAACATTCTAGACGAATACGAATCGTCCTTGAAATTCGTGTCAATTATGTATCTATT 443
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
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                                                                                                           TGGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTT 826
                                                                   TGGTAAAACAATGGCAAGATAAATTCTTTÄÄTAAACGATTTTCTCATTCTGTATTTAACG 1552
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51.4%;
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                                                                                                                                                                                                                                                                                                                         Score 38.8; DB 4;
Pred. No. 0.15;
0; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                      Length 1755;
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Sequence 20, Application US/0 Patent No. 5872237 GENERAL INFORMATION: APPLICANT: Feder, John N.

Application US/08724394A

APPLICANT:

Kronmal,

Gregory S.

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RESULT 6
US-08-724-394A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Applicat Patent No. 6420135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles F
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         8192 AGACTTCTGCGGTTTTAGCTTGCAAGTCCAGTAATTTCTCCACAGCTTGGGACGTATTTT 8251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1613 CTCCAGATAAATTAGAATCTTCAATTGATGAAGCATTTGCAT 1654
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                                                                           8312 TT 8313
                                                                                                                                                    8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        682 CT 683
                                                                                                                                                                                     622 TTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAACAC 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: HP Vectra
OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                    TTCTCATTTTTTCCTCAAAAACTGCTCCCAAAAGAACGAAAAAGAGGATAAATCCAGCAC 8311
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                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                    4.2%;
56.6%;
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Pred. No. 1.3;
0; Mismatches
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Sequence 21, Application US/08724394A PARLENT NO. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       52945 AGGAGGTTTGAGTAAATAAGGTTAAAAGTGATGGTGTTCTAGACTATTTGTGTCTTTATA 53004
                                                                                                                                                                                                                                                                                                                                                                        53065
                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION USON DATA: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Megabase Transcript Map: No. 58
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APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                          494
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                                                                                                                                                                                                                                                                                                                                                                                                          434 CCCAAAGCTGAACAGTAGTAGGAAGAAAAAAAAGGGATTGATGTGAAGAAATAAAGAGGCAGA 493
                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..24624
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                     GTCTGTTTTTTTAATTCAATCT 53086
                                                                                                                                                                                                     GGCTGTATTTCTTACTTTATCT 635
                                                                                                                                                                                                                                                                                                                                     AGATGGATTCAATAGCTCACTAAAATTTTATATATTTGTATGATGATTGTGAACCTCCTG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
99; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2%;
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Patent No.

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

Feder, John N.
Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.

Sequence 22, Application US/08724394A

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US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                                                     Query Match 4.2%;
Best Local Similarity 49.0%;
Matches 99; Conservative
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                                                                                                                                                                                                                                                                     52945
                                                                                                                                     53005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and
STREET: Two Embarcadero
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Thomas, Winston
APPLICANT: Tsuchhlashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                          614 GGCTGTATTTCTTACTTTATCT 635
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                   494 AGATGGATTCAATAGCTCACTAAAATTTTATATATTTGTATGATGATTGTGAACCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1...246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                 GTCTGTTTTTTAATTCAATCT 53086
                                                                                                                                    AGGAGGTTTGAGTAAATAAGGTTAAAAGTGATGGTGTTCTAGACTATTTGTGTCTTTATA 53004
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                                                                                                                                                                                                                                                                                                                                                      Score 37.2;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                       Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                        Length 246240;
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                                                                                                                                                              RESULT 9
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                                                                                      Sequence 1, Application US/08971395
Patent No. 6359197
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palasson.
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                                                                                                                                                                                                                                                                                                                                                        52945
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Amasino,
APPLICANT: No. 6359
APPLICANT: Gan, Sush
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                53065 GTCTGTTTTTTTAATTCAATCT 53086
                                                                                                                                                                                                                                                                                    53005 TTAAAGTGAATTTTTTGTAGGCAGCATGTTGTGGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Megabase Transcript Map: No. 58' TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                               GGCTGTATTTCTTACTTTATCT 635
                                                                                                                                                                                                                                                                                                                     AGGAGGTTTGAGTAAATAAGGTTAAAAGTGATGGTGTTCTAGACTATTTGTGTCTTTATA 53004
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Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                   Amasino, Richard M
No. 6359197, Yoo-Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                      Susheng
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 Transgenic Plants with Altered Senescence Characteristics
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ER: 017957-000100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.2; DE Pred. No. 3.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-971-395-1
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                                                                                                                                                                                                                                                                                                          RESULT 10
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Best Local S
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                                                                                                                                                                                                                                                         Sequence 1, Application US/08413135 Patent No. 5689042
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Amasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 60 INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 608-251-9166
WFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                            317 TCCAAGTTTTATATACGAAACTTGTTTTTTTAATGAAAACAGTTGAATAGTTGATTATGA 376
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                                                                                                                                                                                                                                                                                                                                                                                         748 TTTTGATGAAAAGTTTCCCAAGCTA 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polania
                                   COUNTRY: US
ZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 53701-2113
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ilarity 48.3%;
Conservative
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                                                                                                                                                                     Transgenic Plants with Altered Senescence Characteristics
                                                                                                                                                                                                                        Richard M
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Best Local Similarity 48.3%;
Matches 99; Conservative
                                                         APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REPERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-10
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
SOPTWARE: FastSEQ for Windows Version 3.0 Mg ID NO 766 LENGTH: 569
                                                                                                                                                                                                                                                                                                                              APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H. APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                               APPLICANT: Derti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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DESCRIPTION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,135
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6262333
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DEDNESS: double
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SYSTEM: PC-DOS/MS-DOS
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/desc = "SAG12-1 Promoter DNA"
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Pred. No. 1.8;
0; Mismatches 106;
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; MOLECULE TYPE:
US-08-630-822A-82
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; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(569)
; OTHER INFORMATION: n = A,T,C or
US-09-328-111-766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-630-822A-82
Query Match
Best Local Similarity
Matches 86; Conserv
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Best Local Similarity 52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,822A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 TGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCCAAAGC 441
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                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 11-APPLICATION: 43:
                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1700
CITY: Denver
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                                                                                                                                                                    LENGTH:
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                                                                                                                                                                  1383 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                Linear
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                                                                                                                                                                                                                                                                                                                                                                   11-APR-1996
                                                                                                                                                                                                                        863-0223
                  3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND APPARATUS
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                                                                                                                                                                                                                                                                                              32,020
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   Score 35; DB 2; Length 1383.
Pred. No. 1.6;
O; Mismatches 85; Indels
                                                                                                                                                                                                                                                                               2618-17-C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Indels
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387 TCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAAC 446

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Conservative

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TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-069-82
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                                                                                                                                                                                                                                                          Query Match 3.9%;
Best Local Similarity 50.3%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6:
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                447
                                                                                                                                                                      690 TCTAGATACGAAAACGAAAGAAAATTATAAAATCTCCTGGTCGTGTGCAGGATATCACGAA 749
                                                                                                                                                                                                           387 ТСААТСТАТСОВАААТССАВААТАТТААЛАВТВААСТААЛАТАТОТССССАВАВСТВААС 446
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sheridan Ross P.C.
                    AGAACATAAAAAAGTGAAAGATATCAAACCTGATTTCGAATCTTCTCAAAG
                                                        AGCTCACTAAAATTTTATATATTTTGTATGATGATTGTGAACCTCCTGAATG
                                                                                             AATAATAGATGAGAAACAAAAGTCGTCAAAAGACACAGAGTGGCATAATAAGAAAGTGAA
                                                                                                                                  AGTAGTAGGAAGAAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAAT 506
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No. 5932470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTCACTAAAATTTTATATATTTGTATGATGATTGTGAACCTCCTGAATG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAATAGATGAGAAACAAAAGTCGTCAAAAGACACAGAGTGGCATAATAAGAAAGTGAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTAGTAGGAAGAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAAT 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80203
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                                                                                                                                                                                                                                                        Score 35; DB 2; Length 1383; Pred. No. 1.6; Mismatches 85; Indels
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Sequence 67, Application US/08630822A
Patent No. 5840695
Patent No. 5840695
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
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RESULT 15
US-08-630-822A-67
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MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-171-156A-28
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US-09-171-156A-28
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Best Local Similarity
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09171156A Patent No. 6368846 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                       910
                                                                                          507 AGCTCACTAAAATTTTATATATTTTGTATGATGATTGTGAACCTCCTGAATG
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                                                                                                                                                                                                                                    387 TCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAAC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/171,156A
FILING DATE: 04-Mar-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: SHERIDAN ROSS P.C.
STREET: 1560 BROADWAY, SUITE 1200
                                                              AGAACATAAAAAGTGAAAGATATCAAACCTGATTTCGAATCTTCTCAAAG 860
                                                                                                                                 AATAATÄGATGAGĀĀĀCĀAAĀGTCGTCAAĀĀGĀCĀCĀGĀGTGĢCĀTĀĀTĀĀGAĀAGTGĀĀ
                                                                                                                                                                    AGTAGTAGGAAGAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAAT 506
                                                                                                                                                                                                   TCTAGATACGAAAACGAAAAATTATAAATCTCCTGGTCGTGCAGGATATCACGAA 749
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TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA
APPARATUS TO COLLECT SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hunter, Shirley
                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                           Score 35; DB 4; Length 1383; Pred. No. 1.6; Dismatches 85; Indels
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ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,822A
FILING DATE: 11-APR-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
Search completed: April 15, 2003, 22:46:45 Job time : 346.483 secs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 24..1409
                                                                                                                                                                                                                                                                                                                                            387 ТСААТСТАТССБАААТССАБААТАТТААААБТБААСТААААТАТБТССССАААБСТБААС 446
                                                                                                                                                                                                                                           447 AGTAGTAGGAAGAAAAAAGGATTGATGTGAAGAATAAAGAGGCAGAAGATGGATTCAAT 506
                                                                                                                                                                                                                                                                                              713 TCTAGATACGAAAACGAAAGAAATTATAAATCTCCTGGTCGTGTGCAGGATATCACGAA 772
                                                                                                                                      507 AGCTCACTAAAATTTTATATATTTGTATGATGATTGTGAACCTCCTGAAIG 557
                                                                                                                                                                                                   773 AATAATAGATGAGAAACAAAAGTCGTCAAAAGACACAGAGTGGCATAATAAGAAAGTGAA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
                                                                                                     AGAACATAAAAAGTGAAAGATATCAAACCTGATTTCGAATCTTCTCAAAG 883
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linear
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Result
No.
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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Maximum DB
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                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    710.6
669.4
629.2
598.2
577
575.8
                                                                                               Score
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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em_gss_hum:*
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em_gss_mam:*
em_gss_orber:*
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gb_htc:*
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 BM697544
BE856875
BF791178
BF790243
BF672902
BF671987
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BM697544 UI-E-DX0-
BE856875 7£70c03.x
BF791178 602251278
BF790243 602249777
BF672902 602152759
BF671987 602152408
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RESULT 1
BM697544
LOCUS
DEFINITION
UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
DEFINITION
UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
BM697544

VERSION
REST.
ACCESSION
WESST.
ACCESSION
UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
BM697544.1 GI:19010802
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541 'TGTACATTTATATCTCCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTGG
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les 713; Conserv
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                                                                                                                                                                                                                                                                                            GAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAAAAAG
                                                                                                                                                                                                                                                                                                                                         GAAGCCAATTCCAGGAGCGAAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCA_{\mu^{\mu}}^{\nu \sigma}_{\mu^{\nu}\sigma}^{\nu \sigma}
                                                                                                                                                                                                                                                                                                                                                                                               GAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAAAGAATGTACTCCTGAAGTGGAGGAGGATGTTTCCTCCCACCTCGGATGAGGAGAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGCAGGGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGCAGGGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCAT 225
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                                     TGTACATTTATATCTCTTCCTTCTTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTTGG 645
                                                                                                                       TATTTGTATGATGATTGTGAAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
                                                                                                                                                                              GATTGATGTGAAGAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA
                                                                                                                                                                                                                                                                     GAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAAAAAG
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Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="fetal"
//dev stage="fetal"
//dev stage="fetal"
//lab_host="PHIOB (Life Technologies) (T1 phage resistant)"
//lab_host="PHIOB (Life Technologies) (T1 phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DXO is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonuc/Ecotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library as AGANTCAAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-E-DX0-agn-i-12-0-UI"
/clone_lib="UI-E-DX0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Matches
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                                                                                                       CGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGT 319
                                                                                                                                                                                                 CAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAGATATCAATATTCCAATGGGAGCC-TT 625
GTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGA 379
                                                                 CGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAAATGTACTCCTGAAGTGGAGGAGGGT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTC 719
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                                                                                                                                                                                                                                                                                                                                            681;
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Unpublished (1997)
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1 (bases 1 to 683)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE856875 683 bp mRNA linear EST 29-SEP-2000 7f70c03.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:3300004 3' similar to TR:Q9UHP9 Q9UHP9 SMALL MUSCULAR
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Location/Qualifiers
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/db_xref="taxon:9606"
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99.7%;
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Pred. No. 6.7e-141;
0; Mismatches 1;
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JOURNAL
COMMENT
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AUTHORS
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                                                                        Unpublished (1999)

Contact: Robert Strausberg, ph.D.

Email: Gappbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genemics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM1214 row: 1 column: 19

High quality sequence stop: 619.
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                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BF791178
BF791178.1 GI:
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 756)

NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                    BF791178 756 bp mRNA linear EST 12-JAN-2
                                                               Location/Qualifiers
/organism="Homo Bapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4338594"
/clone_lib="NIH_MGC_81"
                                                                                                                                                                                                                                                                                                                                                 GI:12096232
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RESULT 3 BF791178 LOCUS

VERSION

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/lab host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccgctcggcc); Site_2: SfiI
(ggccattateggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTACAGGCCCAGGCGCGCCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
Alto, 158
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ATACATAAAGCAGGGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAG 180 219

AGCCATCCAGGCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACC AGCCATCCAGGCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACC ATACATAAAGCAGGGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAG 279 240

CCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGA

GAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGA GGAGAAGGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGA

459 360 399 300 339

519 420

AAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAAT AAAAAGGATTGATGTGAAGAAATAAAGAGGGCAGAAGATGGATTCAATAGCTCACTAAAAT

TTTATATATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAG-AAATG TTTATATATTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAAATG 540 578 480

GCCTGTTTGTACATTTATATCTCTTCCTTCTAGTTGGCTGT-ATTTCTTACTTTATCTTC GCCTGTTTGTACATTTATATCTCTTCCTTCTAGTGGGCTGTAATTTCTTACTTTATCTTC 600 637

ATTTTTGGCACCTCACAGAAC-AAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTT TTGAGGAGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGA 756 ATTTTTGGCACCTCACAGAACAAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGCG 660 696

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TCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGG
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                                                            TATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTAC
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National Institutes of Health, M
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602249777F1 NIH_MGC_81 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
cound through the I.M.A.G.E. Consortium/LLNL at:
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quality sequence stop: 626.
Location/Qualifiers "
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/clone lib="NIH_MGC_81"
/lab_host="DH10B (TT phage-resistant)"
/lab_host="DH10B (TT phage-resistant)"
/lab_host="DH10B (TT phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/clontech); Site_1: SfiI (ggccgcctcggc); Site_2: SfiI
/ggccattattggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T. Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
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db_xref="taxon:9606"
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Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1122 row: e column: 15
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1 (bases 1 to 855)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                              /clone=IMAGE:4233878"
/clone lib="NIH MGC 81"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
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1 (bases 1 to 793)

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1141 row: o column: 02
High quality sequence stop: 665.
Location/Qualifiers
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/clone="MAGE:4293721"
/clone="IbAGE:4293721"
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/lab host="DH10B (Ti phage-registant)"
/lab host="DH10B (Ti phage-registant)"
/lab host="DH10B (Ti phage-registant); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-L
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                                                                             ATAGTGGAGGAGGTGTTCCCTTCCCACATCGCATGAGTAGAAAATGCCAATTCCAGGAGC
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Eukaryota; Metazoa;
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Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:3523462"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                Score 560; DB 12;
Pred. No. 3.4e-116;
0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 683;
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                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 906)
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BF672126
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                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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/clone="IMAGE:4293763"
/clone lib="NIH MGC 81"
/lab_host="DH10B (TI phage-resistant)"
/labe="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
                                                                                                                  organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                              Location/Qualifiers
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s cDNA clone IMAGE:4293763 5',
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ORIGIN
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Best Local Similarity
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602134792F1 NIH_MGC_81 Homo s
mRNA sequence.
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3 208 c 200 g 213 t
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94.3%;
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Pred. No. 6.9e-115;
0; Mismatches 28;
                                                                              879 bp n
mo sapiens
                                                                              cDNA clone
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Best Local Similarity 95.8
Matches 660; Conservative
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1131 row: h column: 24

High quality sequence stop: 595.

Location/Qualifiers
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                                                                                          AATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGA
                                                                                                                                                                      GGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGA 399
                                                                                                                                                                                                                                                          CCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGA
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AAAAAGGATTGATGTGAAGAAATAAAGAGGGCAGAAGATGGATTCAATAGCTCACTAAAAT
                                                              AATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGA
                                                                                                                                                GGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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147 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4289735"
/clone=lib="NIH MGC 81"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/ggccattatggcc); 5' and 3' adaptors were used In cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30) BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 3.1e-111;
0; Mismatches 16;
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                 Query Match
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      Matches · 572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTATATATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAATGG 579
                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LINL
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 587)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Watterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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Eukaryota; Metazoa;
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IMAGE:562057 3', mRNA
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                    Similarity
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    Conservative
                                                                   TTGTATGATGA-TGTGAACCTCCTGAATGCCTGAGA-TCTAGCAGAAATGG 536
                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/db_xref="GDB:4595347"
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                                                                                                                                                                                                                                                 clone="IMAGE:562057"
                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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97.1%;
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Primates;
 Score 531.8; Pred. No. 7.9e

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451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Pax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                           Program for Rat Gene
University of Iowa
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 541)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                        BM717052
BM717052.1
                                                                                                                                                                                                                                                                                                                                                                                                                                    BM717052 541 bp mRNA linea UI-E-EJO-ahk-c-03-0-UI.r2 UI-E-EJO Homo sapiens UI-E-EJO-ahk-c-03-0-UI 5', mRNA sequence.
                                                                                                                                                                                               Contact: Soares,
                                                                                                                                                                                                                   97044477
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                      TGAGTTCAAATAAATATTTGACTAAAATGTAAAATGTGA 887
                                                                                                                                                                                                  TGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTG
                                                                                                                                                                                                                                                                       TAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGGGGATATGATTTTATGGAGAATGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stuges="fetal and adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/note="organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-B-EJO is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. Pirst strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CGGCG; Retina Foveal and
Macular, GTCC; RPE and Chorold, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="UI-E-EJO-ahk-c-03-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to
Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 544)
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UI-E-EJO-ahk-c-03-0-UI.sl UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahk-c-03-0-UI 3', mRNA sequence.
BM674432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                       171
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                                                                                          modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJO is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
                                                                         TAG_TISSUE=Foveal and Macular Retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choroid"
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/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
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/db_xref="taxon:9606"
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Query Match Best Local ! Matches 518;

Similarity

Conservative

0

Score 518; DB 14; Pred. No. 1e-106; 0; Mismatches 0;

Length 544; Indels

0

Gaps

370 ACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATA 429

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 457.
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495 bp mRNA linear EST 18-AUG-1998
qa70d01.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:1692097 3', mRNA sequence.
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1 (bases 1 to 495)
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NCI-CGAP http://www.ncbi.nlm.ńih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI090520.1 GI:3429579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1692097"
                                                                                                                                /clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                         sex="unknown"
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76 g 160 t
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cive 0; Mismatches 0;
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Thmor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through ruther information.
                         IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 494)
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IMAGE:562057 5', mRNA sequence.
AA211521
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/lab_host="DH10B"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moo, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Bothlenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, B. Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags of 180,000 human expressed sequence tags of 180,000 human expressed sequence tags
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Washington University School of Medicine Louis, ð 63108 Trevaskis, E.,

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 443.

Location/Qualifiers

/clone="IMAGE:562057"
/clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin_resistant)" /organism="Homo sapiens"
/db_xref="GDB:4595347"
/db_xref="taxon:9606"

52.9**%**; 98.8**%**; Score 469.6; DB 9 Pred. No. 8.8e-96; 0; Mismatches 4 DB 9; Length

0;

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Gaps

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AGCAGGTCAACCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGTGTTCCTCC AGCAGGTCAACCCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGTGTTCCTCC 239 327

CAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACA CACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGT CAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACA CACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAGATTCCAGGACCTGCAGT 387 359 447 299

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

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ALIGNMENTS

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cDNA encoding human chisel (Csl) gene.
                                  17-JAN-2000 (first entry)
                                                                    AAX90904;
                                                                                                       AAX90904 standard; cDNA;
                                                                                                       887
                                                                                                       ВP
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Chisel gene; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; regulation; Xq21.3-q22; adaptive process; muscle homeostasis; skeletal myopathy; detection; diagnosis; prophylaxis; treatment; cardiac hypertrophy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; differentiation; exon; gene therapy; transgenic animal; drug screening; ss.

Homo sapiens

# # # # # # # # # # # # # # # # # # #		FFXS	X	RESULT 1 AAX90904 ID AAX XX AC AAX XX AC TAX A
CDS	exon	Homo sapiens. Key exon	Chisel gene; Cs heart/skeletal Xq21.3-q22; and detection; diag muscular and my Becker's myoton gene therapy; t	LT 1 0904 AAX90904 standard; cDNA; 8 AAX90904; 17-JAN-2000 (first entry) cDNA encoding human chisel
/label= Exon_2 /label= Exon_2 /note= "Corresponds to residues 15687-15631 of human cosmid clone U228D4" / 185451	'rtag a' label=Exon 1 note= "Corresponds to residues 19497-19327 of human cosmid clone U228D4" 173229	Location/Qualifiers	Chisel gene; CS1; EF-Hand protein super family; muscle development heart/skeletal muscle cell development; signalling pathway; regulixq21.3-q22; adaptive process; muscle homeostasis; skeletal myopati detection; diagnosis; prophylaxis; treatment; cardiac hypertrophy muscular and myotonic dystrophy; Duchenne muscular dystrophy; the: Becker's myotonic dystrophy; heart failure; differentiation; exon gene therapy; transgenic animal; drug screening; ss.	T 1 904 AAX90904 standard; cDNA; 887 BP. AAX90904; 17-JAN-2000 (first entry) cDNA encoding human chisel (Csl) gene.

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                                                                                                                                                                                                The present sequence is the cDNA encoding the human chisel gene (Cs1)
C that is mapped to the human chromosome Xq21.3-q22. It comprises 5 exons.
C It is a member of the BF-Hand protein super family and is involved in
Signalling pathways. It is predominantly expressed in heart and skeletal
muscles and is activated after the differentiation of cells. Cs1
C functions in regulation aspects of differentiation or adaptive processes
C that maintain muscle homeostasis. This sequence can be used in the
C detection, diagnosis, prophylactic and therapeutic treatment of diseases
Such as those involving aberrant muscle cell development and functional
activity. It is also used in the treatment of muscular and myotonic
C dystrophies, skeletal myopathies such as Duchenne muscular dystrophy and
Becker's myotonic dystrophy, heart failure, cardiac hypertrophy,
myocarditis, myofiber atrophy, etc. The Cs1 gene sequence can also be
used in gene therapy, for the production of transgenic animals and for
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(GEHO )
(HALL-)
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                          AGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT
                                           AGATCGCAGCTCAGAGGACACCGGGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT
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/product= "Chisel
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                   AACTTTGTATGAGTTCAAATAAATATTTGACTAAATGTAAAATGTGA 887
                                                                                                                                                                                                                                                                             TGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGTACATTTATATCT
                                                 AGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTA
                                                                          AGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTA 840
                                                                                                   AGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTTCCCAAGCTACTTCCTAC
                                                                                                                              AGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTTCCCAAGCTACTTCCTAC
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AAD27216 standard; DNA; 886 ВP

(first entry)

Human 66214 EST clone DNA.

RRSULT 2
AAD27216
ID AAD2
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XX AAD2
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XX expr
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XX Homo Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; yene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone 66214; ds.

Homo sapiens

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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                CC The patent discloses novel target genes abnormally expressed in heart CC tissues and their corresponding proteins. The invention also relates to CC methods for assessing the expression level of these genes. The method CC is used for testing the predisposition of mammals and preferably humans CC for a heart disease or for an acute state of such a disease. It is also useful to treat diseases for the heart such as congestive heart failure, CC dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, CC syncope and sudden death, coronary heart disease, systemic arterial theart disease, pulmonary heart disease, valvular CC heart disease, congenital heart disease, pericardial disease and CC endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart disease. The present DNA sequence is expressed sequence tag CC (EST) 66214 clone
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Best Local S
Matches 885
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                                                                               TGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATCAAT 241
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ATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAGAATGTACT
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/product= "Human 66214 proteir
298. 588
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/note= "66214 cDNA fragment"
857. 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human benign prostatic hyperplasia gene #82.
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                                                                                               Munger WE,
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Identifying

drugs for

and

diagnosing benign prostatic hyperplasia,

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detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
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Disclosure; Page 104; 444pp; English

The invention relates to a method of diagnosing (I) the onset or CC progression of benign prostatic hyperplasia (BPH), or screening (II) for CC or identifying an agent that modulates the onset or progression of BPH. CC The method is based on changes in gene expression in BPH tissue isolated CC from patients exhibiting different clinical states of prostate (CC from patients exhibiting different clinical states of prostate cells (II) compared to normal prostate tissue. (I) compared to normal prostate tissue or more genes in prostate cells (CC from the subject that are differentially regulated compared to normal CC prostate cells. (II) comprises preparing a first gene expression profile of EPH cells or EPH-like cell population, exposing the cells to the CC agent, preparing a second gene expression profile of the agent exposed (CC lis, and comparing the first and second gene expression of EPH. (II) is CC useful for diagnosing the onset or progression (CC lis useful for diagnosing the onset or progression (CC lis). The methods are useful to present information identifying the expression of EPH. (II) is compared to properly in a tissue or cells, by comparing the expression (CC level of genes given in the specification in the tissue or cells to the compared to the expression level in BPH. Agents using (II) are useful for creating EPH or prostate cancer. ABK64106-ABK64860 represent human CC benian prostate cancer. ABK64106-ABK64860 represent human CC benian prostate cancer. ABK64106-ABK64860 represent human CC compared to the expression level in a semisore of the invention human constatic human prostate cancer. ABK64106-ABK64860 represent human CC compared to the expression level in a semisore of the invention human constatic human prostate cancer. ABK64106-ABK64860 represent human can be semisored to the cancer of the constant of the cancer. prostatic hyperplasia gene sequences of the invention.

Sequence 587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;

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                                          GCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAA
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                                                                    GCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTTCACCTTTTAA
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Pred. No. 5.1e-139;
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RESULT 4
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AC' ABL64590;
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DT 15-MAY-2002 (first entry)
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STORMACH; lung; prostate; gene therapy; activated ger
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Human; cancer; colon; breat
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Human; cancer; colon; breat
XX
Stomach; lung; prostate; fix
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CS Homo sapiens.
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PD 13-DEC-2001; 2000US-20947; pr
RC 15-UN-2000; 2000US-23361; pr
RC 18-SEP-2000; 2000US-23465; pr
RC 20-SEP-2000; 2000US-23465; pr
RC 20-SEP-2000; 2000US-23492; pr
RC 20-SEP-2000; 2000US-23563; pr
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therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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WPI; 2002-188264/24
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene

Claim 1; SEQ ID 2927; 44pp; English.

CC The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stometh, lung, thyroid, CC ceopphageal, ovarian, kidney, prostate or pancreatic cancer, CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.

Sequence 587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;

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                                                                 GCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAA 828
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ATTATGTCACTAAACTTTGTATGAGTTCAAATAATATTTGACTAAATG
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The present sequence is the cDNA encoding the murine chisel gene (Cs1) that is mapped to the mouse X chromosome. It is a member of the EF-Hand protein super family and is involved in signalling pathways. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle of differentiation or adaptive processes that maintain muscle continuous prophylactic and therapeutic treatment of diseases such as those prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, because of myotonic dystrophy, heart failure, cardiac hypertrophy, and Becker's myofiber atrophy, heart failure, cardiac hypertrophy, myocarditis, cardiac hypertrophy, for the production of transgenic animals and for drug screening.

Claim 3; Page 148; 157pp; English

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5 CTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGAT

Query Match Best Local S Matches 562

al Similarity 562; Conserv

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Mismatches

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Length

778; 51;

43.9**%**;

Score 389.8; DE Pred. No. 4e-99;

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Chisel gene; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart fallure; cardiac hypertrophy;
                                                                                                                                                                                           Isolated nucleic acids encoding chisel, used to develop products treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
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(HALL-) HALL INST MEDICAL RES WALTER &
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DB; AAY28650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/product= "Chisel
/note= "Expressed
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RESULT 6
AAC01483
ID AAC0
XX AAC0
XX AAC0
XX Huma
XX Huma
XX Huma
XX Gene
XX Gene
XX Homo
XX Homo
XX Homo
XX Ep10
XX 26-5
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                                                                                                                         Human; 5' EST;
gene therapy; c
26-FEB-1,999;
                       21-FEB-2000; 2000EP-0200610.
                                                   06-SEP-2000
                                                                          EP1033401-A2
                                                                                                    Homo sapiens
                                                                                                                                                                    Human secreted
                                                                                                                                                                                             06-OCT-2000
                                                                                                                                                                                                                                               AAC01483 standard; cDNA; 428
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                                                                                                                                                                                                                                                                                                                           AACACCTGGAGGGTGTGGTTTTGAGGAGGGATATGATTTTATGGA 721
                                                                                                                                                                                                                                                                                                                                                                               TGTATTTCTTACTTTATCTTCATTTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                              GAAATAAACAACTTCCTGAACATTTTATACATTTGTATGATGATCACAAACCTCCTGAAT
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                                                                                                                                                                                                                                                                                                            ACAACCTGGGAAGTGTGGTTTTGAGGAGATGTGATTTTTATGA 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAG
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                                                                                                                                                                                                                                                                                                                                                             CTCACTTTAGCTACATTTTTGGCACCTTGTAGAGCAAATCAGCACACGAATTT
                                                                                                                                                                                           (first entry)
                                                                                                                             chromosome
 99US-0122487
                                                                                                                                                                   protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACTAAAATTTTATATATTTTGTATGATGATTGTGAACCTCCTGAAT
                                                                                                                             sequence tag; secreted protein; cDNA isolation; mapping; ss.
                                                                                                                           mapping;
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RESULT 7
AAD27226
ID AAD2
XX
AC AAD2
XX
AC AAD2
XX
DT 09-A
XX
DE Huma

AAD27226; 09-APR-2002

AAD27226 standard;

cDNA;

Human 66214 cDNA clone

(first entry)

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Best Local Similarity
Matches 364; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain unstream reconstants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 428 BP; 123 A; 111 C; 104 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 1481; 71pp + CD-ROM; English
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362
                                      365
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   GCGA
                                                              CCTGAAGTGGAGGAGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGA
                                                                                                                                    ATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCCAGAAGAAAAAGAATGTACT
                                                                                                                                                                                                          TGCATGAATATGTCGAAACAGCCAGCTTTCCAATGTTAGAGCCATCCAGGCAAATATCAAT
                                                                                                                                                                                                                                                                                                                                  GATCGCAGCTCAGAGGACACCGGGGGGGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTG
                                                                                                                                                                                                                                                                                                                                                                     GATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA
                                    CCTGAAGTGGAGGAGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGA
                                                                                                          ATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAGAATGTACT
                                                                                                                                                                                  TGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATCAAT
                                                                                                                                                                                                                                                          CATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAGAC
                                                                                                                                                                                                                                                                                           CATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAGAC 181
                                                                                                                                                                                                                                                                                                                                                                                                          GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA
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DB; AAG01477.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
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The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, collative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiock syncope and sudden death, coronary heart disease, systemic arterial hypertrension, pulmonary hypertrension, pulmonary hypertrension, pulmonary hypertrension, pulmonary heart disease, valvular cheart disease, congenital heart disease, pericardial disease and condocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of the invention are useful for the development sequence is a cDNA from 66214 clone. This sequence used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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ATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGT
                                                                                                                                                                                                                                                   GAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAAAAAGGATTGATGTGAAG
                                                                                                                                                 AAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATATATTTGTATGATG
                                                                                                                                                                                                                                                                                                                                      GGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 290; DB 24; 100.0%; Pred. No. 2.5e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 69 G;
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Matches Query Match

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RESULT 8
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                                                                                   cobiological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in certaining RNA transcripts and splice variants of human or animal cranscriptomes. The libraries may also be used as specialised mini celetecting RNA transcripts and splice variants of human or animal celetecting RNA transcripts and splice variants of human or animal celetection of tissue- and pathological state, and so allowing the celetection of tissue- and pathology-specific genes such as those genes celetection; to detect developmental specific genes such as those genes celetection; to detect developmental specific genes and to detect RNA celetection; to detect developmental specific genes; and to detect RNA celetection; to detect developmental specific genes; and to detect may celetect genes celetection of the variants of a transcriptome of a pathent suffering celetection of the present invention.

Celetection of the present invention.

Celetectication, but was obtained in electronic format directly from WIPO at figure variation, but was obtained in electronic format directly from WIPO at figure variation, but was obtained in electronic format directly from WIPO at figure variation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a transcription to the property of the prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
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variant; transcriptome; oligonucleotide library; ss.
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ABN58272
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                                                                                                                                                                                         quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN29589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                       transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or manifestively of the services of the profile of the services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                    Sequence
                                                                                                                                                                      specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID 31020; 47pp; English
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364 GAAGAAACTTCCAAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (sub-)transcriptom comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises
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transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                  can be used
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                            Sequence 6115 BP; 1623 A; 47 C; 1519 G;
                                                                                                                                                                                                                                                                                              genes which
                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1773; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene;
                                                                                                                                                                                                                                                           genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                            The present
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                                                                                     703 AGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTT 762
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                  TCCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTTAGTTCTTCACC 822
TTAGGTTTTTTTTTTTTTTTTTTTTTGGTAAATTTTTGGTATTGGATTTTGGGTTTTTATT
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                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                            invention provides a number of human immune system associated
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polymethese are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity disorders involving aberrant protein expression or biological activity. CC associates of the sequences of the realist to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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AAS67967
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      Query Match
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Matches 97
                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                        Sequence
                                                                                                                                                                                                                                                                                                                                         The invention
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 3771; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #3771.
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                                                                          ftp.wipo.int/pub/published_pct_sequences.
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                                                 BP; 325 A; 365 C; 264 G; 180 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism; modulation; lipolysis stimulation; hormone-sensitive lipase stimulation; lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity; functional food; transgenic yeast; fat/lean ratio; food use; ds.
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                                                                                                                                                                                                                                                                     The invention relates to novel transgenic organisms useful in the production of functional food and drink products for the treatment cc or prevention of obesity via the regulation of lipid metabolism. The crystalisms comprise a polynucleotide encoding a growth hormone fragment cc organisms comprise a polynucleotide encoding a growth hormone fragment cc enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key cc enzyme in lipogenesis). The growth hormone fragment preferably contains cc at least the disulphide-bonded loop of a mammalian growth hormone (but is contone to go reterologous fusion protein partner. The transgenic contone to go reterologous fusion protein partner. The transgenic corganism may be a microorganism used to produce a fermented product (e.g., yeast), or an edible plant or animal or cell thereof. Food or cratio, lipid metabolism or food use in a mammal. In particular, the food or drink products may be used to transor used to modify fat/lean cration of inventor, the human growth hormone (hgH) fragment analogue AoD9604 was carped to yeast, optionally fused to the FLAG epitope (AAB73625). The present sequence is described as a DNA sequence from yeast in the sequence listing, but is not further referred to in the
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                             CATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAGAC 181
VVVCHKHIDHDHKGHMCMHCCCMHKMDHAAAANRMACMHHHHADNGCKHADATARAGRAH
                                                                                       GATCGCAGCTCAGAGGACACCGGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTG
                                                                                                                    GHYCHNHNRBDHDHDDNDRBVWBRVHDCDVWBNHNVWDDHDHDHDHDHDHNDWCHNHNBR
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                                                           VHDHDDDDVYYMNRGHMHMHNHNTCDHDHDHDHNTCHABDGKMVVVVVVVVVVVVVVVV
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10.0%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL32420;
                             genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-1032529: 01-SEP-2000; 2000DE-1043826:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune
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                                                                                                                                                                         Claim 1; SEQ ID NO 393; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                        WPI; 2002-130909/17.
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                                                                                                                                         invention provides a number of human immune system associated
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Best Local S
Matches 109
The present invention describes a method of screening for genes which modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably Drosophila, and toxic polyglutamine sequences include the human and (TPR2) and myeloid leukaemia factor 1 (MLP) genes. The model is useful for identifying treatments for neurodegenerative and proliferative disorders, including Aliheimer's disease, Parkinson's disease, Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar
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12-AUG-1999;
18-JAN-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                            Identifying genes or other compounds that modulate toxicity, useful for treating Alzheimer's disease, and Creutzfeldt-Jakob disease -
                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1; heat shock protein 40; tetratricopeppide repeat protein 2; TPR2; stroke myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease; Parkinson's disease; CJD; BSE; Huntington's disease; head trauma;
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2000US-0205720.
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Pred. No. 0.61;
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                                     useful in developmental biology and in elucidating cell signalling interactions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16175) and the encoded proteins (ABL5737-ABS72072).
                       The sequence data for this patent did not for specification, but was obtained in electronic
                                                                                                                       Claim 1; SEQ ID NO 20324; 21pp + Sequence Listing; English
                                                                                                                                                     New isolated nucleic agenes from Drosophila
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Patent No. US20020077470A1

GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Slda
ITITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
CURRENT APPLICATION NUMBER: US/09/880,192

CURRENT APPLICATION SATE: 2001-06-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PERL PROGram
SEQ ID NO
LENGTH: 824

TYPE: DNA
CORRESTED IN A CONTROL OF THE SECTION OF THE SEQ ID NO 4

LENGTH: B24
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; FEATURE:
; FATURE: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1
US-09-880-192-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
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9 US-09-938-842A-4253
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10 US-09-879-536-766
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12 US-10-071-751-28
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14 US-10-071-751-26
15 US-09-938-842A-4090
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Published Applications NA:*

1: /cgn2 6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2-6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2-6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2-6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

5: /cgn2-6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

7: /cgn2-6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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10: /cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

11: /cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2-6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

14: /cgn2-6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Minimum DB Maximum DB

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Total number of hits satisfying chosen parameters:

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593429 seqs, 438583890 residues

Title: Perfect score:

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US-09-960-352-1972	US-09-754-853A-4	US-10-014-799A-3	US-09-764-864-735	US-09-969-347-175	US-09-535-459-2163	US-09-833-263-275	US-09-922-217-275	US-10-025-380-275	US-09-998-598-1439	US-09-864-761-2816	US-09-070-927A-89	US-10-044-090-123	US-09-938-842A-3453	US-09-815-242-9307	US-09-070-927A-394	US-09-960-352-5216	US-09-962-436-468	US-09-880-192-4	ID
\mathbf{r}	Sequence 4, Appli	Sequence 3, Appli	•	Sequence 175, App	Sequence 2163, Ap	Sequence 275, App	Sequence 275, App	Sequence 275, App	Sequence 1439, Ap	Sequence 2816, Ap	Sequence 89, Appl	Sequence 123, App	Sequence 3453, Ap	Sequence 9307, Ap	Sequence 394, App	Sequence 5216, Ap	Sequence 468, App	Sequence 4, Appli	Description

SUMMARIES

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CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
SEQ ID NO 468
LENGTH: 587
TYPE: DNA
                                                              ; ORGANISM: Homo sapiens FEATURE; FEATURE; ; NAME/KEY: misc feature; OTHER INFORMATION: n=a,t,g or US-09-962-436-468
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturitle OF INVENTION: Sets
FILE REFERENCE: 689290-75
   Best Local Similarity
Matches 572; Conserv
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 468, Application US/09962436 Patent No. US20020081301A1
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                60.0%;
 Score 531.8; DB 10;
Pred. No. 6.5e-137;
0; Mismatches 14;
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                               Length 587;
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; LENGTH: 466
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID:
US-09-960-352-5216
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US-09-960-352-5216
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                                                                                                                                                                                                                                      Sequence 5216, Application Patent No. US20020137139A1 GENERAL INFORMATION:
                                                                                                                              Query Match
                                                                                                                                                                                                                            NUMBER OF SEQ
SEQ ID NO 5216
141 TCCCTTAGGCAGTAAACAAATACATAAAGCAGGGATAAGACTGCATGAATATGTCGAAAC
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                                                                                           36.0%;
Local Similarity 83.9%;
1es 387; Conservation
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                                                                     81 CCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACT 140
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                                                                                                 0;
                                                                                                                                                                      23-BOVMS1-014-Q1-E1-F3
                                                                                               Score 319; DB 10;
Pred. No. 3.3e-78;
0; Mismatches 65;
                                                                                                   65;
                                                                                                                            Length 466;
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RESULT 4
US-09-070-927A-394/c
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Patent No. US20020120116A1
GENERAL INFORMATION:
                                                                                                                    INFORMATION FOR SEQ ID NO: 394:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 TTCAAACAAAAATGGCTCACTAAAAAGTTTTATATATGTGT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AGCCAGTTTCCAATGTTAGAGCCATCCAGGCAAATATTCAATATTCCAATGGGAGCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 TTCCTCCCACCTCGGATGAGGAGAAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 GGCCAGGAGCAGGTCAACCCCCCCAGAAGAAAAGAATGTACTCCTGAAGTGGAGGAGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
PILING DATE: 04-May-2000
CLASSIFICATION: <Unknown> /"
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTCCCACTTCGGACGATGAGAAGAAGCCAATTCCAGGAGCTAAGAAACTTCCAGGAC
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                               LENGTH: 14141 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                           TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
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US-09-815-242-9307/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ
SEQ ID NO 9307
LENGTH: 2253
                                                                                                                                                        Matches
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                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Streptococcus
FEATURE:
                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4283 TTCATTATTTGACCTCACTTTTATCTGGTTACCTTCATTATAACAGAGATAAAATTTTTA 4224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4343 TGCGATTGTGCTAAAACAACTGAACGCAATGGTGCAAATTCACTTTCAACATGCATTTTT 4284
622 TTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAACAC 681
                                                                       730
                                                                                                           850 TGAGTTCAAATAAATATTTGACTAAATGTAAAATGT 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                   AGACTTCTGCGGTTTTAGCTTGCAAGTCCAGTAATTTCTCCACAGCTTGGGACGTATTTT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCTTCAATGAAGAAAAAGCAGAACTTCTATACGT 4188
                                                                                                                                                          69;
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Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant J.
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Trawick, John D.
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Zyskind, Judith W.
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                ... (2253)
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52.6%;
                                                                                                                                                                            4.2%;
                                                                                                                                                                                                                                                                                                                              pneumoniae
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                                                                                                                                                    Score 37.2; DB
Pred. No. 5.7;
0; Mismatches
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Pred. No. 13;
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                                                                                                                                                                                                 DB 10;
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US-09-938-842A-3453/c
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                                     US-10-044-090-123
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Olga BANDEMAN
APPLICANT: Olga BANDEMAN
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 123
LENGTH: 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3453
LENGTH: 1875
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  Query Match
                                                                                                                                                                                                                                                                                                                                                                               Sequence 123, Application US/10044090 Patent No. US20020137081A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                               OTHER INFORMATION:
                                                                                   NAME/KEY: misc
                                                                                                        FEATURE:
                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 TCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAAT 391
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Local Similarity 55.0%;
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                                                               Incyte ID
  4.1%;
                                                             No.
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Pred. No. 7.4;
0; Mismatches 59;
Score 36.6;
                                                             US20020137081A1 892168.1
DB 12;
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Length 3633;
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RESULT 8
US-09-070-927A-89
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                                                                              Matches
17319 TAAATTGTGCGCCTGCTAAACGTTGTTTTGAGTAACCATCTTGTTTAATTTAATTTTAAAT 17378
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3241 AAGCCTAGAATTTCTCTTTAGGTATAT 3267
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                                      670 TAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGGGATATGATTTTATGGAGAATGATA 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MSDOS version SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: -CUNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 982
                                                                              99;
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                                                                                                                                                                                                                     LENGTH: 20072 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                           TELEFAX: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09070927A
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                                                                              Conservative
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                                                                                               4.1%;
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                                                                                                                                                                                                                                                                                                                           309-8512
                                                                                                                                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                                                309-8504
                                                                              Pred. No. 30;
0; Mismatches
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                                                                                               Score 36.6;
Pred. No. 30;
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                                                                                                                                                                                 NO: 89:
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                                                                                                                      DB 10;
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                                                                                                                    Length 20072;
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FILE REFERENCE: AGONG CANALISATION ANNALISATION OF THE REFERENCE: AGONG CANALISATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                  SOFTWARE: Annomax
SEQ ID NO 2816
LENGTH: 395
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             ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL033539.17
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron
                                                                                                                                                            TYPE: DNA
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FILING DATE: 2001-01-30
PPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661 APPLICATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                  Sequence
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RESULT 11
US-10-025-380-275/c
; Sequence 275, Application US/10025380
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; OTHER INFORMATION: EXPRESSED II

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Best Local Similarity
Matches 128; Conserv
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CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOPTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1439
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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Best Local Similarity
Matches 65; Conserv
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  339 АGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 GCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTTTAA 828
                                                                                                                 AATTTTATATATTTGTATGATGATTGTGAACCTTCTGAATGCCTGAGACTCTAGCAGAAA 576
                                                                                                                                                                                                                                          CAGATTATGGAATAGTTGCAGATTTATTTAAGGTAGTTCCTGAAATGACTGAGATATTGA
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  TAATTTGAGGGAAAATTTCTAAC
                                       TGGCCTGTTTGTACATTTATATC 599
                                                                         AATCACAGATATTTGTGGGTATTATAACAATCATTGGAAAGCATGGAGAGCTACATTTCA
                                                                                                                                                          AGAAAAATGAATCAGGATCATGCCTTAAAAAGAAACTTTTGTTAAAGTATTCCACTGA
                                                                                                                                                                                               AGAAAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAA 516
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48.7%; Pred. No. 4.2;
ative 0; Mismatches 133;
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Pred. No. 3.8;
0; Mismatches
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IN ADULT LIVER, SIGNAL = 1.8
IN 18474, SIGNAL = 1.8
IN LUNG, SIGNAL = 1.5
IN PLACENTA, SIGNAL = 1.5
IN HELA, SIGNAL = 1.5
IN HELA, SIGNAL = 1.5
IN HELA, SIGNAL = 1.5
IN BRAIN, SIGNAL = 1.5
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GENERAL INFORMA: APPLICANT: Xu,

INFORMATION:

Secrist, Heather Benson, Darin R.

u, Jiangchun Lodes, Michael J.

Publication No.

US20020182191A1

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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 528
TYPED: Transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.1%;
Best Local Similarity 48.7%;
                                                                                                                          GENERAL INFORMATION:
                                                                                                                                          Sequence 275, Application US/09922217 Patent No. US20020076414A1
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
                                                                                     APPLICANT: Xu, APPLICANT: Lo
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LOCATION: 33, 68, 470
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGG 398
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                                                                                                                                                                                                                                                                                                                        210
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                                                                                                                                                                                                                                                  TAATTTGAGGGAAAATTTCTAAC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAA 516
                                                                                                                                                                                                                                                                                                                      AATCACAGATATTTGTGGGTATTATAACAATCATTGGAAAGCATGGAGAGCTACATTTCA
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Wang, Aijun
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Smith, Carole L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meagher, Madeleine Joy
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
                                                   Secrist, Heather
Benson, Darin R.
                                                                                       Lodes, Michael J.
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                                                                                                           Jiangchun
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CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOPTWARE: FASKSEQ for Windows Version 3.0
SEQ ID NO 275
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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                                 US-09-833-263-275
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SEQ ID NO 275
LENGTH: 528
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APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ. ID NOS: 1124
NUMBER OF SEQ. ID NOS: 1124
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. US20020110547A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 33, 68, 470
OTHER INFORMATION: n = A
                                                                                                                                                                                                                                                                                APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER I
FILE REFERENCE: 210121.471C12
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                   NAME/KEY: misc_feature
LOCATION: (1)...(528)
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                             Clapper, Jonathan D. Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09833263
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48.7%;
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Pred. No. 4.
Score 36.2;
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DB 10;
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Length 528;
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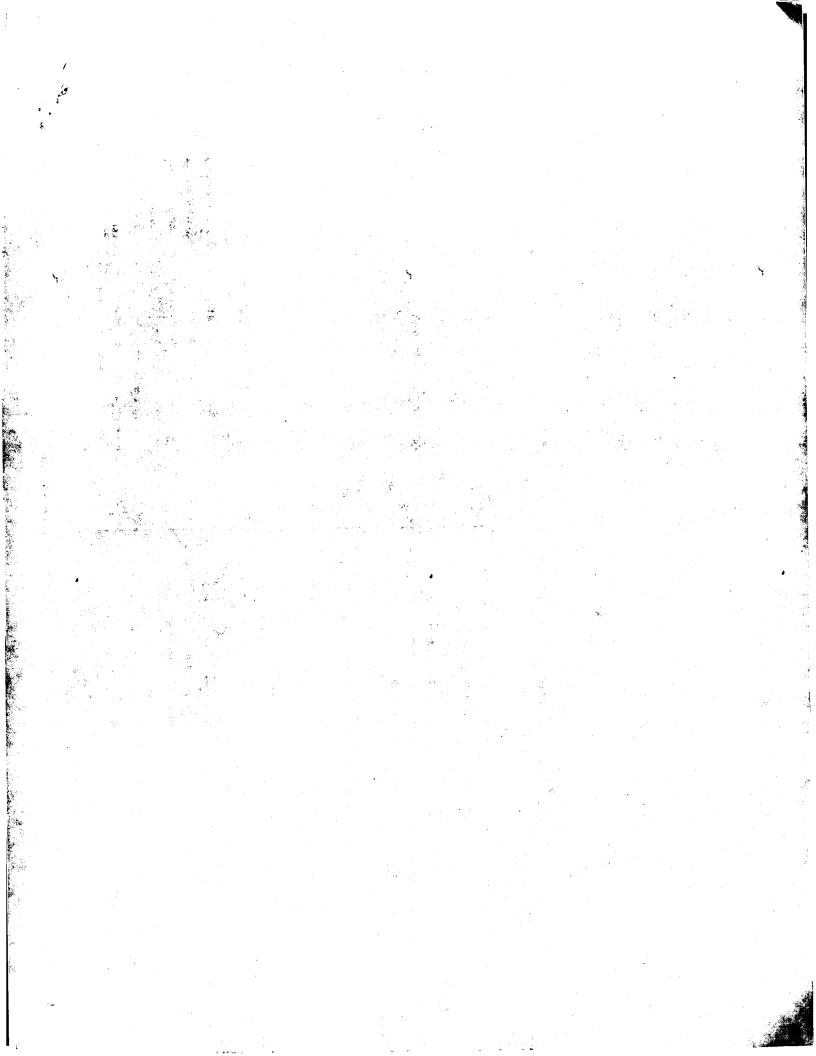
Query Match

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Publication No. US20030040615A1
GENERAL INFORMATION:
APPLICANT: Scilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS; 2170
SOPTWARE: PERL Program
SEQ ID NO 2163
LENGTH: 548
TYPE: DNA
ORGANIAM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030040615A1 hu00992223
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 128; Conserv
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CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECUL
                           577
                                                               383
                                                                                                                                                                          457
                                                                                                                                                                                                                263
                                                                                                                                                                                                                                      399 -- АРАТССАGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGA 456
                                                                                                                                                                                                                                                                           203 AAGACÁGCAÁGACAÁTTGTGGCAATTAÁTAÁGACCCAÁGAÁGCTCCAATTTTCCAÁGTGG 262
                                                                                                                                                                                                                                                                                                               339 АССАВАВАЛАССАЛТТССАССАССАЛОВАЛАСТТССАССАССТССАСТСАЛТСТАТССС 398
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TGGCCTGTTTGTACATTTATATC 599
                                             AATCACAGATATTTGTGGGTATTATAACAATCATTGGAAAGCATGGAGAGCTACATTTCA
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                                                                             AATTTTATATATTTGTATGATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTTAGCAGAAA
                                                                                                                         AGAĀĀĀĀĀTGĀĀTCĀGGATCĀTGCCTTĀĀĀĀĀĀGĀĀĀACTTTTGTTĀĀĀGTĀTTCCĀCTGĀ 382
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ilarity 48.7%;
Conservative
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Pred. No. 4.6;
0; Mismatches 133;
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Search completed: April 16, 2003, 01:13:08 Jab time : 123.63 secs

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; ORGANISM: Homo sapiens
US-09-969-347-175
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US-09-969-347-175
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 175
LENGTH: 1266
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 128;
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Best Local Similarity 48.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 689290-69
CURRENT APPLICATION NUMBER: US/09/969,347
CURRENT FILING DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ebner, Reinhard
                                                                                                                          517
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                                                                                                                                                                                                                                                                                                                                            339 AGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGG 398
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                                                                                                                                                  AGAAAAATGAATGAATCAGGATCATGCCTTAAAAAGAAAACTTTTGTTAAAGTATTCCACTGA 1051
                                                                                                                                                                                                                             CAGATTATGGAATAGTTGCAGATTTATTTAAGGTAGTTCCTGAAATGACTGAGATATTGA 991
TAATTTGAGGGAAAATTTCTAAC 1134
                                     reccremmeracammarame
                                                                    AATCACAGATATTTGTGGGTATTATAACAATCATTGGAAAGCATGGAGAGCTACATTTCA 1111
                                                                                                           AATTTTATATATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAA 576
                                                                                                                                                                                        AGAAAAAAGGATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAA 516
                                                                                                                                                                                                                                                                                                         AAGACAGCAAGACAATTGTGGCAATTAATAAAGACCCAAGAAGCTCCAATTTTTCCAAGTGG 931
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Pred. No. 7.6;
0; Mismatches 133;
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ALIGNMENTS

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KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
1 clases 1 to 886)
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein AP129505 886 bp mRNA linear PRI 22-DEC-1999 Homo sapiens small muscular protein (SMPX) mRNA, complete cds. AF129505 AF129505.1 GI:6625646 Homo sapiens.

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/product="small muscular protein"
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1 (bases 1 to 885)

Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Eastwood, M., Sassoon, D.A. and Coulton, G.R.

Identification of a novel stretch-responsive skeletal muscle gene
                                                                                                                                                                                                                                                                                                    Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial College of Science Technology and Medicine, SAF Bldg, Level 2, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Related sequences:AJ245772, U73508 to U73509.
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/codon_start=1
/product="stretch responsive muscle (X-chromosome)"
/protein_id="CAC08492.1"
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                                                                                                         /gene="Srmx"
                                                                                                                                          /gene="Srmx"
                                                                                                                                                                 1. .183
                                                                                                                                                                            /gene="Srmx"
                                                                                                                                                                                                tissue_type="skeletal muscle"
1. .885
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/db_xref="taxon:9606"
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/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6625646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human (Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Contact: MGC help desk
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Mammalia; Eutheria;
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      Conservative
                                                                                    /product="small muscle protein, x-linked"
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/Cissue_type="Skeletal Muscle"
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Sequence 29
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AX332418.1
       Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screen
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Patent: WO 0194629-A 2927 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                  AF364071
Rattus norvo
AF364071
AF364071.1
         Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M. Identification, mapping, and genomic structure of a novel X-chromosomal human gene (SMFX) encoding a small muscular Hum. Genet. 105 (5), 506-512 (1999)
                                           1 (bases 1 to 892)
Patzak, D., Zhuchenk
                                                                   Rattus.
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Query Match
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Matches 683; Conserv
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CTCCTGAATGCCTGAGACTCTAGCAG-AAATGGCCTGTTTGTACATTTATATCTCTTCCT
                                                            CAATGGGTTGAAATAAACAACTTCATGAGAATTTTATATATTTGTATGATGATGATCACAAAC
                                                                                  AGATGGATTCAA-----TAGCTCACTAAAATTTTTATATATATTTGTATGATGATTGTGAAC
                                                                                                                                          ANAGGTGAACAGTAGTTCAAAGGGGTCAGAAGGCTTGACGTGCTTTCTCAATGGAAAAAA
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Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
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Direct Submission
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/db_xref="taxon:10116"
<1. .892
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/evidence=experimental
183 c 193 g
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862. .867
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/codon_start=1
/product="SMPX protein"
/protein_id="AAK50399.1"
/db_xref="GI:13940510"
/translation="MSKOPIENVRSIQANINIPMGAFRPGAGQPPRRKESTPGTAEGA
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Pred. No. 5.2e-107;
0; Mismatches 174;
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CTGGAGAGAGACAGAGCACTCCAGCTATTTCAGCCACATGAAAAGCACTGGAATTGAGAT
             CTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCCATCGGAATTGAGAT
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AF364070
AF364070.1 G:
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Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                               Submitted (26-MAR-2001) E.M.-Arndt-Uni, Inst. f. H
Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers "
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patzak, D., Zhuchenko, O., Lee, Identification, mapping, and X-chromosomal human gene (SMP Hum. Genet. 105 (5), 506-512
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                                                    52.0%; ilarity 74.2%; Conservative
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                                                                                                                                                           906. .911
                                                                                                                                                                   /Codon_start=1
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<1. .936
                                                                                                                 /evidence=experimental
187 c 203 g
                                                                                                                                                                                                                                                                   /gene="Smpx"
199. .456
                                                                                                                                                gene="Smpx"
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Rodentia;
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                                                   Score 461; DB 10;
Pred. No. 2.1e-103;
D; Mismatches 180;
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n (Smpx)
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Sciurognathi; Muridae;
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              TTCAAATAAATATTTGACTAAATGTAAAA
                                                                    ATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTAAACTTTGTATGAG
                                                                                                                      TGTGC--CTAACGATTTTGATGAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTGGTCA
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                                                                                                        CGTGCAAGCAGTGATTTTGATGTTAAGTACTTTAAGTTACTTCCCACGGTCTTTTGGTCA
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RESULT 8 DEFINITION

Mus musculus mRNA

for

stretch

responsive mRNA

linear muscle (x

(X-chromosome)

ROD 12-APR-2001

đđ

gene)

MMU245772

ACCESSION VERSION KEYWORDS SOURCE protein (Srn AJ245772 AJ245772.1 xmrs)

Srmx gene; stretch responsive musçle (X-chromosome)

Mus musculus house mouse.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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                      CCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGCTTT
                                                                                         CTGGAGAGAGACAGAGCACTCCAGCTATTTCAGCCACATGAAAAGCACTGGAATTGAGAT 86
                                                                                                                  CTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGAT
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Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Important College School Of Medicine, SAF Building, Exhibition Road, Kensington, London SW7 2AZ, UNITED KINGDOM
Location/Qualifiers
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Kemp,T.J., Sadusky,T.J., Simon,M., Brown,R., Eastwood,M.,
Sassoon,D.A. and Coulton,G.R.

Identification of a novel stretch-responsive skeletal muscle
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/codon_start=1
/product="stretch responsive muscle (X-chromosome)"
/protein_id="CAC08493.1"
/db_xref="G1:10178963"
/translation="MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
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                                                                                                                                                                                                                                                                                                                                                         /gene="Srmx"
/function="mRNA of the state of
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/function="mRNA (
585. .590
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/function="mRNA (658. .662
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function="mRNA
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/strain="C57BL/10"
/db_xref="taxon:10090"
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179. .785
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'function="mRNA
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1 Homo sapiens
Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 36503)
Sulston, J.E. and Waterston, R.
Toward a complete human genome se
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                                                             Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JAN-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 36503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 8 (11), 1097-1108 (1998) 99063792
                                                                                                                                                                                                                                                                                                                               This clone is from a chromosome X-specific cosmid library LLOXNCC01 'U'. The source of the chromosomes was a human/hamster hybrid, GM07297-F, from Robert Nussbaum at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livermore National Laboratory at http://www-bio.llnl.gov/genome to obtain the clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPPING INFORMATION:
This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. V., and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomics 44:227-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mailto:sapiens@watson.wustl.edu
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/note="match to EST AA214031 (NID:g1812669) zn58f02.81" complement (3980. .4103) /note="match to EST AA211521 (NID:g1810175) zn55b01.r1"
                                                 /note="match to EST AA211443 (NID:g1810130) 3711. .3929
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                                                                                                                                                                      /clone_
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/chromosome="X"
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4366. .4730
/rpt_family="Malk"
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14804
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24736. .2
                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu"
20137. .20192
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28149. .28286
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.0938. .11032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCACCTCACAGAACAAATTAGCCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGA
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                                                                                                              Bequence.
AL772392
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 124186)
                                                                                                                                        Human DNA sequence
                                                                     Homo sapiens.
                                                                                               AL772392.4
                                                                                                                                                     AL772392
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complement (35221. .35386)
/note="match to EST AA211521 (NID:g1810175) zn55b01.r1"
complement (35243. .35386)
/note="match to EST AA389647 (NID:g2042633)"
36277. .36501
/rpt Eamily="Retroviral"
/rpt Eamily="Retroviral"
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34152. .34277
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30427. .30777
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29526. .29750
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                                                                                                                                        from clone
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om clone RP11-450P7
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Best Local Similarity
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                                      764
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CCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                   TATATTTGTATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTG 100532
                                                                                                                            GGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTT
                                                                                                                                                                                                       GGCACCTCACAGAACAAATTAGCCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGA
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                                                                                         GGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTT 100352
                                                                                                                                                                                                                                          GGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP11-450P7 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      database can be found at
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/clone_lib="RPCI-11.2"
a 24595 c 23947 g 38244 t
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/chromosome="X"
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Matches 562; Conserv
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                                                                                                                      CTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGAT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-FEB-2001) Developmental Biology, Victor Chang Research Institute, 384 Victoria St, Darlinghurst, Sydney, N South Wales 2010, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,(Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentg, Mohun,T. and Harvey,R.P.

The small muscle-specific protein Csl modifies cell shape and promotes myocyte fusion in an insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Palmer, S., Groves, N., Schindeler, A., Yeoh, T., Biben, C., Sparrow, D.B., Barnett, L., Jenkins, N.A., Copeland, N.G., I Mohun, T. and Harvey, R.P.
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                         /product="muscle-specific protein CSL"
/protein id="AAK07682.1"
/bxref="G1:14575062"
/txinslation="MSKOPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
167 c 185 g 202 t
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                  note="ortholog of Homo sapiens SMPX"
                                                                                                                                                                                                                                                                                                                                                     gene="Csl"
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Rodentia;
                                                                                                                                                  Score 389.8; DB 1
Pred. No. 8.5e-86;
0; Mismatches 152
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Koentgen, F.,
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Koentgen, F.,
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Sequence
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Novel target genes for diseases of the
Patent: WO 0192567-A 27 06-DEC-2001;
                                                                                                                                                                                                                                                unidentified unidentified
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299 ACTCCTGAAGTGGAGGAGGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCAAGTCCAA 358

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ACTCCTGAAGTGGAGGAGGGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCA 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 224691 bases at least Q40
Consensus quality: 226148 bases at least Q30
Consensus quality: 226956 bases at least Q20
Insert size: 227331; sum-of-contigs
Insert size: 227331; sum-of-contigs
Insert size: 194478; 8.5% error; agarose-fp
Quality coverage: 6.42x in Q20 bases; sum-of-contigs Quality
coverage: 8.63x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL732396 228031 bp DNA Mus musculus chromosome X clone RP23-93M14, PROGRESS ***, B unordered pleces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 228031)
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AL732396.6 GI:22415936
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                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1 5544: contig of 5544 bp in length
5545 5644: gap of 100 bp
5645 11121: contig of 5477 bp in length
11122 11221: gap of 100 bp
11222 23110: contig of 11889 bp in length
23111 23210: gap of 100 bp
23111 23210: gap of 18936 bp in length
42147 42246: gap of 100 bp
42247 74925: contig of 32679 bp in length
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                           AAATAAATATTTGACTAAATGTAAAATGTGA 887
                                                                                             TTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTAAACTTTTGTATGAGTTC
AAATAAATATTTGAGTAAATGTAACATATGA 187785
                                                                         TTTGAAATG-----GTTTCTTCACCTTTTAAATTATCTCAATTAACTTTTATGAGTTC 187754
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153828: contig of 78803 bp in
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172635: contig of 18707 bp in
172735: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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.----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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                                                                                                                                                              Center project name: GXOD
Center clone name: CH230-20D15
                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
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5, *** SEQUENCING IN PROGRESS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
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TITLE JOURNAL	•	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Qy 855 TO Db 147079 TO RESULT 15 AC096040/c LOCUS DEFINITION	Qy 679 CJ Db 146905 CJ Qy 738 TC Db 146965 TC Qy 795 T7 Db 147025 TJ
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., O'riedo, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., O'riedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wang, S., Williamson, A., Wilczyk, R., Wooden, S., Warlson, M., Y., F., Zhou, J., Zorrilla, S., Nelson, D., Wilpublished	Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Garrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Hollowsy, C., Hollins, B., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lozado, R.J., Lucier, R., Luna, R., Ma, J., Ma, J., Lozado, R.J., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,	46 unordered pieces. AC096040 AC096040.4 GI:21723170 AC096040.4 GI:21723170 AC096040.4 GI:21723170 HTG; HTGS_PHASE1. Norway rat. Norway rat. Rorway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rattus. Rattus. I (baese 1 to 82586) I (baese 1 to 82586) Alsbrooks,S.L., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Barbaria,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,	orves	CACCTGGAGGGTTGGTTTTGAGGAGGGTATGA-TTTTATGGAGAATGATATGGCAATG 737 [

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Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:17943701.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 35907 bases at least Q40
Consensus quality: 40224 bases at least Q30
Consensus quality: 44113 bases at least Q20
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Chemistry: Dye-terminator Big Dye: 100% of reads
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-29I1
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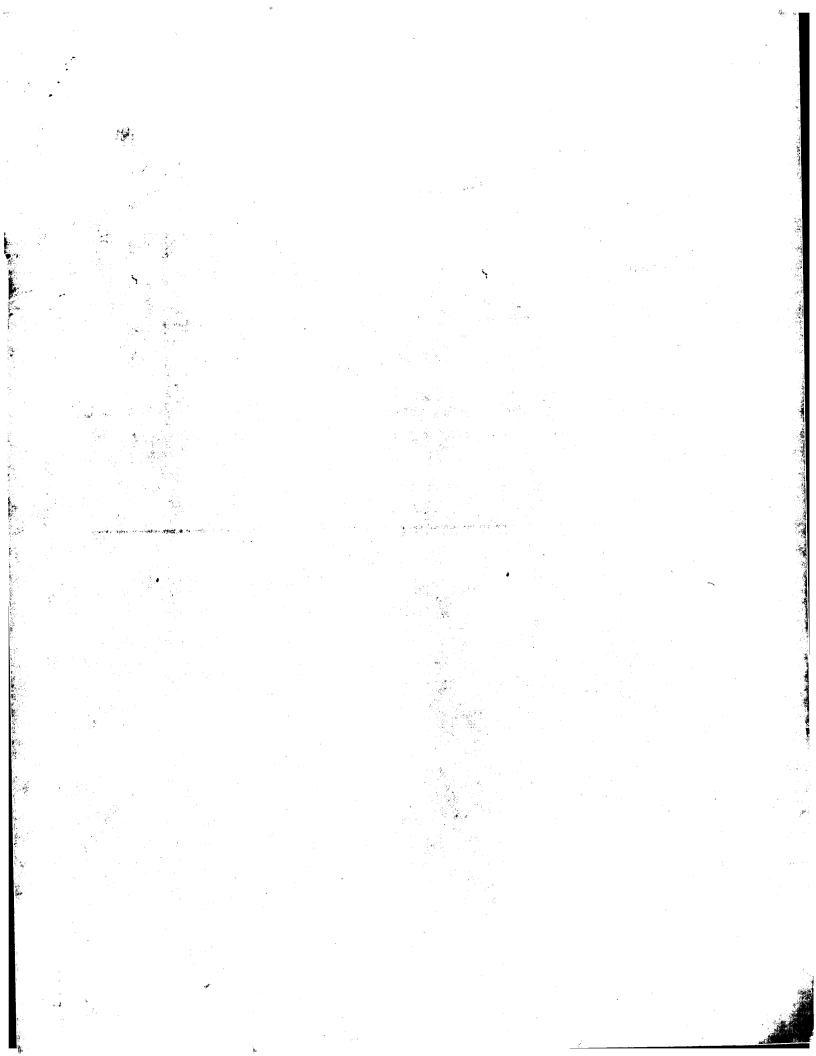
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FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
TYPE: amino acids
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Patent No. 6342593
GENERAL INFORMATION:
Query Match
Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRAELSQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Plowman, Gregory
APPLICANT: Peles, Elor
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8
                                                                                                                MOLECULE TYPE:
                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                TYPE: amino acid
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Sequence Sequence

Description Sequence

67.5 67.5 67.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents AA:*

1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,

/cgn2_6/ptcdata/1/laa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/laa/backfiles1.pep:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Sequence: Perfect score:

Scoring table:

BLOSUM62

1 MMSKQPVSNVRAIQANINI......NLSEIQNIKSELKYVPKAEQ

US-09-647-019-4

Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues

Run on:

OM protein - protein search, using sw model

Copyright

GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.

April 9,

2003, 12:33:56 ; Search time 16.6774 Seconds (without alignments)
155.253 Million cell updates/sec

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RESULT 3
PCT-US95-05008-8
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                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                 -08-426-509A-8
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWAKE: SUCCURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/426,509A
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1181 SSPPP---
                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gishizsky,,
                                                                                                                  173
                                                         220 VALYDYMP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON OPERATING SYSTEM: FastSE
                                                                                                                                       23 GAFRPGAGQPPRRKECTPEVEEGVPPTSDEE---KKPIPGAKKLPGPA---VNLSEIQNI 76
                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 21-APR-1995
                                                                                    77 KSELKYVP 84
                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York,
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                          GSLKPGSS---HRKTKKP-----LPPTPEEDQILKKPLP----PEPAAAPVSTSELKKV 219
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Pred. No. 3
                                                                                                                                                                       Mismatches
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                                                                                                          RESULT 4
US-08-301-162-2
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; TOPOLOGY: unknown ; MOLECULE TYPE: protein PCT-US95-05008-8
                                                                                                                      Sequence 2, Application US/08301162 Patent No. 6022546
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.0%; Score 73.5; DI Best Local Similarity 32.4%; Pred. No. 3.1; Matches 22; Conservative 13; Mismatches
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                                                                              GENERAL INFORMATION: APPLICANT: Knapp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
  APPLICANT: Kupper, Hans
TITLE OF INVENTION: Toxo
TITLE OF INVENTION: Prep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                              173 GSLKPGSS---HRKTKKP-----LPPTPEEDQILKKPLP-----PEPAAAPVSTSELKKV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        220 VALYDYMP 227
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                                                                                                                                                                                                                                                                                                                                                  23 GAFRPGAGQPPRRKECTPEVEEGVPPTSDEE---KKPIPGAKKLPGPA---VNLSEIQNI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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Y: U.S.A.
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                                                        Knapp, Stefan
Ziegelmaier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugen, Inc.
515 Galveston Drive
Redwood City, California 94063-4720
United States of America
Wissenschaften E.V.
Hofgarten Str. 2
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  Toxoplasma Gondii Antigens, Preparation Thereof and the
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The
Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 659;
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MEDIUM TYPE: Floppy disk

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US-09-461-240-2
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Matches
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Patent No. 6326008
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/ACENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 392 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Rel-ease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  207 ELPPP-----TEQELAPSTEQ 222
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                   62 KLPGPAVNLSEIONIKSELKYVPKAEO 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner
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ZIP: 20005-3315
COMPUTER READABLE FORM:
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow,
                                                                                                                                                                     TITLE OF INVENTION: Toxoplasma Gondii Antigens, Preparation Thereof and the
                                                                                                                                                        NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                    APPLICANT: Knapp, Stefan
Ziegelmaier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                               Dunner
STREET: 1300 I Street,
CITY: Washington
                                COUNTRY: USA
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Pred. Nb. 2.4;
3; Mismatches 2
                                                                                   N. W. ,
                                                                                   Suite 700
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RESULT 6
US-09-968-927-2
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TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 ELPPP-----TEQELAPSTEQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 NAQELPPPNVQEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/301,162
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/167,128
FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 02481.1005-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 KLPGPAVNLSEIQNIKSELKYVPKAEQ 88
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108 21; Conservative
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COUNTRY: USA
ZIP: 2005-3315
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNMEER: US/09/968,927
FILING DATE: 03-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knapp, Stefan
Ziegelmaier, Robert
Kupper, Hans
TITLE OF INVENTION: Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      Dunner
STREET: 1300 I Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/461,240 FILING DATE: 16-Dec-1999
                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 392 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.7%; Score 72; DB 4; Length 392; 24.1%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma Gondii Antigens, Preparation Thereof and the
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Use Thereof
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PRIOR APPLICATION DATA

CLASSIFICATION: <Unknown>

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                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kupper, Hans
TITLE OF INVENTION: Toxc
TITLE OF INVENTION: Prep
                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 NAQELPPPNVQEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 ELPPP-----TEQELAPSTEQ 222
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                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
APPLICATION NUMBER:
                              APPLICATION NUMBER:
                                                    FILING DATE:
                                                                   APPLICATION NUMBER:
                                                                                                                      FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                         20005-3315
                                                                                                                                                                                                                                                                                                                        Washington
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/301,162 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/167,128 FILING DATE: <Unknown>
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1300 I Street, N.W.,
                                                                                                                                                                                                                                                                                        USA
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                06-DEC-1990
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24.1%;
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Preparation Thereof and the
20
                               US 07/623,086
                                                                   US/08/167,128
                                                                                                                                       US/08/301,162
DE P3940598.2
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Use Thereof
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 ELPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KLPGPAVNLSEIQNIKSELKYVPKAEQ
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                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                        APPLICATION NUMBER: US/08/167,128
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/461,240
FILING DATE: 16-Dec-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM_PC compati
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Knapp, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                    NAME: Fleshner, Raz E. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/301,162 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09461240
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24.1%; Pred. No. 2.
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                                      02481.1005-00000
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US-09-968-927-18
; Sequence 18, Application US/09968927
; Patent No. 6419925
; GENERAL INFORMATION:
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MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-461-240-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.7%; Score 72; DB 4; Length 428; Best Local Similarity 24.1%; Pred. No. 2.6; Matches 21; Conservative 13; Mismatches 25; Indels
                                                                                            REGISTRATION NUMBER: 34,331
REGISTRATION NUMBER: 02481.1005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,927
FILING DATE: 03-0ct-2001
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/301,162
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/167,128
FILING DATE: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
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Kupper, Hans
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
Preparation Thereof and the Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knapp, Stefan
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                                               TOPOLOGY: linear
                                                                 LENGTH: 428 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunner
STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PPPNVQELPPPTEQELPPPTEQELPP-PTEQ 198
      18:
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Best Local Similarity
Matches 21; Conserv
                                                                                                                             Query Match
Best Local Similarity 36.0
Matches 25; Conservative
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Patent No. 5721354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CBerr, Luann
REGISTRATION UNMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
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APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
181 GRAKDKPK 188
                                                              126 RPGHGDDPDRVICEIVESPPVSAPTVSVPPPSBESHQPVIP---
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                                 78 SELKYVPK 85
                                                                                        26 RPGAGQPPRRKEC----TPEVEE---GVPPTSDEEKKP-IPGAKKLPGPAVNLSEIQNIK 77
                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..257 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/4
FILING DATE: March 31, 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                   /label= UL133
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                                                                                                                             Score 70.5; DB 1;
Pred. No. 2.1;
4; Mismatches 26;
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                                                                                                                           Indels 13;
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RESULT 11
US-08-926-922-7
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US-09-253-682-7
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09253682 Patent No. 6040170
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
FILING DATE: September 10, 1997
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NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAADDRESSE: LAADDRESSEE: LAADDRESSEE: LAADDRESSEE: LATTORESE: ADDRESSEE: LATTORESE: TAITORESE: ADDRESSEE: LATTORESE: TAITORESE: T
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TELEPHONE: 510-834-1448
                                                                                              TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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                                                                  ADDRESSEE:
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                                                                  Luann Cserr Attorney at Law
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Pred. No. 2.1;
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US-09-527-657-7
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Patent No. 6291236
GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: 08/926,922
PILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CSETT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 510-839-7810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GRAKDKPK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 RPGHGDDPDRVICEIVESPPVSAPTVSVPPPSEESHQPVIP-----PQPPAPTSEPKPKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..257 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 SELKYVPK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 94610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/527,657

FILING DATE: 17-Mar-2000
                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Spaete, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94610
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USA
                                                                                                                                                                                                                ADDRESSEE: Luann Cserr Attorney at Law STREET: 750 Arimo Avenue
                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                               STATE: CA
                                                                                                                                                                                            CITY: Oakland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%;
                                                                                                                                                                                                                                                                                                       Tai-An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= UL133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.5; DI
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/926,922 FILING DATE: September 10, 1997

```
# EARLIER APPLICATION NUMBER: 09/086,503
# EARLIER FILING DATE: 1998-05-28
# NUMBER OF SEQ ID NOS: 55
# SOPTWARE: FASTSEQ for Windows Version 3.0
# SEQ ID NO 55
# LENGTH: 667
# TYPE: PRT
# ORGANISM: Toxoplasma gondii
US-09-303-064-55
                                                                                                                                                                                                                                                                                           APPLICANT: MUNT, Jeffery C.
APPLICANT: HUNT, Jeffery C.
APPLICANT: BROJANAC, Susan
APPLICANT: BROJANAC, Susan
APPLICANT: CHOVAN, Linda B.
APPLICANT: CHOVAN, Linda B.
APPLICANT: CHOVAN, Linda B.
APPLICANT: HOWARD, Lawrence V.
APPLICANT: HOWARD, Lawrence V.
APPLICANT: REMINITY, Stephen F.
APPLICANT: REMINITY, Stephen F.
APPLICANT: RABUJO, Fausto
APPLICANT: SUZUKI, Yashuhiro
APPLICANT: LI, Shuli
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THE
FILE REFERENCE: 6361.US.P1
CURRENT APPLICATION NUMBER: US/09/303,064
CURRENT FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein

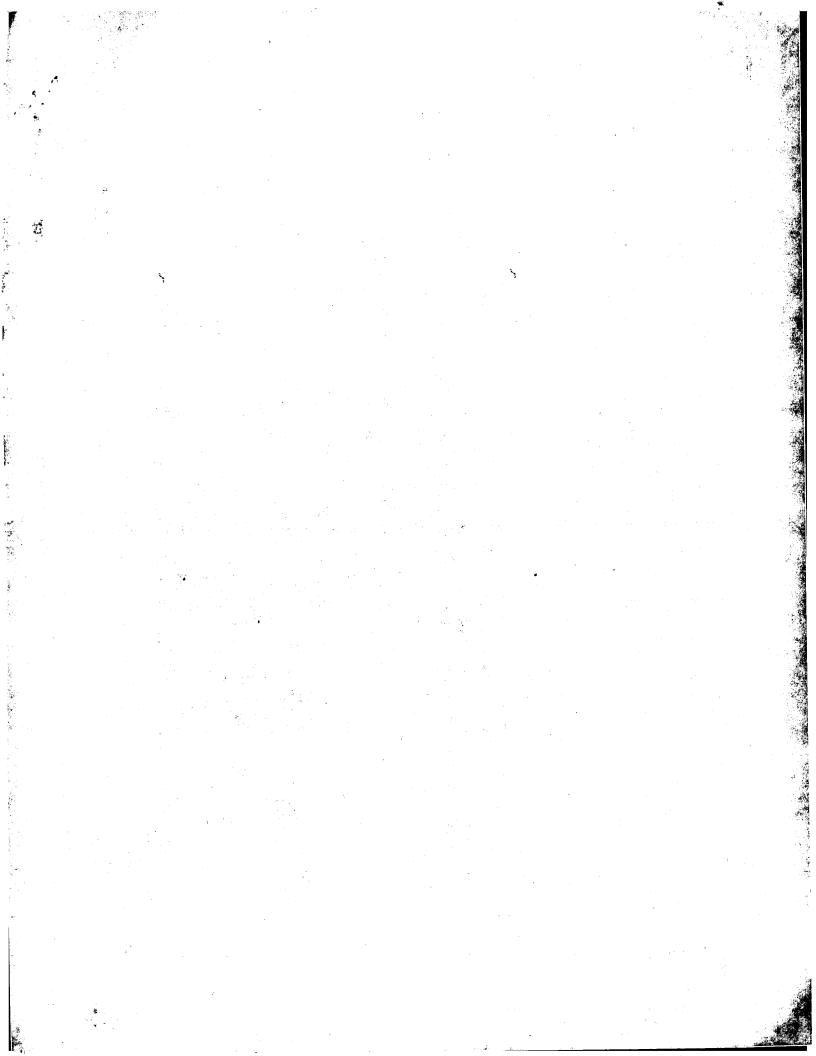
LOCATION: 1..257

OTHER INFORMATION: /label= UL133

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-527-657-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ફ
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US-09-303-064-55
Query Match
Best Local Similarity 24.1
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.8
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 55, Apparent No. 6221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CBETT, LUBIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEPHONE: 510-839-7810
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GRAKDKPK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 RPGHGDDPDRVICEIVESPPVSAPTVSVPPPSEESHQPVIP-----PQPPAPTSEPKPKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 SELKYVPK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 RPGAGQPPRRKEC----TPEVEE---GVPPTSDEEKKP-IPGAKKLPGPAVNLSEIQNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 257 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: CBerr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09303064
           15.3%; Score 70; DB 4; Length 667; 24.1%; Pred. No. 7.7; ative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 70.5; DB 4; Length 257; 36.8%; Pred. No. 2.1; tive 4; Mismatches 26; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 13;
             28;
           Gaps
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APPLICANT: HUNT, Jeffery C.
APPLICANT: HUNT, Jeffery C.
APPLICANT: BROJANAC, Sugan
APPLICANT: CHOVAN, Linda E.
APPLICANT: CHOVAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, LAWTENCE V.
TITLE OF INVENTION: ANTIGEN COCKTAILS AND USES THE FILE REFERENCE: 6361.US.01
CURRENT APPLICATION NUMBER: US/09/086,503A
CURRENT APPLICATION NUMBER: US/09/086,503A
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 55
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-086-503-55
Search completed: April Job time : 18.6774 secs
                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-086-503-55
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Best Local (
                                                                                                                                                                                                                                                       Matches
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Patent No. 6329
                                                                                                                                                               303 NAQELPPRIVQEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 ELPPP-----TEQELPPSTEQ 361
                                                                                                                   62 KLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 15.3%; Score 70; DB 4; Length 667; Local Similarity 24.1%; Pred. No. 7.7; Local Similarity 24.1%; Pred. No. 7.7; Indels
                                                                                                                                                                                 2 NMSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPGAK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KLPGPAVNLSEIQNIKSELKYVPKAEQ 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09086503A
               9, 2003, 12:40:31
                                                                                                                                                         -----PPPNVQELPPPTEQELPPPTEQELPP-PTEQ 345
                                                                                                                                                                                                                                          28;
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Regult
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                          score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                               Pred. No.
                                                                                                                     is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248812 seqs, 61136040 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-647-019-4
459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNMSKQPVSNVRAIQANINI......NLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248812
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No.	Score	Query	Query Match Length	DB	ID	Description
1	84	18.3	523	5	US-09-799-777-76	Sequence 76, Appl
N	76.5	16.7	603	10	US-09-906-779-4	٠.
ω	76.5	16.7	1274	9	US-10-020-215-2	~
4.	73.5	16.0	659	ø	US-09-977-260-8	Φ.
ຫ	73.5	16.0	659	9	US-10-045-202-2	Sequence 2, Appli
0	73.5	16.0	659	ø	US-09-977-261-8	ω.
7	73.5	16.0	659	10	US-09-977-269-8	œ
8	70	15.3	667	10	US-09-896-852-55	Sequence 55, Appl
9	68.5		978	10	US-09-815-242-5456	
10	68.5	14.9	1001	10	US-09-815-242-12686	Sequence 12686, A
1	68		196	10	US-09-858-664A-16	Sequence 16, Appl
12	69		247	9	US-09-981-353-95	Sequence 95, Appl
13	68	14.8	280	10	US-09-925-300-1411	Sequence 1411, Ap
14	67.5	14.7	2441	12	US-10-109-886-8	
15	67	14.6	180	10	US-09-864-761-45128	
16	67	14.6	437	10	US-09-864-761-36083	
17	66.5	14.5	238	10	US-09-864-761-34591	
18	66.5	14.5	2005	10	US-09-735-367B-3	
19	66.5	14.5	2063	10	US-09-735-367B-2	ν,

4 U	;	44	43	42	41	40	39	38	37	36	ه 35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
6	;	62	62	62	62.5	63	63.5	63.5	63.5	63.5	64.5	64.5	64.5	64.5	64.5	65	65	65	65	65	65	65.5	65.5	65.5	65.5	65.5
13.5		13.5	13.5	13.5	13.6	13.7	13.8	13.8	13.8	13.8	14.1	14.1	14.1	14.1	14.1	14.2	14.2	14.2	14.2	14.2	14.2	14.3	14.3	14.3	14.3	14.3
808	, ,	771	603	546	1907	360	930	466	403	212	630	559	468	212	212	2266	1530	774	616	546	363	659	512	512	512	108
v	, ,	ø	ø	10	9	9	9	10	5	10	ø	۲	10	10	9	9	9	9	9	10	ب	9	5	ø	9	10
US-10-108-605-127		US-09-982-107-8	US-09-764-868-705	US-09-839-743-3	US-09-832-292-39	US-10-149-819-6	US-10-113-794A-1	US-09-925-301-1355	US-09-731-872-249	US-09-733-507-12	US-09-742-096-5	US-08-781-986A-5251	US-09-884-260A-53	US-09-925-300-1577	US-09-742-096-25	US-10-118-513A-14	US-10-118-513A-6	US-10-162-706-5	US-10-243-735-4	US-09-901-884-5	US-08-781-986A-5237	US-10-045-202-4	US-09-977-269-16	US-09-977-261-16	US-09-977-260-16	US-09-864-761-35589
Sequence 127, App		Þ	Sequence 705. App	Sequence 3, Appli	Sequence 39, Appl	Sequence 6, Appli	Sequence 1, Appli	S	249,	Sequence 12, Appl	Sequence 5, Appli		Sequence 53, Appl	e 15	25,	Sequence 14, Appl	Sequence 6, Appli	Sequence 5, Appli	· ·	Sequence 5, Appli	52	•	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 35589, A

ALIGNMENTS

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US-09-799-777-76
US-09-799-777-76
Sequence 76, Application US/09799777
Patent No. US2002091244A1

GENERAL IMPORMATION:
Hilman, Jennifer L.
CORLEY, Nail C.
GENERAL IMPORMATION: HILMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OSS/MS-DOS
OPERATING SYSTEM: PC-OSS/MS-DOS
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OSS/MS-DOS
OPERATING S
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; SEQ ID NO 4
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-779-4
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                                                                                                                                                                                                                   RESULT 3
US-10-020-215-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-906-779-4
                                                                                                                                                           Sequence 2, Application US/10020215 Publication No. US20030008347A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Shi et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09906779
Patent No. US20020064844A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                     APPLICANT: PLOWMAN, GREGORY
APPLICANT: PELES, BIOR
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 038602/1290
CURRENT APPLICATION NUMBER: US/10/020,215
CURRENT FILING DATE: 2001-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/906,779
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US01/01563
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/176,306
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 09/095,443
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/049,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Protein Tyrosine Phosphatase Polynucleotides, Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PT040P1
                                                                                                                                                                                                                                                                                       461 PISSIQATIAKLSIRPPGGLESPVASLPGPAEPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 SSQTPFP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 PISSIQATIAKLSIRPPGGLESPVASLPGPAEPP---
                                                                                                                                                                                                                                                                                                                         60 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AKKLPGP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 32.8
mes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 3125156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 523 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: LNODNOT05
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76.5; DB
Pred. No. 3.8;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84; DB 10
Pred. No. 0.52;
10; Mismatches
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                                                                                                             ALP RELATED DISORDERS
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                                                                                                                                                                                                             US-10-045-202-2
                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                   Sequence 2, Application US/10045202
Publication No. US20030040461A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: 1
                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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APPLICANT: ULLRICH, AXEL
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APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
CURRENT APPLICATION NUMBER: US/09/977,260
CURRENT FILING DATE: 2001-10-16
                                                   APPLICANT: Bristol-Myers Squibb
APPLICANT: Bristol-Myers Squibb
APPLICANT: Bristol-Myers Squibb
TITLE OF INVENTION: MODULATORS OF BRUTON'S TYROSINE KINASE AND BRUTON'S TYROSINE KINATITLE OF INVENTION: INTERMEDIATES AND METHODS FOR THEIR IDENTIFICATION AND USE IN TITLE OF INVENTION: PREVENTION OF OSTEOPOROSIS AND RELATED DISEASE STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-06-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/10/045,202
CURRENT FILING DATE: 2002-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
                                     FILE REFERENCE: D0032 NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                      227
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Pred. No. 9.4;
13; Mismatches
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sequence
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; ORGANISM: Homo sapiens
US-09-977-261-8
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US-09-977-261-8
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US-10-045-202-2
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SEQ ID NO 8
LENGTH: 659
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Publication No. US20030054527A1
GENERAL INFORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
                                                                                                                                                                           Sequence 8, Application US/09977269
Patent No. US20020082037A1
GENERAL INFORMATION:
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SEQ ID NO 2
LENGTH: 659
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                                         APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTJC PROTEIN TYROSINE KINASES
PILE REFERENCE: 038602/1260
CURRENT APPLICATION NUMBER: US/09/977, 269
CURRENT FILING DATE: 2001-10-16
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CURRENT APPLICATION NUMBER: US/09/977,261
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
           CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
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PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 12
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APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
NUMBER OF SEQ ID NOS: 24
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NUMBER OF SEQ ID NOS: 24
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nes 22; Conservative
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Local Similarity 32.4%;
nes 22; Conservative 1
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; Pred. No. 8.7;
13; Mismatches
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Pred. No. 8.7;
.3; Mismatches
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US-09-815-242-5456
; Sequence 5456, Application US/09815242
; Patent No. US20020061569A1
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US-09-896-852-55
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-269-8
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APPLICANT: Maine, Gregory T.
APPLICANT: Hunt, Jeffery C.
APPLICANT: Brojanac, Susan
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 55
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 667
TYPE: PRT
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Best Local Similarity 32.4
Matches 22; Conservative
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Patent No. US20020025542A1
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                                          APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jhy-Tsing Sheu, Michael
APPLICANT: Chovan, Linda E.
APPLICANT: Tyner, Joan D.
APPLICANT: Howard, Lawrence V.
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35,
FILE REFERENCE: 6361.US.D1
CURRENT APPLICATION NUMBER: US/09/896,852
CURRENT FILING DATE: 2001-06-29
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                    APPLICANT:
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                                                                                                                                                                                                                                                                 346 ELPPP-----TEQELPPSTEQ 361
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les 21; Conserv
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                Carr, Grant J.
Yamamoto, Robert T
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H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB:
Pred. No. 20;
13; Mismatches
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Pred. No. 8.7;
13; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                      PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                             PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Local Similarity 31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T
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Pred. No. 47;
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SEQ ID NO 12686
• LENGTH: 1001
                                                                                                                                                                                                         Sequence 95, Applica Patent No. US2002016 GENERAL INFORMATION:
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                               SOFTWARE: PERL Program
SEQ ID NO 95
LENGTH: 247
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CURRENT APPLICATION NUMBER: US/09/858,664A
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 09/711,134
PRIOR FILING DATE: 2000-11-11
                                                                                CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
                                                                                                                                       APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON
FILE REFERENCE: PA-0038 US
                                                                                                                                                                        APPLICANT: Lasek, Amy W. APPLICANT: Jones, David
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
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                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      61 KKLPGP---AVNLS 71
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26; Conservative
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Pred. No. 48;
7; Mismatches
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RESULT 14
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US-09-925-300-1411
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// OTHER INFORMATION: Incyte ID No. US20020160382A1 2054053CD1
US-09-981-353-95
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10109886
Patent No. US20020119499A1
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                               TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND TITLE OF INVENTION: ANTAGONIST TO PPAR FILE REPERENCE: TANIGUCHI-6 CURRENT APPLICATION NUMBER: US/10/109,886 CURRENT FILING DATE: 2002-04-01 PRIOR PILICATION NUMBER: 09/514,247 PRIOR PILICATION NUMBER: 09/514,247 PRIOR PILING DATE: 2000-02-28 PRIOR APPLICATION NUMBER: PCT/JP98/03734 PRIOR FILING DATE: 1998-08-24 PRIOR FILING D
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SEQ ID NO 1411
LENGTH: 280
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Best Local Similarity
                     PRIOR APPLICATION NUMBER: JP231084/1997 PRIOR FILING DATE: 1997-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
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OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steve Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 68; DB 10; Length 280 31.9%; Pred. No. 11;
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Pred. No. 9.7;
14; Mismatches
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; LENGTH: 2441
; TYPE: PRT
; ORGANISM: mouse
US-10-109-886-8
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PRIOR PILLING DATE: 2000-02-04
PRIOR PEPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 04263.6
PRIOR APPLICATION NUMBER: US 06/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 07/US01/00666
PRIOR APPLICATION NUMBER: US 07/US01/00666
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                                                 PRIOR FILING DATE: 2000-09-21
FRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                           PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1975 RANINNGMPPGRDGMGTPGSQMTPVGLNVPRPNQVSGPVMSSMPP-GQWQQAPIPQQQPM 2033
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00661
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o. US20020048763A1
Annomax Sequence Listing Engine
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Hanzel, David K.
Chen, Wensheng
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Pred. No. 1.8e+02;
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Page 6
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB
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seq length: 2000000000
A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to l score greater than or equal to the score of the result being and is derived by analysis of the total score distribution to have being pr printed,

SUMMARIES	
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10	00 <	1 ON UT	1.4-1	- מי	Result No.
76.5	78.5 77	84	274	459 451	Score
16.7	16.8	19.6	59.7	100.0	Query Match Length DB
691	1098	143 523	75	888	Length
222	22	22	200	20	DB .
AAU04485 ABB03068	AAY53666 ABG20365	AAV21855 AAY21855	AAY28650 AAY28834	AAY28651 AAE16632	ID
Human protein tyro Human expressed po	Sequence gi/101742 Novel human diagno	Novel human secret Human signal pepti	Murine chisel (Csl Xenopus chisel (Cs	Human chisel (Csl) Human 66214 protei	Description

(CHAN-) CHANG CARDIAC RES INST VICTOR. (GEHO) GEN HOSPITAL CORP. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

27-MAR-1998; 26-MAR-1999; 07-OCT-1999. WO9950410-A1. Homo sapiens.

98AU-0002634. 99WO-AU00220

human se	AAU30349	22	188	15.0	69	45
protein	AAB95327	22	452	15.1	69.5	44
	AAB95276	22	452	15.1	69.5	ι W
protein s	AAB92644	22	452	15.1	69.5	42
TT.	ABB50737	22	452	15.1	69.5	41
	AAW88812	20	452	٠	69.5	40
thali	AAG09575	21	202	15.1	69.5	39
	AAG73842	22	197	15.1	69.5	88
fusio	AAY57754	21	654	٠	70	37
	AAG26404	21	172	15.3	70	36
Arabidopsis thalia	AAG26405	21	151	15.3	70	35
	AA006906	22	146	15.3	70	34
റ	AAW05502	17	257	15.4	70.5	33
	ABB58382	22	3502		71	32
	ABB63768	22	874	•	71	31
Human ÖRFX ÖRF1406	AAB41642	21	131	•	71	30
7	AA004777	22	91	15.5	71	29
	ABB58108	22	515	•	71.5	28
	AAR12352	12	428	•	72	27
ipooc	AAR12345	12	392	15.7	72	26
dopsis thali	AAG49497	21	222	15.7	72	25
Novel human secret	AAU33195	22	2153	15.8	72.5	24
Ę	ABB58850	22	1178	•	72.5	23
Human Bruton's tyr	ABB76487	23	659	•	73.5	22
ָם פּ	AAR94534	17	659	•	•	21
Human Bruton's tyr	AAU09009	22	635	•	٠	20
Ω.	AAG24005	21	191	٠	73.5	19
-	AAB94408	22	870	٠	74	18
human diac	ABG27048	22	249	16.1	74	17
histidin	AAB29661	21	1636	16.7	76.5	16
tyrosi	AAB29662	21	1583	16.7	•	15
ALP. Hor	AAW89253	20	1274	16.7	•	14
tyrosine	AAB29664	21	1264	16.7	•	13
_	AAB29663	21	1253	16.7	76.5	12
Novel human enzyme	AAU23180	22	691	16.7	•	11

ALIGNMENTS

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RESULT 1
AAY28651
ID AAY2
Chisel protein; Cs1; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; regulation; Xq21.3-q22; adaptive process; muscle homeostasis; cardiac hypertrophy; detection; diagnosis; prophylaxis; treatment; differentiation; nucleus; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; skeletal myopathy; Becker's myotonic dystrophy; heart failure; transgenic animal; drug screening; gene therapy; homology; scallop regulatory myosin light chain.
                                                                                                                                                                                                                                                                                                                         Human chisel (Csl) protein.
                                                                                                                                                                                                                                                                                                                                                     17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                AAY28651;
                                                                                                                                                                                                                                                                                                                                                                                                       AAY28651 standard; Protein; 88
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RESULT 2
AAE16632
THE REPORT OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart desease; pericardial disease; congenital heart disease; yene therapy; syncope; transgenic animal; expressed sequence tag; EST; 66214 protein.
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N-PSDB; AAX90904.
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                                                                                                                                                                                             30-MAY-2001;
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                                         (MEDI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 3; 157pp; English
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Pred. No. 1.5e-40;
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary heart disease, congenital heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present sequence is 66214 protein encoded by an expressed sequence tag (EST) DNA.
                                                                                                                                                                                 Chisel protein; CB1; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably human for a heart disease or for an acute state of such a disease. It is all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful to treat diseases of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardio-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1a; Fig 9c; 154pp; English
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                                                                                                                                                        Mus sp
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Pred. No. 1.1e-39;
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27-MAR-1998; 26-MAR-1999;

98AU-0002634 99WO-AU00220

RES INST VICTOR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the murine chisel protein (Csl), that is a common control of the EF-Hand protein is super family and is involved in signalling pathways. Csl protein is localised to the nucleus and does not show significant homology to any known protein. Structural homology between Csl and scallop regulatory myosin light chain is however detected. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle condifferentiation or adaptive processes that maintain muscle chambers and the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those convolving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, skeletal myopathies such as Duchenne muscular dystrophy, myocarditis, myofiber atrophy, heart failure, carddac hypertrophy, myocarditis, cmyofiber atrophy, etc. The Csl gene sequence can also be used in gene to therapy, for the production of transgenic animals and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                            Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; xenopus; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; buchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heat failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain.
                                                                      07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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            26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus chisel (Csl) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY28834 standard; Protein; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                               WO9950410-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPGPVVNLSEIQNVKSELKFVPKGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPGPAVNLSEIQNIKSELKYVPKAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-610852/52
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GEN HOSPITAL CORP
HALL INST MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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            99WO-AU00220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES WALTER & ELIZA.
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Pred. No. 1.4e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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RESULT 5
AAU32495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the xenopus chisel protein (Cs1), that is a C member of the EF-Hand protein super family and is involved in signalling pathways. Csl protein is localised to the nucleus and does not show cs significant homology to any known protein. Structural homology between CC sl and scallop regulatory myosin light chain is however detected. It is compared to the differentiation of cells. Csl functions in regulation aspects of differentiation or cells. Csl functions in regulation aspects composition in the detection, diagnosis, csp from the differentiation or adaptive processes that maintain muscle chameostasis. This sequence can be used in the detection, diagnosis, csp prophylactic and therapeutic treatment of diseases such as those ccl involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, cs keletal myopathies such as Duchenne muscular dystrophy, and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, cm myofiber atrophy, etc. The Csl gene sequence can also be used in gene creating.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating muscular
                                                                                                                                                           Human; vaccination; gene stem cell proliferation; immune suppression; immur
                                                                                                                                                                                                                        Novel human secreted protein #2986.
                                                                                                                                                                                                                                                                                                                   AAU32495 standard; Protein; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids encoding chisel, used to develop products treating cardiomyopathy, cardiac hypertrophy, heart failure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvey RP,
                                                                                                     WO200179449-A2
                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                          18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610852/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHAN-)
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                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                          59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 MSKOPVSNVRAIQANINIPMGAFRPGAGOPPRRKECTPEVEEGVP-PTSD---EEKKPIP
                                                                                                                                                                                                                                                                                                                                                                                                               GAKKLPGPAVNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSKQPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPIP
                                                                                                                                                                                                                                                                                                                                                                                             GAVKLPGPAFNLSE
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GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myopathies -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98AU-0002634.
                                                                                                                                                           gene therapy; nutritional supplement;
tion; haematopoiesis; nerve tissue regeneration;
immune stimulation; anti-inflammatory; leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%;
75.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmer SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274; DB 20;
No. 2.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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18-APR-2000; 2000US-0552929 26-JAN-2001; 2001US-0770160

16-APR-2001; 2001WO-US08656

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RESULT 6
AAY21855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in toone, cartilage, tendon and/or nerve tissue growth or regeneration; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid in treatment of leukaemias. AAU29510-A5133304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 26
                                                                                                                                                                         ulcerative colitis; atopic dermatitis; dermatomyositis; emphysema; diabetes mellitus; atrophic gastritis; glomerulonephritis; gout; trauma; Grave's Disease; hypereosinophilia; irritable bowel syndrome; infection; lupus erythematosus; multiple sclerosis; myasthenia gravis; inflammation; osteoarthritis; osteoporosis; pancreatitis; polymyositis; scleroderma; osteoarthritis; osteoporosis; pancreatitis; polymyositis; scleroderma;
                                                                                                                                                                                                                                                                                     Signal-peptide containing protein; SIGP; human; cancer; immune response; addenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 623; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                      08-JUL-1999.
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          Human signal peptide-contianing protein (SIGP) (clone ID 3125156).
                                                                                                                                                                                                                                                                                                                                                                                                                                       20-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY21855 standard; Protein; 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in treatment of leukaemias. AAU29510-AAU33304 represent the sequences of novel human secreted proteins of the invention
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                                                                               WO9933981-A2
                                                                                                                                                                 rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 PVRASSNDSFEQSIKAEIE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 GAFREGAGOPERR----KECTPEVEEGVEPTSDEEKKPIPGAKKLPGPAVNLSE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IQNIKSELK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                            Sjogren's
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Pred. No. 0.089;
8; Mismatches
                                                                                                                                                               syndrome;
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22-DEC-1998;

98WO-US27598.

25-NOV-1999

Unidentified

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AAY53666
IID AAY5
XX
XX
AC AAY5
AC Sequ
DT 22-F
XX
DT Sequ
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DE Sequ
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XX
Mech
KW Mech
KW bone
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SO Unid
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PN W099
XX
PD 25-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR (AAY21841-855) and polymucleotides (AAX82076-90) encoding the proteins (SIGP) CR (AAY21841-855) and polymucleotides (AAX82076-90) encoding the proteins. CR (AAY21841-856) and be computed to conjuncture of the SIGP protein can be used to revent a cancer. An antagonist of the SIGP protein can be used to treated or prevented include sarcomas, adenocarcinomas, leukemia's, lymphomas, melanomas, bladder, concers of the adrenal gland, bladder, concers of the adrenal gland, bladder, concers (CR (CR)) bone marrow, brain, breast, cervix, gall bladder, ganglia, creation, breast, cervix, gall bladder, ganglia, creation, breast, cervix, gall bladder, ganglia, creation, breast, creation, gallone, covary, concers, parathyroid, and uterus. The immune responses that can be created or prevented include, AIDS, Addison's disease, adult respiratory concentration, cholecystitus, Crohn's disease, understive colitis, atopic concernatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic creatitis, glomerulonephritis, Grave's disease, unltiple sclerosis, constitutis, osteoporosis, pancradial inflammation, rheumatoid creativitis, scleroderma, Sjogren's syndrome, and autoimmune thyroditis, complications of cancer, infections, and trauma.
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Best Local (
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N-PSDB; AAX82090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human signal-peptide containing protein coding sequences used treat cancer and immune responses
                                                                                                                                                                          Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608
                                                                                                                                                                                                                                                                                              AAY53666 standard; Protein; 4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 88-89; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-1997;
                                                                                                               Mechanical stress; gene therapy; protein 608; osteoporosis; bone density; bone development; gi/1017427/emb/CAA62189.
                                                                                                                                                                                                                   22-FEB-2000
                                                                                                                                                                                                                                                         AAY53666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                           484 SSQTPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 PIŚSIQATIAKLSIRPPGGLESPVASLPGPAEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AKKLPGP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley NC,
Shah P;
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB 2
Pred. No. 1.6;
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPPASLPESTPIPS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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RESULT 8
ABG20365
   The present sequence is obtained from a clustral X alignment with CC protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the CC 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the CC identification of genes responsive to a specific mechanical stress. The CC method comprises applying the mechanical stress to an organism (tissue CC or cells comprising bone cells), isolating the specific cellular CC fractions and extracting mRNA from them, and differentially analysing the CC genes whose expression is responsive to a specific stress. The identified genes whose expression is responsive to a specific stress. The identified CC genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or CC disease state. The risk determination methods are used for testing a cC medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating to osteoporosis or controlling a physiological or disease state (especially osteoporosis or the symptoms or other factors causing or contributing to osteoporosis or class symptoms or other conditions involved in mechanical stress or its bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3735 PPKKPEVTPVKVPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVPKVAVPEKKVPEA 3790
                               31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensions of supplement; medical imaging; diagnostic; genetic disorder
(HYSE-) HYSEQ INC
                                                                                                                       11-OCT-2001
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                               13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   ABG20365 standard; Protein; 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of stress induced genes for determining risk and preventing, treating or controlling osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (QUAR-) QUARK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 PPRRKECTP-EVEEGVPPTSDEEKKPIPGAKKLPGPAVNLSEIQNIKSELKYVPKA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development.
                                                                                                                                                                                                                                                                            human diagnostic protein #20356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Fig 6A-R; 308pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4412 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78.5;
Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Homo sapiens.

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RESULT 9
AAU04485
ID AAU0
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AC AAU0
XX
AC AAU0
XX
DT 26-S
XX
DT 26-S
XX
DE Huma
XX
Prot
KW Alzh
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KW Tour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at first polynument of the printed specification, but was obtained in electronic format directly from WIPO at first polynuments.
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Matches
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                                                                                                                                              Protein tyrosine phosphatase; PTPase; human; nervous system; dementia; Alzheimer's disease; Huntington's disease; Parkinson's disease; autism; Tourette's syndrome; obsessive compulsive disorder; schizophrenia; mania cardiovascular disorder; atherosclerosis; myocarditis; Addison's disease; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; vitiligo; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; vitiligo; ankylosing spondylitis; Sjogren's syndrome; asthma; atopic dermatitis; diabetes mellitus; inflammatory disorder; pancreatitis; sarcoidosis; allogenic transplant rejection; multiple myeloma; Burkitt's lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein tyrosine phosphatase (PTPase) polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU04485 standard; Protein; 603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                eukaemia; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMSKQPVSNVRAIQANINIPMGAFRP---GAGQPPRRKECTPEVEEGVPPT----SDEE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTPRP----PAPA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKPIPGAKKLPGPA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                neoplasm
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Pred. No. 19;
7; Mismatches
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                                                                                                                                                                                                                                                                                     disease;
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ARBSULT 10
ARBO3
XX ARBO3
XX ARBO3
XX ARBO3
XX ARBO3
XX O7-JF
XX O7-JF
XX CYtos
KW ARLis
KW Vulns
KW Cardi
KW cardi
KW cardi
KW Ineuro
XX Homo
XX Homo
XX Homo
XX Homo
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autism), cardiovascular disorders (e.g. atherosclerosis and myocarditis), autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, ankylosing spondylitis, Addison's disease, Sjogren's Syndrome, vitiligo, asthma, attopic dermatitis and diabetes mellitus), inflammatory disorders (e.g. pancreatitis, sarcoidosis and allogenic transplant rejection) and cancers and neoplasms (e.g. leukaemia, Burkitt's lymphoma and multiple myeloma). The presence or absence of a mutation in the nucleic acid encoding the protein allows for diagnosis of or susceptibility to a pathological condition. The sequences are also useful in screening for agonists and antagonists of PTPase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a human protein tyrosine phosphatase (PTPase) polypeptide. PTPase proteins and nucleic acids are useful for preventing, treating or ameliorating a medical condition. The medical conditions are disorders of the central and peripheral nervous system (e.g. Alzheimer's disease, Huntington's disease, Parkinson's disease, Tourette's syndrome, disease, Tourette's syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obsessive compulsive disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 283-285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2000; 2000US-0176306.
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                                                                                                                                              Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                     Human expressed polypeptide SEQ
                   02-AUG-2001
                                                    WO200155167-A1
                                                                                                               cardiant; gene
neurological di
                                                                                                                                                                                                                                                       07-JAN-2002
                                                                                                                                                                                                                                                                                                                        ABB03068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                           SSPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PISSIQATIAKLSIRPPGGLESPVASLPGPAEPP
                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS08886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENOME
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                                                                                                                    therapy; cancer; immune disorder; isease; infection; human; secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           -LSSPLPEAPQPKE 527
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                                                                                                                                                                                                                                                                                                                          691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  schizophrenia, mania, dementia and
                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                     ID NO 41.
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                                                                                                                                      cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603;
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                                                                                                                                       disorder,
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Matches
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04-FEB-2000;
26-SEP-2000;
01-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAI99614-AAI99654) and proteins (ABB03062-ABB03085) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's allergies, autoimmune allergies, autoimmune cancer and controllers autoimmune cancer and cancer and controllers autoimmune cancer and controllers autoimmune cancer and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with polypeptides and for treating autoimmune diseases e.g., multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                 Human; oxidoreductase enzyme; transferase; hydrolase; lyase; is
ligase; hyperproliferative disorder; immunodeficiency disorder;
autoimmune disorder; neurological disorder; metabolic disorder;
                                                                                                                                                                                                                                                                AAU23180 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                   AAU23180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549
                                                                                                                                                                                                                                                                                                                                                                                      598 SSPPP------LSSPLPEAPQPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parasitic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691 AA;
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2000US-0251988.
2000US-0251479.
2000US-0251990.
2000US-0254097.
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2000US-0180628.
2000US-0235484.
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                                                                                                                                                                      (first entry)
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                                                                                                                   polypeptide
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27.0%;
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                                                                                                                        #266.
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                                                                                                                                                                                                                                                                     A
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No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      did not form part of the in electronic format directly
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                                                                           isomerase;
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4:

disorder;

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
blood-related nephrotropic; Homo sapiens. WC200155301-A 02-AUG-2001; 11-JAN-2000; 04-FEB-2000; 04-FEB-2000; 04-FEB-2000; 16-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-JUL-2000; 12-JUN-2000; 11-JUL-2000; 11-SEP-2000;
diborder; infect anticoagulant. 2001W0-US01239. 2000US-013065. 2000US-0180628. 2000US-018064. 2000US-021688. 2000US-021688. 2000US-021688. 2000US-021688. 2000US-0225214. 2000US-0225266. 2000US-0225268. 2000US-0231414. 2000US-0231414. 2000US-0231244. 2000US-02323399. 2000US-02332400. 2000US-02332400. 2000US-0234274.
lous disorder; cyt
cytostatic; anti a
arthritic;
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25-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 13-OCT-2000 11-NOV-2000 11-NO
2000US-023583 2000US-023583 2000US-023583 2000US-023583 2000US-023583 2000US-023636 2000US-023636 2000US-023636 2000US-023636 2000US-023636 2000US-023636 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-024178 2000US-024178 2000US-024178 2000US-024417 2000US-024661 2000US-024921
Caller Color

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RESULT 12
AAB29663
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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14-APR-2000; 2000WO-JP02455.
                                                                                                                                                                                                                                                                                                                 Human; histidine domain-protein tyrosine phosphatase; chromosome 3p21.3; gene deletion; tumour suppressor; c
                                                                                                                                                                                                                                                                                                                                                                                                                    Human tyrosine phosphatase HD-PTP cKAL16 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB29663 standard; Protein; 1253 AA.
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                                                                     26-OCT-2000
                                                                                                                                 WO200063392-A1.
                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                   chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic;
lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 SSPPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te: The sequence data for this patent did not form part of the printed ecification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
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27.0%;
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Pred. No. 13;
13; Mismatches
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16-APR-1999;

99JP-0108842.

(KYOW) KYOWA HAKKO KOGYO KK

14-APR-2000; 2000WO-JP02455

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors and host cells containing human HD-PTP nucleic acids; the recombinant production of HD-PTP, anticancer drugs containing HD-PTP; gene therapy compositions containing DNA encoding HD-PTP; diagnostic reagents containing HD-PTP oligonucleotides; antibodies specific for HD-PTP; and an immunoassay method using HD-PTP-specific antibodies for use in cancer diagnosis and investigation. HD-PTP proteins, nucleic acids and antibodies may be used in the treatment, investigation and diagnosis of cancers, particularly those of the lung. The present sequence represents a human HD-PTP fragment encoded by the cKAL16 cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain-protein tyrosine phosphatase (HD-PTP; AAB29661) and to human HD-PTP nucleic acids (AAC81224, AAC812825, AAC81262, AAC81263). The HD-PTP gene is located on chromosome 3p21.3. This region is frequently found to be deleted in lung cancers, and is therefore thought to contain a tumour suppressor gene. The invention also relates to expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tyrosine phosphatase with oncostatic activity encoded frequently deleted in lung cancer, useful for treatment and of tumors -
                                                                                                                                                                                                     Human; histidine domain-protein tyrosine phosphatase; HD-PTP; chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic; lung cancer; tumour; gene therapy; diagnosis; recombinant produc
                                                                                                                                                                                          lung cancer; tumour;
anticancer.
                                                                                                                                                                                                                                                                       Human tyrosine phosphatase HD-PTP cKAL11 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1160 SSPPP----
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                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                          23-FEB-2001
                                                                                                                                                                                                                                                                                                                                          AAB29664;
                                                                                                                                                                                                                                                                                                                                                                        AAB29664 standard; Protein; 1264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel human tyrosine phosphatase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 98-106; 134pp; Japanese
                                                                                             26-OCT-2000
                                                                                                                            WO200063392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                          (first entry)
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27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LSSPLPEAPQPKE 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76.5;
Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                         recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLPPASLPESTPIPS 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1253;
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I diagnosis
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AAW89253
ID AAW89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel human tyrosine phosphatase, histidine cdomain-protein tyrosine phosphatase (HD-PTP; AAB29661) and to human cdomain-protein tyrosine phosphatase (HD-PTP; AAB29661) and to human characteristic acids (AAC81224, AAC81265, AAC81262, AAC81263). The characteristic acids (AAC81224, AAC81265, AAC81263). The contain contain to be deleted in lung cancers, and is therefore thought to contain contain to be deleted in lung cancers, and is therefore thought to contain contain suppressor gene. The invention also relates to expression contain production of HD-PTP; anticancer drugs containing HD-PTP; containing HD-PTP; and an immunoassay method using HD-PTP; algencific for come in cancer diagnosis and investigation. HD-PTP proteins, nucleic acids of cancers, particularly those of the lung. The present sequence represents a human HD-PTP fragment encoded by the cKALII DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 24
                 23-OCT-1997;
28-APR-1997;
20-MAY-1997;
11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             PTP04; PTP05; PTP10; SAD; ALF; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphom neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.
                                                                                                                                                                                                         27-APR-1998;
                                                                                                                                                                                                                                                                8661-AON-50
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW89253 standard; Protein; 1274 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tyrosine phosphatase with oncostatic activity encoded frequently deleted in lung cancer, useful for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of tumors
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           97US-0063595.
97US-0044428.
97US-0047222.
97US-0049477.
97US-0049756.
97US-0049914.
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Pred. No. 25;
13; Mismatches
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diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated, enriched or purified nucleic colds encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The CC present sequence represents human ALP. The above proteins, other than CC ALK-7, are protein tyrosine phosphateases (PTP6) and are used to identify concluding NBP) in vivo or in vitro. These substances are used to treat colding NBP) in vivo or in vitro. These substances are used to treat colding NBP) in vivo or in vitro. These substances are used to treat colding NBP) in vivo or in vitro. These substances are used to treat colding NBP) in vivo or in vitro. These substances are used to treat colding NBP in vivo or in vitro. These substances are used to treat coldinary that involve the proteins, particularly cancer (e.g. leukaemia coldinary), while modulators of ALK-7 (which is a type I receptor coldinary), while modulators of ALK-7 (which is a type I receptor coldinary) for treating Alzheimer's, Parkinson's or Huntington's coldinary for treating Alzheimer's, Parkinson's or Huntington's coldinary the coldinary cancer (e.g. and long related sequences, uncleased as probes to identify and clone related sequences, coldinary coldinary coldinary to generate transgenic animals and in contents the therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 24
                                               16-APR-1999;
                                                                           14-APR-2000; 2000WO-JP02455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1181 SSPPP------LSSPLPEAPOPKE 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132
                                                                                                                     26-OCT-2000
                                                                                                                                                                                                                           Human; histidine domain-protein tyrosine phosphatase; HD-pTP; chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic; lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                     WO200063392-A1
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                      Human tyrosine phosphatase HD-PTP fragment.
                                                                                                                                                                                                                                                                                                                                                23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                               AAB29662 standard; Protein; 1583
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Markby D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-009434/01.
N-PSDB; AAV81748.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                               99JP-0108842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%;
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Pred. No. 26;
13; Mismatches
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owman GD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GLPPASLPESTPIPS 1180
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(KYOW) KYOWA HAKKO KOGYO KK

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The invention relates to a novel human tyrosine phosphatase, histidine CC domain-protein tyrosine phosphatase (HD-PTP, ABR2661) and to human CC HD-PTP nucleic acids (AAC81224, AAC81225, AAC81262, AAC81263). The CC HD-PTP gene is located on chromosome 3p21.3. This region is frequently CC found to be deleted in lung cancers, and is therefore thought to contain CC atumour suppressor gene. The invention also relates to expression CC vectors and host cells containing human HD-PTP nucleic acids; the CC recombinant production of HD-PTP; anticancer drugs containing HD-PTP; CC creagents containing HD-PTP oligonucleotides; antibodies specific for CC HD-PTP; and an immunoassay method using HD-PTP proteins, nucleic acids and antibodies may be used in the treatment, investigation and diagnosis CC crepresents a substantial portion of the human HD-PTP proteins.
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Search completed: April Job time : 32.5806 secs
                                                                                                                                                                                                                                       Query Match 16.7%; Score 76.5; DB 21; Best Local Similarity 27.0%; Pred. No. 32; Matches 24; Conservative 13; Mismatches 23;
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N-PSDB; AAC81225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimizu K;
                                                                             1490 SSPPP------LSSPLPEAPQPKE 1507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of tumors
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                             1441 PISSIQATIAKLSIRPPGGLESPVASLPGPAEPP------
                                                                                                                   60 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                               7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                         1583 AA;
                  9, 2003, 12:35:31
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Result
No.
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Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      364.5
364.5
338
85.5
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                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrat:
6: sp_mamal:*
7: sp_mbc:*
9: sp_phage:*
9: sp_phage:*
                                                                                                                                                                                         Match Length
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459
1 MNMSKQPVSNVRAIQANINI......NLSEIQNIKSELKYVPKAEQ 88
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sp_organelle:*
sp_phage:*
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ap_rodent:*
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Q9er98 mus musculu
Q925f0 rattus norv
Q90258 xenopus lae
Q9y4d3 homo sapien
Q9ykd3 homo sapien
Q9yke6 rattus morv
Q8r1z5 mus musculu
Q66579 eastern equ
Q95v2 dictyosteli
Q9pzx7 eastern equ
Q10465 homo sapien
Q8w242 homo sapien
Q8w242 homo sapien
Q8w242 homo sapien
Q9pzx3 eastern equ
Q88790 eastern equ
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ALIGNMENTS

RP SEQUENCE FROM N.A. RA PATZAK D.; RA PATZAK D.;	Genomics 72:260-271(2001). [2] SEQUINCE FROM N.A. MEDLINE=20065879; PubMed=1059 Patrak D., Zhuchenko O., Lee "Identification, mapping, and chromosomal human gene (SMPX) Hum. Genet. 105:506-512(1999)	OX WGBI_TaxID=10090; OX WGBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=C57BL/10; TISSUE=SKELETAL MUSCLE; RX MEDLINE=21295047; PubMed=11401441; RA Kemp T.J., Sadusky T.J., Simon M., Brown RA Sassoon D.A., Coulton G.R.; RT "Identification of a Novel Stretch-Respond	QUERUB; QUERUB; Ol-MAR-2001 (TrEMBLrel. 16, La Ol-MAR-2001 (TrEMBLrel. 19, La Ol-DEC-2001 (TrEMBLrel. 19, La Stretch responsive muscle (X-c (Muscle-specific protein CSL). SMPX OR SRMX OR CSL. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalia, Enthoria, Deforata;	SULT 1 ER98 PRELIMINARY;
EMBL/GenBank/DDBJ databases. 81084; eler A., Yeoh T., Biben C., Wang CC.,	8820; C.C., Wehnert M.; genomic structure of a novel X- encoding a small muscular protein.";	Stretch-Responsive Skeletal Muscle Gene	, Created) , Last sequence update) , Last annotation update) (X-chromosome) (SMPX protein) SL). SL).	PRT; 85 AA.

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MGD; MGI:1913356; Smpx.
SEQUENCE 85 AA; 9253 MW; 43863840A65DA6BC CRC64;
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Patzak D., Zhuchenko O., Lee C.C., Wehnert M.;
"Identification, mapping, and genomic structure of a novel chromosomal human gene (SMPX) encoding a small muscular profilm. Genet. 105:506-512(1999).
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"Identification, mapping,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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es. 5:169-176(1998).
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                                                                                                                                                                                                                                                                                                                                                        MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   Score 85.5; D
Pred. No. 1.3;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
3.3e-29;
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                                                                                                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                                                                      33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka A.,
                                                                                                                                                                                                                                                                                                          Length 1209;
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brain which c
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InterPro; IPR001478; pDZ.
InterPro; IPR0012965; P_rich_extensn.
Pfam; pP00168; C2; 2.
Pfini; PP001217; PRICHEXTENSN.
SMART; SM00239; C2; 2.
SMART; SM00229; PDZ; 1.
PROSITE; PS00499; C2 DOMAIN 1; 1.
PROSITE; PS0049; C2 DOMAIN 2; 2.
PROSITE; PS50106; PDZ; 1.
Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11285225;

Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;

"An unusual C(2)-domain in the active-zone protein piccolo:
implications for Ca(2+) regulation of neurotransmitter release.";

EMBO J. 20:1605-1619(2001).

-I- FUNCTION: MAY ACT AS A SCAFFOLDING PROTEIN INVOLVED IN THE
ORGANIZATION OF SYNAPTIC ACTIVE ZONES AND IN SYNAPTIC VESICLE
TRAFFICKING (BY SIMILARITY).

-I- SUBURIT: INTERACTS WITH RABAC1/PRA1 AND PROFILIN.

-I- SUBCULTIAR LOCATION: CONCENTRATED AT PRESYNAPTIC SIDE OF SYN.
                                                                                                                                                                                                                                                                                                                                                                                                   -i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
PRODUCED BY ALTERNATIVE SPLICING.
-i- DOMAIN: C2 DOMAIN 1 IS INVOLVED IN BINDING CALCIUM AND PHOSPHOLIPIDS. CALCIUM BINDS WITH LOW AFFINITY BUT WITH SPECIFICITY AND INDUCES A LARGE CONFORMATIONAL CHANGE.
-i- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-i- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; AF138789; AAF070822.2; -.
EMBL; AF237534; AAF63196.1; -.
HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
Fenster S.D., Cases-Langhoff C., Gundelfinger
Fubmitted (JAN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABAC1.
MEDLINE=20170257; PubMed=10707984;
Fenster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Garner A.M., Kaempf U., Kindler S., Gundelfinger B.D., Garner C.(
"Piccolo, a presynaptic zinc finger protein structurally related bassoon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Piccolo protein (Multidomain presynaptic cytomatrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALICUM-BINDING ACTIVITY, AND VAL-4688; MET-4689; VAL-4690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JKS6 PRE
Q9JKS6; Q9JLT1;
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4968
4876
4881
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                                                                                  547
1033
2362
4536
4752
5059
4880
5085
PDZ.

C2 DOMAIN 1.

C2 DOMAIN 1.

C2 DOMAIN 2.

C2 DOMAIN 2.

TKPTN -> SKRRK (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

D->A: COMPLETE LOSS OF CALCIUM-BINDING AND CALCIUM-BEPENDENT PHOSPHOLIPID BINDING ACTIVITY.
                                                                                                                                                               C4-TYPE (
C4-TYPE (
POLY-PRO.
                                                                                                                                                                        12 X 10 AA TANDEM APPROXIMATE REPEATS P-A-K-P-Q-P-Q-P-X.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS OF ASP-4668; ASP-4674;
SER-4691; GLN-4692; ASN-4693 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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databases.
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CHANGE.
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Best Local S
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Matches
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Q8R1Z5;
01-JUN-2002 (TrEMBLrel. 21, Cree
01-JUN-2002 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 54.5 kba protein (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
NON TER 1
SEQUENCE 496 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=EYE;
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MUTAGEN
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ilarity 27.0%;
Conservative 1
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Rodentia;
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36.8%;
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                                                                                                                                                                                                                                                                                                                                                   Score 80.5; DB
Pred. No. 1.6;
L4; Mismatches
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Last annotation updat
in (Fragment).
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Pred. No. 20;
5; Mismatches
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QN->AA: MODERATE
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VV->SS: 10-FOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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BINDING ACTIVITY.
V->S: SMALL INCREASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D->A: COMPLETE LOSS OF CALCIUM-BINDING AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VM->SS: 10-FOLD INCREASE IN AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                         8E5EA796262B60DE CRC64;
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20;
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                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5085;
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                                                                                                                                                                                                                                                                        GLPPASLPESTPVPS
                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                   Indels
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IN AFFINITY
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Q923E6 PKBLL....
Q923E6;
Q923E6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLRel. 20, Last annotation update)
Q1-MAR-2002 (Tremblical 20, Last annotation update)
Q1-MAR-2002 (Tremblical 20, Last annotation update)

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RESULT 8
Q66579
ID Q66579
AC Q665
AC Q
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Best Local
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Query Match
Best Local Similarity
Matches , 17; Conserv
                                                                                                                                                                                                                                           InterPro; IPR001836; Alpha Core.
InterPro; IPR001836; Alpha E1_glycop.
InterPro; IPR0002548; Alpha E2_glycop.
InterPro; IPR000253; Alpha E2_glycop.
InterPro; IPR000253; Alpha E3_glycop.
InterPro; IPR000253; Togavirin.
Pfam; PF00944; Alpha Core; 1.
Pfam; PF01984; Alpha E1_glycop; 1.
Pfam; PF01983; Alpha E2_glycop; 1.
Pfam; PF01963; Alpha E3_glycop; 1.
Pfam; PF01563; Alpha E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q66579;
Q66579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00102; Y_phosphatase; 1.
PROSITE; PS00383; TYR PHOSPHATASE_1; UNKNOWN_1.
PROSITE; PS50056; TYR PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC006582; AAH06582.1; Interpro; IPR000387; TYR_phosphatase. Interpro; IPR000242; Tyr_pp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO1. Gen. Mikrobiol. Virus
EMBL; X63135; CAA44845.1;
HSSP; P03315; IVCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encephalomyelitis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SSP. NORTH AMERICAN VARIANT; , ' MEDILINE=91375524; PubMed=1896061; Wolchkova V.A., Netessov S.V.; "Complete nucleotide sequence of the genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATLAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eastern equine
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                                                                                                                                                                       CHAIN
CHAIN
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                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TIEMBLrel. 01, Created)
(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 19, Last annotation update)
ine encephalomyelitis virus RNA sequence.
ine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
          Conservative
                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55561 MW; 6B13C359FDE21513 CRC64;
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Rodentia;
                                                                                                                             1241
                                                                                                                                                 260
323
743
800
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27.0%;
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                                17.2%;
                                                                                                         137559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80.5; DB
Pred. No. 1.7;
14; Mismatches
          14;
          Score 79; DB
Pred. No. 6.7;
14; Mismatches
                                                                                                         MW.
                                                                                                                             C PROTEIN.
E3 PROTEIN.
E2 PROTEIN.
6K PROTEIN.
E1 PROTEIN.
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                                                                                                         B9668EB7416F0882
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                           DB
6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA stage; Togaviridae;
                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA
               24;
                                                       Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
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                                                                                                           CRC64;
               Indels
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                 6
                 Gaps
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Q9PZX7
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   DR RAC DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q95VZ3;
Q95VZ3;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MA38-MASS;
Brault A.C., Powers A.M., Kang W., Tesh R.B., Shope R.
Brault A.C., Powers A.M., Kang W., Tesh R.B., Shope R.
"Genetic and Antigenic Diversity among Eastern Equine
"Genetic and Antigenic Diversity among Eastern Equine
viruses from North, Central and South America.";
viruses from North, Central and South America.";
viruses from North, Central and South America.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PZX7;
Q9PZX7;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21319145, PubMed=11425877;
Jung G., Remmert K., Wu X., Volosky J.M., Hammer J.A. II
"The Dictyostelium CARMIL protein links capping protein
complex to type I myosins through their SH3 domains.";
J. Cell Biol. 153:1479-1497 (2001).
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InterPro; IPR001993; Mitoch carrier.
PROSITE; PS00215; MITOCH CARRIER, UNKNOWN 1.
SEQUENCE 1050 AA; 113866 MW; D6F18849AA9C692B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carmil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Structural polyprotein.
Eastern equine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                    viruses from North, Central Submitted (JUN-1999) to the EMBL; AF159550; AAF04792.1; HSSP, P03315; IVCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus)
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InterPro; IPR001836; Alpha_core.
InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR002530; Togavirin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926
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1 (TrEMBLrel. 19,
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Pred. No. 6.3;
12; Mismatches
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Best Local Similarity
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Best Local
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NON TER
SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscle protein; CyToskeleton; Structural protein; Phosphorylation; Serine/throonine-protein kinase; Alternative splicing; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Titin, skeletal muscle isoform (EC 2.7.1.-) (Connectin) (Fragment)
Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00944; Alpha_core; 1.
Pfam; PF01589; Alpha_E1 glycop;
Pfam; PF005943; Alpha_E2 glycop;
Pfam; PF01563; Alpha_E3 glycop;
Pfam; PF01563; Alpha_E3 glycop;
PARINTS, PR00798; TOGAVIRIN.
                                                                                                                                                                                                      Pfam; PF00047; 1g; 59.
Pfam; PF02818; PPAK; 53.
SMART; SM00408; IGc2; 43.
SMART; SM00410; IG_like; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: MUSCLE-SPECIFIC
-i- SIMILARITY: TO THE CATALYTIC DOMAINS
                                                                                                                                                                                                                                                                                 InterPro; IPR003598; Ig c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR004168; PPAK_motif.
                                                                                                                                                                                                                                                                                                                                                                         EMBL; X90569; CAA62189.1;
HSSP; P56276; 1TLK.
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MEDLINE=96026330; PubMe
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Kolmer B.;
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Pred. No. 7.6;
L4; Mismatches
                                                                                                  GLU/LYS/PRO/VAL-RICH
                                                           B85240533CBADE58 CRC64;
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                   Length 7962;
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                                PROBOTI; PROUDON; ENE, DRINABB; 1.

S.MART; SMO0060; FN3; 133.

S.MART; SM00060; FN3; 137.

S.MART; SM00408; IG-2; 1148.

S.MART; SM00406; IG-2; 1148.

S.MART; SM00210; IT-YKG; 1.

S.MART; SM00210; IT-YKG; 1.

PROSITE; PS00033; FGGY KINASES 1; UNKNOWN 1.

PROSITE; PS00033; FGGY KINASES 1; UNKNOWN 1.

PROSITE; PS00033; FGRIX LOOP HELIX; UNKNOWN 1.

PROSITE; PS00013; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS0011; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS00119; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.

PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.
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Q8WZ42;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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InterPro;
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InterPro; IPR002290; Ser thr pkinase
InterPro; IPR001245; Tyr pkinase.
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Pfam; PF02818;
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EMBL; AJ277892; CAD12456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21573839; PubMed=11717165;
Bang M.L., Centner T., Fornoff F., Geach J
MCNabb M., Witt C.C., Labeit D., Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granzier H., Labeit S.;
"Series of exon-skipping events
as the structural basis for myof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Titin.
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Z-line to I-band linking system.
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Centner T., Kolmerer
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Mammalia; Eutheria;
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  Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o; IPR000282; Cytck receptor 2.
c; IPR000719; Euk pkinase.
c; IPR000577; FGGY kin.
c; IPR003561; FN III.
c; IPR001092; HLH basic.
c; IPR003599; Ig.
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Trombitas K., Hell W.,
Kolmerer B., Witt C., B
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PPAK; 53.
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Primates;
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Ig.wHC.
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17.1%;
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Query

Score 78.5;

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RESULT 13
Q9ADV0
RESULT 14

Q9PZX3

ID Q9PZX

AC Q9PZX

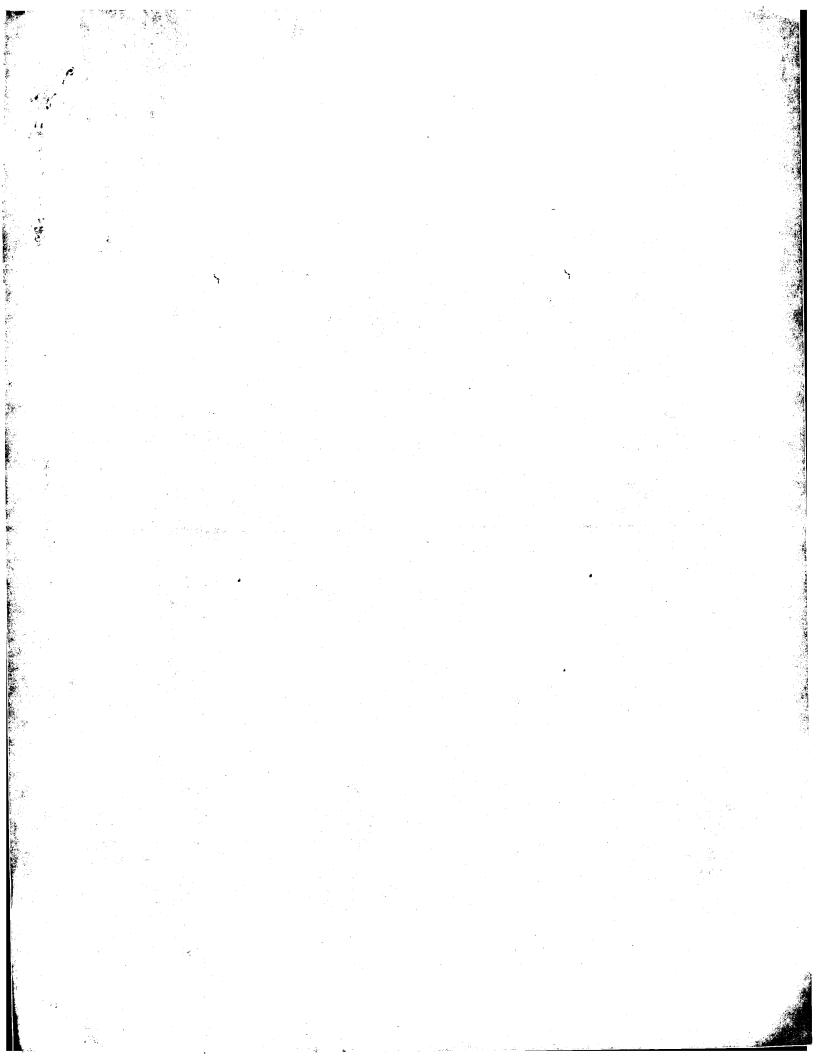
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01-JUN-2001 (TrEMBLrel. 17, Creat
01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 17, Last
Hypothetical 19.7 kDa protein.
Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chaffeensis.";
Infect. Immun. 69:2083-2091(2001).
EMBL; AF078553; AAK28702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anaplasmataceae; Ehrlichia.
NCBI_TaxID=944;
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                                 STRAIN=FL93-939;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PZX3;
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Ohashi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serodiagnosis.";
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   Brault, A.C., Powers
                                                                                                                                                                                                                                  virus)
                                                                                                                                                                                                                                                                Eastern equine
                                                                                                                            NCBI_TaxID=11021;
                                                                                                                                                                        Alphavirus.
                                                                                                                                                                                                Viruses; ssRNA positive-strand
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19; Conserv
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19; Conser
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182 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                encephalitis virus (Eastern equine encephalomyelitis
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   A.M.,
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31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78;
Pred. No.
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); Mismatches
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   Σ.
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InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR002548; Alpha_E2_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR002533; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_core; 1.
Pfam; PF001589; Alpha_E1_glycop; 1.
Pfam; PF001589; Alpha_E2_glycop; 1.
Pfam; PF001583; Alpha_E3_glycop; 1.
Pfam; PF01583; Alpha_E3_glycop; 1.
PRNNTS; PR00798; TOGĀVIRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF159554; AAF04796.1; HSSP; P03315; IVCP.
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Weaver S.C., Hagenbaugh A., Bellew L., Nett
Chang G.J., Clarke D.K., Gousset L., Scott
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Eastern equine encephal
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01-NOV-1996
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InterPro; IPR000936; Alpha E2 glycop.
InterPro; IPR002533; Alpha E3 glycop.
InterPro; IPR000930; Togavirin.
                                                                                                                                                                                                                              related RNA viruses.";
Virology 197:375-390(1993).
EMBL; U01034; AAC53735.1; -
HSSP; P03315; 1VCP.
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01-JUN-2001
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PR01589; Alpha E2_glycop;
PR00943; Alpha E2_glycop;
PR01563; Alpha E3_glycop;
PR01563; TOGĀVIRIN.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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InterPro; IPR00036; Alpha_E2_glycop.
InterPro; IPR000336; Alpha_E2_glycop.
InterPro; IPR001836; Alpha_Core.
InterPro; IPR001836; Alpha_Core.
InterPro; IPR000930; TogavTrin.
Pfam; PP00943; Alpha_E2_glycop; 1.
Pfam; PF00944; Alpha_E2_glycop; 1.
Pfam; PF001583; Alpha_E3_glycop; 1.
Pfam; PF01583; Alpha_E3_glycop; 1.
PRINTS; PF00798; TOGAVIRIN.
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) [Contains: Coat protein C (EC 3. (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang G.-J.J., Trent D.W.;

Chang G.-J.J., Trent D.W.;

Chang G.-J.J., Trent D.W.;

"Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins.";

J. Gen. Virol. 68:2129-2142(1987).

J. Gen. Virol. 68:2129-2142(1987).

J. Gen. PURCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

J. PURCTION: THE CENTYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

J. PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE STHE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
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Bastern equine encephalitis virus (Bastern equine encephalomyelitis
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; P03315; 1VCP.
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                                                                                                                                                                                                                                                                                                  Polyprotein;
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SPIKE GLYC
SPIKE GLYC
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(BY SIMILARITY).
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                       InterPro; IPR002548; Alpha_E1_glycop
InterPro; IPR000356; Alpha_E2_glycop
InterPro; IPR000353; Alpha_E3_glycop
InterPro; IPR001836; Alpha_core.
InterPro; IPR001836; Alpha_core.
InterPro; IPR000930; TogavIrin.
Pfam; PP00944; Alpha_E2_glycop; 1.
Pfam; PP00944; Alpha_E3_glycop; 1.
Pfam; PF01589; Alpha_E3_glycop; 1.
Pfam; PF01589; Alpha_E3_glycop; 1.
Pfam; PF01589; Alpha_E3_glycop; 1.
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (Pi30) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein E1].
6 kDa peptide; Spike glycoprotein E1].
Eastern equine encephalitis virus (strain va33[ten broeck]) (Eastern equine encephalitis virus).
viruses; seRNA positive-strand viruses, no DNA stage; Togaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                          Weaver S.C., Scott T.W., Rico-Hesse "Molecular evolution of eastern equi
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                               EMBL; M69094; AAA42980.1; PIR; A39992; VHWVEV. HSSP; P03315; 1VCP. MEROPS; S03.001; -
                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                North America.";
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91220727; PubMed=2024496;
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                      PRINTS; PR00798;
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Pred. No. 8.7;
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Best Local &
Matches 17
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      TYPOSINE PHOSPHATE.

-I- TISSUE SPECIFICITY: EPITHELIAL CELLS.
-I- SIMILARITY: BELONGS: TO THE TYR FAMILY
-I- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
-I- SIMILARITY: CONTAINS 5 ANK REPEATS.
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         EMBL; U00936; AAC27350.1; HSSP; P08631; IAD5.
                                                                                                                                                                                                     Chan T.A., Chu C.A., Steele R.E.;
                                                                                                                                                                                                      MEDLINE=94181280; PubMed=8134129;
Chan T.A., Chu C.A., Rauen K.A., Kroiher M., Tatarewicz S.
                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Irvine;
                                                                                                                                                                                                                                                                                                                                                              HYDAT
                                                                                                                                                                                                                                                                   Eukaryota, Metazoa;
Hydridae, Hydra.
                                                                                                                                                                                                                                                                         Hydra attenuata (Hydra) (Hydra vulgaria)
Eukaryota, Metazoa; Cnidaria, Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                        Tyrosine-protein
                                                                                                                                                                                                                                                         NCBI_TaxID=6087;
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(Rel.
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41, Last annotation update)
kinase HTK16 (EC 2.7.1.112).
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27.4%;
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Best Local Similarity
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PRINTS; PRO0109; TYRKINASE.

PRODOM; PD000001; Euk pkinase; 1.

ProDom; PD000003; SH2; 2.

SMART; SM00248; ANK; 4.

SMART; SM00252; SH2; 2.

SMART; SM00219; TYPKC; 1.

PROSITE; PS50008; ANK REPEAT; 2.

PROSITE; PS50018; ANK REPEAT; 1.

PROSITE; PS500107; PROTEIN KINASE TOM; 1.

PROSITE; PS50011; PROTEIN KINASE TOM; 1.

PROSITE; PS500101; PROTEIN KINASE TYR; 1

PROSITE; PS500101; PROTEIN KINASE TYR; 1

PROSITE; PS50011; PROTEIN KINASE TYR; 1
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P36225;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29; Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Microtubule-associated protein 4 (MAP 4) (Microtubule-associated
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                                                    "Molecular cloning of a ubiquitously distributed microtubule-associated protein with Mr 190,000.";
J. Biol. Chem. 265:13849-13855(1990).
                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL (MEDLINE=90338002; PubMed=2380192 Aizawa H., Emori Y., Murofushi H
                                                                                                                                                                                                    NCBI_TaxID=9913;
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Suzuki K.;
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Mammalia; Eutheria;
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MEDLINE=91236765; PubMed=2033072;
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PROTEIN KINASE.
PROTE (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
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Pred. No. 8.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-4 (MAP-U)
J. Biol. Chem. 26
-!- FUNCTION: NON
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PIR; A37127; A37127
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TISSUE SPECIFICITY: IS DISTRIBUTED UBIQUITOUSLY AMONG ALL ?

BUT AMOUNTS ARE LOWER IN CEREBELLUM AND LIVER.

PYM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMIN

NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE
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                                                                                                                                          DLSRPKSTTTSSVKKSTTVPGTA--PPAGAPSRARPTATPPRPSGTPPVDKKPTAAKPTS 86
                                                                                                                                                            NMSKQPVSNVRAIQANINIPMGAFRPGAGQPPR-RKECTPEVEEGVPPTSDE--EKKPIP 58
                                                                                                  SAPRIGRVAANASAPDIKNVRSKV
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Pr00418; tubulin-binding; 3
PF; PS00229; TAU MAP; 3
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TAU/MAP MOTIF 1
TAU/MAP MOTIF 1
TAU/MAP MOTIF 1
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Pred. No. 16;
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P48634;
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Biochem. Biophys. Res. Commun. 239:488-492(1997).
-!- SUBUNIT: Interacts with the SH3-containing re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98008866; PubMed=9344857; Matuoka K., Miki H., Takahashi K., Takena "A novel ligand for an SH3 domain of the
                     Perrot V.,
Cohen D.;
                                                                                                                                               MEDLINE=90192810; PubMed=2156268;
Banerji J., Sands J., Strominger J.L., Spies T.;
Rage pair from the human major histocompatibility complex.encodes
"A gene pair from the human major histocompatibility complex.encodes
large proline-rich proteins with multiple repeated motifs and a
single ubiquitin-like domain.";
Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                         MEDLINE=93272029; PubMed=8499947; Iris F.J.M., Bougueleret L., Prieur Perrot V., Jurka J., Rodriguez-Tome
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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TISSUE=T-cell;
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TISSUE SPECIFICITY: Expressed in fetal and adult brain,
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Catarrhini;
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BTK_HUMAN
ID BTK_HUMAN STANDARD;
AC Q06187;
DT 01-JUN-1994 (Rel. 29, Created)
                                                                                    RESULT 8
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Best Local S
Matches 21
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EMBL; M33518; AAA35586.1; --
EMBL; M3512; AAA35586.1; --
EMBL; M3512; CAA78744.1; --
EMBL; B35098; B35098
PIR; B35098; B35098
PIR; S36152; S36152.
Genew; HGNC:13918; BATZ.
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CONFLICT
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Nat. Genet. 3:137-145(1993).
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                                                                                                                      NIPMGAFRPGAGQPPRRKECTPEVEEG-VPPTSDEEKK-----PIPGAKK-----LPGP 66
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TISSUE SPECIFICITY: LIMITED TO
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3; Mismatches
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Flinter F., Ha
Smith C.I.E.,
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"Deficient expression of a B cell cytoplasmic tyrosine kinass cell 72:279-290(1993).
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MEDLINE=93145329; PubMed=8425221;
Tsukada S., Saffran D.C., Rawlings
Klisak I., Sparkes R.S., Kubagawa F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ
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SEQUENCE FROM N.A.
MEDLINE-93140868; PubMed=8380905;
MEDLINE-931408; PubMed=8380905;
MEDLINE-93140868; PubMed=8380905;
MEDLINE-931408; PubMed=8380905;
MEDLINE-9314086; PubMed=8380905;
MEDLINE-931408; PubMed=8380905;
MEDLINE-9314
                                                                                                                                               PHOSPHORYLATION OF GTF21, AND MUTAGENESIS MEDLINE=97165069; PubMed=9012831;
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Ohta Y., Haire R.N., Litman R.T., Fu S.M., Nelson R.P., Kratz J.,
Kornfeld S.J., la Morena M., Good R.A., Litman G.W.;
"Genomic organization and structure of Bruton agammaglobulinemia
tyrosine kinase: localization of mutations associated with varies
clinical presentations and course in X chromosome-linked
agammaglobulinemia.";
                                                           Yang W., Desiderio S.;
"BAP-135, a target for Bruton's tyrosine kinase in response
                                                                                                                                                                                           PHOSPHORYLATION OF GTF2I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sixty-nine kilobases of contiguous human genomic sequence containing the alpha-galactosidase A and Bruton's tyrosine kinase loci."; Mamm. Genome 6:334-338(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95352959;
Oeltjen J.C., Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cinter F., Hammarstroem Smith C.I.E., Bentley D.R. Nature 364:362-362(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95012452; Po
Rohrer J., Parolini
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Mammalia; Eutheria;
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15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase BTK (EC 2.7.1.112) (Bruton's tyrosine kinase)
(Agammaglobulinaemia tyrosine kinase) (ATK) (B cell progenitor
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engagement.";
tl. Acad. Sci. U.S.A.
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94:604-609(1997)
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Biochemistry 37:2912-2924(1998)
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Kwan S.-P., Lappalainen I., Lehvaeslaiho H., Lester T., Meindl A.,
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Vihinen M., Iwata T., Kinnon C.,
Vorechovsky I., Smith C.I.E.;
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[16]
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Levinsky R.J., Kinnon C.
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MEDLINE=94214481; PubMed=8162056;
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MEDLINE=97169387; PubMe
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MEDLINE=94214435; PubMed=8162018;
de Weers M., Mensink R.G.J., Kraa
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                                             "Screening of gene
Bruton's tyrosine
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                                                                                            Conley M.E., Fitch-Hilgenberg
                                                                                                         VARIANTS XLA D-113; C-361; Q-520
MEDLINE=95152494; PubMed=7849697
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          MEDLINE=95152522;
                        VARIANTS XLA H-28; P-33;
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sson_P.T., Allard
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PubMed=9218782;
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24:160-165(1996)
  Winkelstein
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RESULT 9
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EXAA HUMAN STANDARD; PRT; 393 AA. 1931260; Q15949; Q43505; Q43370; Q1-JUL-1993 (Rel. 26, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-UN-2002 (Rel. 41, Last annotation update)

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[19]
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Biochemistry 34:1475-1481(1995).
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Smith C.I.E.;
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                                                                                                                                                                                Gaspar H.B., Bradley L.A.D., Katz F., Lovering I
Morgan G., Levinsky R.J., Kinnon C.;
"Mutation analysis in Bruton's tyrosine kinase,
agammaglobulinaemia gene, including identificat:
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                                                                                                                          VARIANTS XLA ASN-429 AND ARG-477.
MEDLINE=96177680; PubMed=8634718;
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L3; Mismatches
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Sowadski
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mith C.I.E.,
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J.M.,
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EMBL; X58430; CAB86198.1; ALT_FRAME.
EMBL; AF040714; AAB96917.1; --
EMBL; AF004080; -; NOT_ANNOTATED_CDS.
EMBL; M30599; AAA36006-1; --
EMBL; S69027; AAD14030.1; --
EMBL; S69029; AAD14030.1; --
EMBL; S69029; AAD14030.1; --
EMBL; S14930; S14930.
PIR; S14930; S14930.
PIR; S26402; S26402.
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PIR; S26403; S26402.
PIR; AA425; A34425.
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MEDLINE-9128229; PubMed=10,00000...

Lowney P., Corral J.C., Detmer K., Lebeau M.Pi., J.,

Lawrence H.J., Largman C.;

"A human Hox 1 homeobox gene exhibite myeloid-specific expression alternative transcripts in human hematopoietic cells.";

arids Res. 19:3443-3449(1991).
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as incident and this statement is not removed. Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem.
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Castronovo V., Kusaka M., Charlot A., Gielen J., Sobel M.;
"Homeobox genes; potential candidates for the transcription of the transformed and invasive phenotype.";
Biochem. Pharmacol. 47:137-143(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90098876; PubMed=2574852; Acampora D., D'Esposito M., Faiella A., Morelli F., Stornaiuolo A., Nigro V., Si"The human HOX gene family."; Nucleic Acids Res. 17:10385-10402(1989).
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Submitted (FEB-1998) t
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Bradshaw H., Hinds
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PL1 (SARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE ABD-B HOMEOBOX
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.
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b the EMBL/GenBank/DDBJ
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lmeone A., B
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Boncinelli E.;
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RESULT 10
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Q63003;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                   STRAIN=Wistar; TISSUE=Brain; MEDLINE=96015159; PubMed=8537300; Suzuki E., Kojima N., Yoshimura K., "Cloning and sequence analysis of cprotein 5E5 in the nervous system."

J. Biochem. 118:122-128(1995).
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                               This SWISS-PROT entry is copyright. It is produced through a copyright in the produced through a copyright in the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content in
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Mammalia; Eutheria; Rodentia;
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PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental
                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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ProDom; PD000010; Homeobox
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Pfam; PF00046; homeobox;
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                                                                                   FUNCTION: MIGHT HAVE DNA-BINDING ABILITY. SUBCELLULAR LOCATION: Nuclear. TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
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DNA-binding; Nuclear prote
SEQUENCE 825 AA; 86831
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MEDLINE=97042057; PubMed=8887328
Wang W., Chen X., Xu H., Lufkin
"Msx3: a novel murine homologue
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01-NOV-1997 (Rel. 35, Last sec
15-JUN-2002 (Rel. 41, Last and
                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
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EMBL; AF0602229; AAC15459.1; -.

EMBL; X96518; CAA636567.1; -.

HSSP; P14653; 1B72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimeld S.M., McKay I.J., Sharpe P.T., "The murine homeobox gene Msx-3 shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: RESTRICTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the developing neural tube.
Mech. Dev. 55:201-210(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97014264; PubMed=8861099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 73-204 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The mechanism of
                                                                   MGD; MGI:106587; Msx3.
                                                                                                                                                                                                                                                                                                                                                                                                           - I - SIMILARITY: BELONGS TO THE MSH HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 PAVNLSEIQNIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                    NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMGAFRPGAGQPPRRKECTPEVEEGVP------PTSDEEKKPIPGAKKLPG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEGAF - PGGG
Pro; IPR001356; Homeobox
PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a novel murine homologue of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the dorsal embryonic 58:203-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi T., Raghow R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biogenesis, developmental regulation and wo alternatively spliced mRNAs encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8887328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r protein;
86831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%;
                                          Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEEEGVPRPRAPPEPPDPGAPRPPPDPGPLPLPGSQEKPT 180
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annotation update)
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Pred. No. 42;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6,
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AF667FE2FD555BDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.T.;
shows highly restricted
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Drosophila msh homeobox gene central nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE DORSAL
                                                                                                                                                                                                                                                                                 There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                    . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBRYONIC CENTRAL
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the murine
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                                                                                                                                                                                                                                                                                                                                                         a collaboration
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                                                                                                                                                                                                                                                                                                                                     outstation
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE STANDARD; PRT; 874 AA.

BCA1 MOUSE STANDARD; PRT; 874 AA.

Q61140; Q60869;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CRK-associated substrate (P130CAS) (Breast cancer anti-estrogen resistance 1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000010; Homeobox; 1.

SMART; SM00389; HCX; 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein; Multigene family.

Multigene family.

DNA_BIND

B7

146

CONFLICT

75

75

CONFLICT

76

CONFLICT

77

78

CONFLICT

79

CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance 1 protein).
BCAR1 OR CRKAS OR CAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20249316; PubMed=10739664; Donaldson J.C., Dempsey P.J., Redd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                               ÷
                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanks S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH NEPHROCYSTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Interaction between focal adhesion kinase substrate pl30Cas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96068679; PubMed=7479864; Polte T.R., Hanks S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOCAL ADHESION KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crk-associated substrate p130(Cas)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ALERKFHQKQYLSIAER 117
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                                                                                             SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADHESION KINASE 1,
ADAPTE PROTEIN CRKL AND LYN KINASE CAN HETERODIMERIZE WITH C.
(BY SIMILARITY). INTERACTS WITH NEPHROCYSTIN AND PTKZB.
SUBCELLULAR LOCATION: FOCAL ADHESIONS. UNPHOSPHORYLATED FORM
LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO THE MEMBRANE UPON
TYROSINE PHOSPHORYLATION (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAS-B (SHOWN HERE) AND CAS-A
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                     . Cell Res. 256:168-178(2000).
FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL FOR TYROSINE KINASE-BASED SIGNALING RELATED TO
                                                                                                                                                                                                                                                                                                                     IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY). H. BEEN SHOWN TO BE ESSENTIAL IN CARDIOVASCULAR DEVETORMENT OF THE PROPERTY OF T
                       DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QANINIPMGAFRPGAGQPPRRKECTPEVEEGVPPTSDEEK---KPIPGAKKLPGPAVNLS
                                                                                                                                                                                                                                                                                                             EMBRYOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELGVERPLGASKPGAWPPPVAHSCPPRAPSPPPCTLRKHKTNRKP-----RTPFTTAQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92:10678-10682(1995)
                                                                                                                                                                                                                                                                                                                                          IN CARDIOVASCULAR DEVELOPMENT DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interacts with nephrocystin and contacts of polarized epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bouton A.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Crk-associated tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                                                                                                                                                                                                                       COORDINATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204;
                                                                                                                                  AND CAS-A;
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RESULT 13
BCA1_RAT
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Best Local S
Matches 23
                                                                                                BCA1_RAT STANDARD; PRT; 968 AA. 963767; Q63766; Q637676 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) CRK-associated substrate (P130CAS) (Breast cancer anti-estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                     resistance 1 protein).
BCAR1 OR CRKAS OR CAS.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U28151; AAA93
HSSP; P07751; 1BK2.
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                                                                                                                                                                                                                                                                                                                          377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS50002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000066;
SMART; SM00326; SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001452; SH3. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U48853; AAA93381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0452; SH3DOMAIN.
                                                                                                                                                                                                                                                           435 STGSTRSSQSASSLEVV 451
                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                19 NIPMGAFRPGAG----QPPRRKECTPEVEEG------VPPTSDEEKKPIPGAKKLPGP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSSUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL. DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE) (BY SIMILARITY) DOMAIN: THE SH3 DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH REGION OF FOCAL ADHESION KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT 7 YOVVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORYLATED OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATEO OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                   DVPPGLRRPGPGTLYDVPRERVLPPEVADGSVVDDGVYAVPPPAERE-APTDG-KRLSAS 43
                                                                                                                                                                                                                                                                                         AVNLSEIQNIKSELKYV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:108091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U28151; AAA93248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     23,
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e aplicing.
6 26
74 87
119 420
426 618
639 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                   874 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS 1 SH3
BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   94256
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₩.;
                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 69; DB 1;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO-RICH.
SUBSTRATE FOR KINASES ()
SER-RICH.
SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVERGENT HELIX-LOOP-HELIX MOTIF. MTVP -> MKYL (IN ISOFORM CAS-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3-binding; Cell adhesion;
                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                               589EDD76532BDBBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR KINASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 874;
                                                                                                                                                                                                                                                                                                                                                                                Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN AT THE
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J. Biol.
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- INDMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POYENTIAL SAY.—BINDING SITES AND A C.—TERMINAL DOMAIN CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF: THE SH2-BINDING SITES PUTARIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HILH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.

- IDOMAIN: THE SH3 DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROTEIN TO POCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH PRESERVED AND AND INTERACTS WITH ONE PROLINE-RICH PRESERVED AND AND INTERACTS WITH ONE PROLINE-RICH
                                                                                                                    PRINTS; PR00452; SH3DOMAIN PRODOM; PD000066; SH3; 1. SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                 EMBL; D29766; BAA06169.1;
EMBL; D29766; BAA06170.1;
HSSP; P07751; 1BK2.
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION OF FOCAL ADHESION KINASE 1.

-!- PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE YDYVHL MOTIF: THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORYLATE SITES AND CAN PHOSPHORYLATE OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX.

-!- DISEASE: APPEARS TO HAVE A CENTRAL FUNCTION IN TRANSFORMATION OF CELLS TO THE CONTRACT PROCESSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTS WITH NEPHROCYSTIN AND PTK2B (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: FOCAL ADHESIONS AND STRESS FIBERS.
UNPHOSPHORYLATED FORM LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO
THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)
AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tyrosine phosphorylation of Crk-associated substrates by focal adhesion kinase. A putative mechanism for the integrin-mediated tyrosine phosphorylation of Crk-associated substrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel signaling molecule, p130, forms stable complexes in vivo with v-Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
    Alternative splicing.
DOMAIN 97 159
DOMAIN 168 181
DOMAIN 213 514
                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakai R., Iwamatsu A., Hirano
Yazaki Y., Hirai H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL S. TISSUE-Fibroblast; MEDLINE-94349922; PubMed-8070403;
                                                                               PROSITE; PS50002; SH3; 1. Phosphorylation; SH3 domain;
                                                                                                                                                                               Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       +
                                                                                                                                                                                                 InterPro; IPR001452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tachibana K., Urano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98030588; PubMed=9360983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE PHOSPHORYLATION BY FOCAL ADHESION KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: BELONGS TO THE CAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY). SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADDRESION KINASE 1, ADAPTER PROTEIN CRKL AND LYN KINASE. CAN HETERODIMERIZE WITH C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 272:29083-29090(1997).
FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL FOR TYROSINE-KINASE-BASED SIGNALING RELATED TO C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOME CELL TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morimoto C
                                                                                                                                                                                                                                     BAA06169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T., Fujita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND PARTIAL SEQUENCE
SH3.
PRO-RICH.
SUBSTRATE
                                                                               SH3-binding; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohashi Y., Kamiguchi K.,
                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO CELL ADHESION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COORDINATING
                                                                                                                                                                                                                                                                                                                                                                        restrictions
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                                                                                                                                                                                                                                                                                                                                                                                            EMBL
                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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FOR KINASES

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CES2_HUMAN
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM A).

(MEDINE-21275466; PubMed-11381032;

Footz T.K., Brinkman-Mills P., Banting G.S., Maier S.

Frootz T.K., Brinkman-Mills P., Banting G.S., Maier S.

Fridgland L.J., Hu S., Birren B., Minoshina S., Shimi
Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S.,

Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe

McDermid H.E.,

McDermid H.E.,

Manalysis of the cat eye syndrome critical region in

region of conserved synteny in mice: a search for car

or near the human chromosome 22 pericentromere.";
                                                                                                                                                                                                                                                                         Nagase T., Kikuno k., nauvolation of Prediction of the coding sequences of The complete sequences of 100 new cDNA for large proteins in vitro."; DNA Res. 7:347-355 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                        Genome
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Cat eye syndrome critical region protein 2.
CECR2 OR KIAA1740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                         "Sequence analysis of LRPPRC and its SEC1 domain interaction partners suggests roles in cytoskeletal organization, vesicular trafficking, nucleocytosolic shuttling, and chromosome activity."; Genomics 79:124-136 (2002).
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 346-1484 FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BXF3; Q9C0C3; Q96P58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CES2
and B/CECR2B; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Highly expressed in skeletal mu
, placenta and lung. Expressed at lower level in braicolon, spleen, kidney.
                                                                                                                                                                                                                  MEDLINE=21686162;
                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529
                                                        remodeling and cytokinesis.
-!- SUBUNIT: Interacts with LRPPRC.
-!- ALTERNATIVE PRODUCTS: 2 isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 NIPMGAFRPGAG---QPPRRKECTPEVEEG-----VPPTSDEEKKPIPGAKKLPGP 66
                                                                                                the integration of cytoskeletal network with vesicular trafficking, nucleocytosolic shuttling, transcription,
                                                                                                                                FUNCTION: May be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STGSTRSSQSASSLEVV
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                                                                                                                                                                                                                                                                                                                                                                                                                    Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
23; Conser
                                                                                                                                                                                                   McKeehan W.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            896
                                                                                                                                                                                                                                                                                                                                                                                                                    11:1053-1070(2001).
                                                                                                                                                                                                                                                           168-1484 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                                                                                                  PubMed=11827465;
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741
894
98
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                                                                                                               involved through its interaction with of cytoskeletal network with vesicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SER-RICH.
SH3-BINDING (POTENTIAL).
DIVERGENT HELIX-LOOP-HELIX
MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                           (ISOFORM B),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E861641BFD68D377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                 Kondo Y., Okumura K., Ohara O.; es of unidentified human genes. XIX. CDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1484 AA
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ein 2.
                                                         A (shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu N
Shimizu N
1 S., Phan
, Roe B.A.
                in brain,
                                                                                                                                                                                                                                                          INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              in humans candidate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phan B.A.,
                             muscle, thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N., Pan H.,
an S., Yao Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTIF.
                 heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan Yao
                                                                                                    chromosome
                                                                                                                               LRPPRC in
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                                                                                                                                                                                                                                                                                                                                                                                                                                             and the genes at
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VGLI_HS

- HSV2H - VGLI HSV2H P13291; 01-JAN-1990 01-JAN-1990 01-NOV-1997

STANDARD;

PRT;

372

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Glycoprotein

(Rel. (Rel. (Rel. n I.

13, 13,

Created)
Last sequence up

update)

OR US7.

AC OCC OCC RAY

Alphaherpesvirinae; NCBI_TaxID=10315;

EQUENCE

FROM

N.A.

Herpes simplex virus (type 2 / strain Viruses; dsDNA viruses, no RNA stage;

Simplexvirus

Herpesviridae;

HG52)

MEDLINE=87111457; PubMed=3027242; McGeoch D.J., Moss H. W.M., McNab D., Frame M.C.; "DNA sequence and genetic content of the HindIII 1 short unique component of the herpes simplex virus identification of the gene encoding glycoprotein G,

region in the type 2 genome: , and evolutionary

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                                                     Matches
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VARSPLIC
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CONFLICT
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES),
                                                                                                                                                                                                                                                                                                              InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                      PROSITE; PS00633; BROMODOMAIN_1; PROSITE; PS50014; BROMODOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:1840; CECR2
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q92831; 1B91.
943 MSVTVSAPKPALGNPGR----APENSEAQEPEND-QAEPLPGLEEKP-PGVGTSE
                         18 INIPMGAFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPGAKKLPGPAVNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental disorder associated with the duplication of a 2 M region of 22q11.2. Duplication usually takes in the form of a surpernumerary bisatellited isodicentric chromosome, resulting four copies of the region (represents an inv dup(22) (q11)). CES characterized clinically by the combination of coloboma of the iris and anal atresia with fistula, downslanting palpebral fissures, presurricular tags and/or pits, frequent occurrence of
                                                                                                                                                                                                                                                                                                                                                                                 AF336133; AAK15343.1; -. AB051527; BAB21831.1; -. AF411609; AAL07393.1; -.
                                                     18;
                                                                                                                                                                                                                                                                                                    SM00297;
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and renal malformations, and normal or near-normal mental
                                                                                                         re splicing.
451 521
333 337
611 614
1250 1253
1250 1253
519 526
527 1484
370 389
1045 1045
1484 AA; 16
                                                     Conservative
                                                                                                                                                                                                                                                                                                   BROMO;
                                                                    15.0%;
                                                                                                           164214
                                                                                                   POLY-GLU.

POLY-SER.

POLY-PRO.

MISSING (IN ISOFORM B).

EYTKMSDN -> GKQGRSLC (IN
MISSING (IN ISOFORM B).

MISSING (IN REF. 2).

C -> S (IN REF. 2).

R -> W (IN REF. 2).

14 MW; 049AA844E51AF63F CRC
                                                    11;
                                                    Pred. No. 85;
L; Mismatches
                                                                                Score 69;
                                                                                                           049AA844E51AF63F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.
                                                                                DΒ
                                                                              1;
                                                       20;
                                                                               Length 1484
                                                       Indels
                                                                                                                                                                              ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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Search completed: April 9, 2003, 12:36:14 Job time : 15.0645 secs
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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CARBOHYD 156 1
CARBOHYD 169 1
CARBOHYD 175 1
CARBOHYD 243 2
SEQUENCE 372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X04798; CAA28485.1; -. EMBL; 286099; CAB06714.1; -. PIR; P34674, P43674. InterPro; IPR002874; Herpes_gI. Pfam; P701688; Herpes_gI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of BioidfFormatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Dolan A.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSVI AND

2: GH, GB, GC, GG, GD, GI, AND GE.

-1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPIV,

AND TO PRV GP63.
                                                                                                                                                          196 PSSVYTPGASRPTPPRTTT---
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J. Gen. Virol. 68:19-38(1987).
                                                                                                                                                                                                                      21 PMGAFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPGAKKLPGPA 67
                                                                                                                                                                                                                                                                                                   14.9%; Score 68.5; DB 1; Length 372; ilarity 31.9%; Pred. No. 22; Conservative 5; Mismatches 20; Indels ...
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169 N
175 N
243 N
39558 MW;
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M; COD4A22CAB16E8D7 CRC64;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                              Searched:
PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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459
1 MNMSKQPVSNVRAIQANINI......NLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                       283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                April 9, 2003, 12:33:21 F Search time 22.3548 Seconds (without alignments) 378.434 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                      283224
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	200	27	8) N	24	2.5	2 2	21	20	19	18	17	16	15	14	13	12	11	10		0	7	6	· UT	4	L	N	-	NO.	Result
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JC4163	A75531	JE0367	T17229	H83619	D84688	T30692	G90053	AE2596	G97378	G86168	818	B35098	615	S37671	T13065	A37127	T42567	AI2016	T14756	T04104	T04106	A56605	VHWVEV	S72350	I38346	S26373	æ	T00373	ID	
DNA-binding	hypothetical	zinc finger	hypothetical	μ.		probable r	rt .	tonB protein	hypothetical	hypothetical	rt -				PIP82 pro	₽	tegument)	hypothetical		B-type cyc	B-type cy	structural	structural		elastic t	genome po		hypothetical	scripti	
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45	44	43	42	41	40	39	38	37	36	Ç	34	ü	32	31	30
67.5	67.5	67.5	67.5	68	68	89	68	89	68	68	68	68.5	68.5	69	69
14.7	14.7	14.7	14.7	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.9	14.9	15.0	15.0
2441	2440	854	422	1415	745	710	614	514	407	249	170	880	372	968	408
N	N	N	N	N	N	N	N	N				N		N	N
S39161	S39162	S02003	T24865	T21244	T12528	D96728	T16268	A33879	I52703	JH0629	T48144	B87222	F43674	S46992	T32767
			hypothetical prote	zyg-9 protein - Ca			hypothetical prote	aminopeptidase ysc	42K membrane glyco	cleavage signal-1	hypothetical prote	7	ein - h	_	hypothetical prote

ALIGNMENTS

NESULT 2 VINVEE Structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137) N.Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein C;Species: eastern equine encephalomyelitis virus C;Species: 31-Mar-1999 #sequence_revision 31-Mar-1999 #text_change 16-Jul-1999 C;Accession: A26816 R;Chang, G.J.J.; Trent, D.W. J. Gen. Virol. 68, 2129-2142, 1997 A;Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equinus region and the sequence of the genome region encoding the 26S mRNA of eastern equinus region and the sequence of the genome region encoding the 26S mRNA of eastern equinus region and the sequence of the genome region encoding the 26S mRNA of eastern equinus re	Query Match Best Local Similarity 35.1%; Pred. No. 2.6; Matches 27; Conservative 6; Mismatches 33; Indels 11; Gaps Qy 13 AIQANINIPMGAFRPGAG	RESULT 1 T00373 Typothetical protein KIAA0649 - human C;Species: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00373 R;Ishikawa, K:, Nagase, T.; Suyama, M:, Miyajima, N.; Tanaka, A.; Kotani, H.; DNA Res. 5, 169-176, 198 A;Title: Prediction of the coding sequences of unidentified human genes. X. Th A;Reference number: Z14142; MUID:98403880; PMID:9734811 A;Accession: T00373 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1209 <ish>A;Residues: 1-1209 <ish>A;Residues: 1-1209 <ish>A;Residues: EMBL:AB014549; NID:g3327111; PIDN:BAA31624.1; PID:g3327112 C;Genetics: A;Note: KIAA0649</ish></ish></ish>
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A; Molecule type: mRNA
A; Residues: 1-1241 <VOL>
A; Cross-references: EMDL: X63135; NID:959185; PIDN:CAA44845.1; PID:959186
A; Cross-references: EMDL: X63135; NID:959185; PIDN:CAA44845.1; PID:959186
A; Note: sequence could not be checked because of bad print in paper
C; Superfamily: togavirus structural polyprotein
C; Keywords: capsid protein; envelope protein: glycoprotein; polyprotein
C; Keywords: capsid protein C #status predicted <CAP>
F; 260/Product: capsid protein E3 #status predicted <EP3>
F; 324-743/Product: envelope protein E3 #status predicted <EP2>
F; 744-800/Product: envelope protein E1 #status predicted <EP1>
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                                                   C;Accession: 138346
R;Labeit, S.; Kolmerer, B.
R;Labeit, S.; Kolmerer, B.
R;Labeit, S.; Kolmerer, B.
R;Cience 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: 138346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V. Mol. Gen. Mikrobiol. Virusol. 8-15, 1980 and 1980 encephalomyelitis virus A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus A;Reference number: S26369; MUID:91375524; PMID:1896061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome polyprotein - eastern equine encephalomyelitis virus N;Contains: 6K protein; capsid protein C; Envelope protein E1; envelope protein C;Species: eastern equine encephalomyelitis virus C;Species: eastern equine encephalomyelitis virus C;Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
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                                                                                                                                                                                                   elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38346
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A;Status: preliminary; translated A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
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27.9%;
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Pred. No. 11;
14; Mismatches
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Pred. No. 11;
4; Mismatches 2
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R;Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.B.; Chang, G.J Virology 197, 375-390, 1993
A;Title: A comparison of the nucleotide sequences of eastern and western equine encephal A;Reference number: S72349; MUID:94025587; PMID:8105605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structural polyprotein - eastern equine encephalomyelitis virus N;Contains: 6K protein; capsid protein; E1 protein; E2 potein; E3 protein C;Species: eastern equine encephalomyelitis virus C;Species: eastern equine encephalomyelitis virus C;Date: 04-May_1998 #sequence_revision 15-May-1998 #text_change 26-Aug-1999
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C;Genetics:
F;261-323/Product: membrane glycoprotein E3 #status predicted <EG3>
F;324-743/Product: membrane glycoprotein E2 #status predicted <EG2>
F;324-743/Product: membrane glycoprotein E2 #status predicted <EG2>
F;695-712/Domain: transmembrane #status predicted <TM2>
F;722-738/Domain: transmembrane #status predicted <TM3>
F;744-799/Product: 6K protein #status predicted <KP6>
F;781-799/Domain: transmembrane #status predicted <TM4>
F;880-1240/Product: membrane glycoprotein E1 #status predicted <EG1>
F;1212-1236/Domain: transmembrane #status predicted <TM5>
F;1212-1236/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                       A;Molecule type: genomic RNA
A;Residues: 1-1240 cwtsp.
A;Rote: the authors translated the codon AGC for residue 836 as Arg and GUI
A;Note: the authors structural polyprotein
C;Supperfamily: togavirus structural polyprotein; transmembrane protein
C;Reywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;4-260/Product: coat protein C #status predicted <CPC>
F;259-276/Domain: transmembrane #status predicted <TM1>
F;259-276/Domain: transmembrane #status predicted <TM1>
C;000 coat protein C #status predicted <TM1</pre>
F;259-276/Domain: transmembrane #status predicted <TM1</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structural polyprotein - eastern equine encephalomyelitis virus (strain VA33[Ten Broeck] N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein C;Species: eastern equine encephalomyelitis virus A;Note: host Equis caballus (domestic horse)
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A;Cross-references:
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A;Title: Molecular evolution of eastern equine encephalomyelitis virus in North A;Reference number: A39992; MUID:91220727; PMID:2024496
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Weaver, S.C.; Sco
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Pred. No.
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Pred. No. 94;
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Gene 195, 167-175, 1997
A;Title: Alternative splicing of cyclin transcripts in maize endosperm A;Reference number: Z15213; MUID:97449292; PMID:9305761
A;Accession: T04106
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A;Residues: 1-1242 <WEA>
A;Residues: 1-1242 <WEA>
A;Cross-references: GB:L20951; NID:g405814; PIDN:AAA02897.1; PID:g305047
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:119924, NCBIP:119931)
C;Superfamily: togavirus structural polyprotein
C;Keywords: polyprotein
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A;Title: Genetic characterization of an antigenic subtype of eastern equine encephalomy. A;Reference number: A56605; MUID:93090093; PMID:1280945
A;Accession: A56605
                                                                                                                                                                      A;Cross-references: EMBL:U66662; NID:g1546054; PIDN:AAB72019.1; PID:g1546055
A;Experimental source: cultivar Pioneer 3925
C;Superfamily: cyclin
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-458 <SUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-type cyclin homolog (clone CycZme3) - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04106
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                                     10 NVRAIQANINIPMGAFRPGAGQPPRRKEC--TPEVEEGVPPTSDEEKKPIPGAKKL 63
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NDRAAPANROKPLDAVFNRNGKAVKLKECKVKPEVIVSIPDSEKEKKSKFPGGOKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEDLRRSIANLTLKQRAPNPPAGPPAKRKKPAPKPKPAQAKKKRPPPPAKKQKRKPKPGK 100
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                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                         16.8%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 77.5; E
27.4%; Pred. No. 16;
tive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77.5; D
Pred. No. 16;
14; Mismatches
                                                                                        8;
                                                                                                              Score 77; DB 2; Length 458; Pred. No. 6.2;
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1240;
                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                      <u>ب</u>
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                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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R;Sun, Y.; Flannigan, B.A.; Madison, J.T.; Setter, T.L. Gene 195, 167-175, 1997
A;Title: Alternative splicing of cyclin transcripts in maize A;Reference number: Z15213; MUID:97449292; PMID:9305761
A;Accession: T04104
                                                                                                                                                  C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. A;Noto: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B-type cyclin hómolog - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z18181
A; Accession: T14756
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                                                                                                                                                                                                                 hypothetical protein alr1687 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                        AI2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AL110210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-990 <WAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein DKFZp564F0923.1 - C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-479 <SUN>
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                                                                                                                                                                                                                                                                                                                  897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 NVRAIQANINIPMGAFRPGAGQPPRRKEC--TPEVEEGVPPTSDEEKKPIPGAKKL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                               60 AKKLPGPAVNLSEIQNIKSELKYVPKAEQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                        7 PVSNVRAIQANINI-PMG-----AFRPGAGQPPRRKECTPEVEEGVPPTSDEEKKPIPG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKFZp564F0923.1
                                                                                                                                                                                                                                                                                                              SSPPP-----LSSPLPEAPQPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195/3; 434/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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ilarity 35.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetal brain; clone DKFZp564F0923
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Pred. No. 6.5;
8; Mismatches
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Pred. No. 1
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30-Jun-2002
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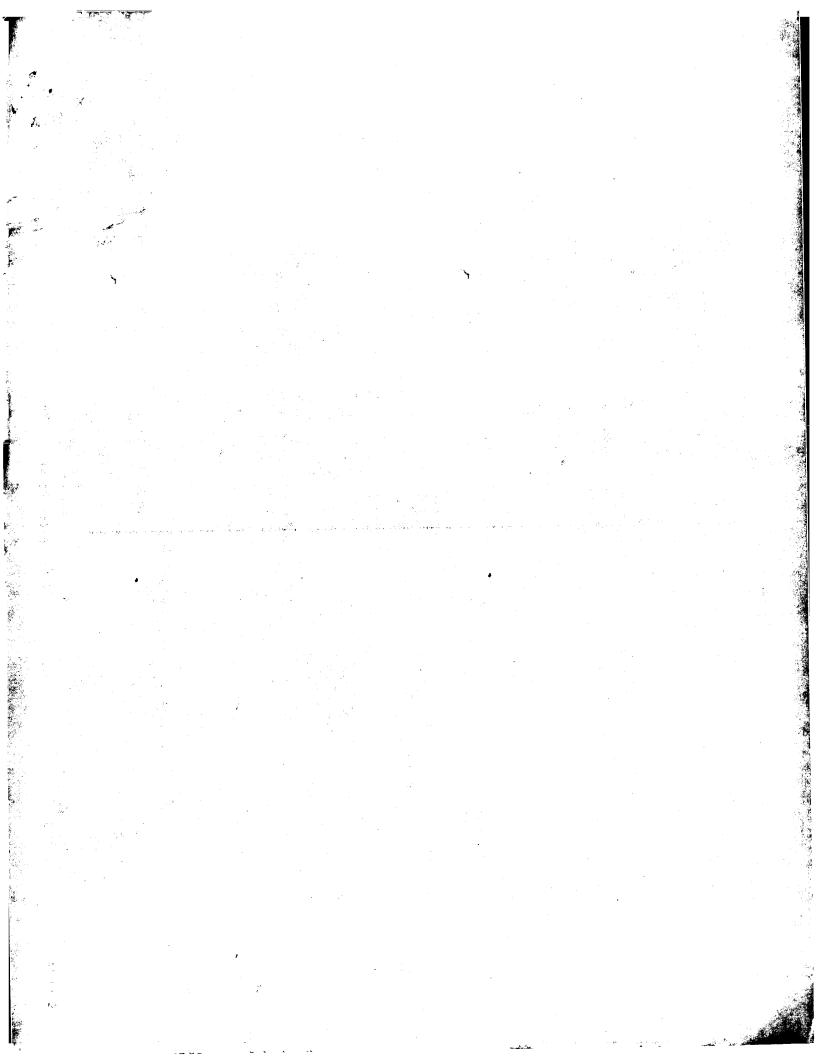
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A;Molecule type: DNA
A;Residues: 1-3534 <TEL>
A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59539.1;
A;Sperimental source: strain NS80567
C;Cenetics:
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C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_re
C;Accession: T42567
R;Telford, E.A.; Watson, M.S.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000019; PIDN:BAB78053.1; PID:g17135507; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1687
                                                                                                     C;Accession: A37127; A32866
R;Aizawa, H.; Emori, Y.; Murofushi, H.; Kawasaki, H.; Sakai, H.; Suzuki, K.
J. Biol. Chem. 265, 13849-13855, 1990
A;Title: Molecular cloning of a ubiquitously distributed microtubule-associated A;Reference number: A37127; MUID:90338002; PMID:2380192
A;Accession: A37127
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KUR>
               A;Molecule type: mRNA
A;Residues: 1-1072 <AIZ>
A;Cross-references: GB:D90149; GB:J05557;
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.;
                                                                                                                                                                                                                                C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change
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A;Title: The DNA sequence of equine herpesvirus 4.
A;Reference number: Z22173; MUID:98264497; PMID:9603335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                               N; Alternate names: 190K microtubule-associated protein; MAP-U
                                                                                                                                                                                                                                                                                                      microtubule-associated protein U - bovine
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Biol.
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Pred. No. 4.8;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVNLSEIQNIK
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                    Ξ.,
               NID:g217577; PIDN:BAA14179.1; PID:d1014882; Kotani, S.; Suzuki, K.; Sakai, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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C; Generator: 6p21.3
A; Map position: 6p21.3
A; Introns: 38/2; 97/2; 129/3;
A; Introns: 3e/2; collagen alpha
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C;Keywords: microtubule binding; tandem repeat
C;Keywords: microtubule binding; tandem repeat
F;877-907/bomain: MAP2/tau repeat homology <MT1>
F;880-901/Region: microtubule binding #status predicted
F;833-945/bomain: MAP2/tau repeat homology #status atypical <MT2>
F;937-1004/bomain: MAP2/tau repeat homology <MT3>
F;977-1004/bomain: MAP2/tau repeat homology *#status atypical <MT4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; PLICULE VIE SURS
A; Residues: 1-1171 <SURS
A; Cross-references: EMBL: AF067153; NID: 93171244; PID: 93171245;
A; Cross-references: Strain Canton-S, photoreceptor
                                                                                             A;Molecule type: DNA
A;Residues: 1-1870 <BOU>
A;Cross-references: EMBL:Z15025;
                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: $37671 A; Accession: $37671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z17597; A; Accession: T13065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Suri, V.; Qian, Z.; Hall, J.C.; Rosbash, M.
Neuron 21, 225-234, 1998
A;Title: Evidence that TIM light response is relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIP82 protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
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                                                                                                                                                                                                                                                           R;Bougueleret,
                                                                                                                                                                                                                                                                                                   C; Date: 20-Feb-1995
                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                 MHC class III histocompatibility antigen HLA-B-associated protein 2 [similarity]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
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                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                  Accession: S37671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 OPPRRKECTPEVEEGVPPTSDEEKKP-----IPGAKKLPGPA
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27.4%; Pred. No. 21;
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           154/1; 202/1; 252/3; 279/2; 327/1; 357/2; 429/3; 588/1; 6 1(IV) chain
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                                                                                                NID:g29374; PID:g29375
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Search completed: April 9, 2003, 12:39:40
Job time : 26.3548 secs Query Match 16.1%; Score 74; DB 2; Length 1870; Best Local Similarity 35.0%; Pred. No. 54; Matches 21; Conservative 8; Mismatches 15; Indels 16; Gaps 4.

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Sequence:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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           protein search, using sw model
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1 MSKQPASNIRSIQA
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ster than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/backfIles1.pep:*
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16.9
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                                                                                                                                                                                                                                                                                                                                                                                                         Length
          2003, 12:33:56;
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                                            US-08-696-827-1
US-08-680-326-36
5223391-5
US-09-149-476-623
US-08-839-008-9
US-08-839-008-9
US-08-9-095-443-2
5273901-7
54827-757-0228-14
US-07-757-0228-74
US-07-757-0228-74
US-07-757-0228-10
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155.253 Million cell updates
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Sequence 623, Appli Sequence 9, Appli Sequence 9, Appli Patent No. 5482709 Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 58, Appl Sequence 44, Appl Sequence 44, Appl Sequence 42, Appl Sequence 50, Appl Sequence 50, Appl Sequence 60, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 2, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli
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Sequence 36, Appl
Patent No. 5223391
                                                                                                                                                                                                                                                                                                                                                                                                    Description
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  Query Match
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Database

Minimum DB Maximum DB

Result

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19.1%;

Score 74.5;

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Length 244;

RESULT 1 US-08-696-827-1 US-08-696-827-1 Sequence 1, Application US/08696827 Patent NO. 5798213 GENERAL INFORMATION: APPLICANT: MIYADERA KAZUTAKA APPLICANT: YAWADA, Yuji APPLICANT: YAWADA, Yuji APPLICANT: YAWADA, Yuji APPLICANT: YAWADA, Shinichi TITLE OF INVENTION: MONOCLONAL ANTIBODIES NUMBER OF SEQUENCES: 2 CORRESSONDENCE ADDRESS: ADDRESSERE SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W., Suite 800 CITY: Washington, D.C. STATE: D.C. COUNTRY: U.S.A. ZIP: 20037 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER, IEMP PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/696,827 FILING DATE: 21-AUG-1996 PRIOR APPLICATION NUMBER: US/08/696,827 FILING DATE: 25-DEC-1995 PRIOR APPLICATION NUMBER: 9CT/USJP/02661 FILING DATE: 25-DEC-1995 PRIOR APPLICATION NUMBER: 03.764 REFERENCE/DOCKET NUMBER: 0-764 REFERENCE/DOCKET NUMBER: 0-7656 REFERENCE/DOCKET NUMBER: 0-76	28 63 16.2 489 4 US-09-249-200-7 29 63 16.2 518 1 US-08-392-367B-2 30 63 16.2 518 3 US-08-893-467A-2 31 63 16.2 905 2 US-08-893-467A-2 31 63 16.2 905 4 US-09-357-014-9 32 63 16.2 1135 2 US-08-574-959A-7 34 63 16.2 1135 2 US-08-574-959A-7 35 62.5 16.0 83 2 US-08-499-676A-10 36 62 15.9 169 4 US-09-483-533-28 37 62 15.9 169 4 US-08-483-533-28 38 62 15.9 169 4 US-08-483-533-28 39 62 15.9 355 4 US-08-483-533-41 40 62 15.9 355 4 US-09-283-471A-41 40 62 15.9 355 4 US-09-283-471A-41 40 62 15.9 355 9 US-08-483-532-3 41 62 15.9 1400 3 US-08-080-255-7 42 62 15.9 1400 3 US-08-080-255-7 43 62 15.9 1400 3 US-08-061-376-5 44 62 15.9 340 4 US-09-61-376-5 45 61.5 15.8 179 4 US-09-612-126-11
	Sequence 7, Appli Sequence 2, Appli Sequence 9, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appli Sequence 28, Appli Sequence 28, Appli Sequence 41, Appli Sequence 41, Appli Sequence 7, Appli

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                                                                                                                                                     5223391-5
                                                                                                                                                                     RESULT 3
SEQ
                                                                                                  Patent No. 5223391
APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
TITLE OF INVENTION: INHIBITIORS OF HERPES SIMPLEX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 36, Application US/08680326 Patent No. 5925733
                                                                                     REPLICATION
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,326
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
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CORRESPONDENCE ADDRESS:
            NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,634
FILING DATE: 21-FEB-1990
 ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                       641 GRFRGAGGEAPKRPAAAREDEER---PEEEGEDEDEREEGGGEREPDGA 686
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                        Local
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STRAND, KURT
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RESULT 4
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Best Local Similarity
Matches 15; Conserv
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CURRENT APPLICATION NUMBER: US/09/149,476
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                                                                                                                                                                                              FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/040,163
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                                                   APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598
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                                                                                                           FILING DATE: 1997-05
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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Pred. No. 8.6;
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8R APPLICATION NUMBER: 60/056,911

8R PILING DATE: 1997-08-22

8R APPLICATION NUMBER: 60/056,636

8R FILING DATE: 1997-08-22

8R APPLICATION NUMBER: 60/056,874

8R FILING DATE: 1997-08-22

8R APPLICATION NUMBER: 60/056,910

8R FILING DATE: 1997-08-22

8R FILING DATE: 1997-08-22 ER APPLICATION NUMBER: 60/056,895
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ER APPLICATION NUMBER: 60/048,974
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,876
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ER APPLICATION NUMBER: 60/056,877
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ER APPLICATION NUMBER: 60/056,889
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ER APPLICATION NUMBER: 60/056,893
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APPLICATION NUMBER: 60,
FILING DATE. 100 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,888
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APPLICATION NUMBER: 60/056,879
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APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: PILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-05-APPLICATION NUMBER: 6 FILING DATE: 1997-05-FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568 APPLICATION NUMBER: 60 FILING DATE: 1997-05-FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-05-APPLICATION NUMBER: 60/047,632 : 1997-05-23 NUMBER: 60/ 1997-04-60/043,569 60/043,674 60/047,601 60/047,596

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2R FILING DATE: 1997-09-05
2R APPLICATION NUMBER: 60/056,884
2R FILING DATE: 1997-08-22
2R APPLICATION NUMBER: 60/057,669
2R FILING DATE: 1997-09-05
2R APPLICATION NUMBER: 60/049,610 R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: FILING DATE: 1997-05 APPLICATION NUMBER: FILING DATE: FILING DATE: APPLICATION NUMBER: FILING DATE: 1997-0 FILING DATE: APPLICATION NUMBER: FILING APPLICATION NUMBER: 60/043,578 APPLICATION NUMBER: 6 FILING DATE: 1997-05-FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/057,761 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 APPLIATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 FILING LING DATE: DATE: DATE: NUMBER: 60/061,060: 1997-10-02 NUMBER: 60/048,964 NUMBER: NUMBER: NUMBER: 60/047,588: 1997-05-23 1997-06-13 1997-06-06 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-04-11 1997-04-1 1997-08-22 1997-05-23 1997-04-1 1997-05-23 1997-08-2 1997-05-23 60/056,908 60/056,887 60/056,909 60/056,632 60/043,670 60/047,501 60/043,576 60/047,614 60/047,599 60/047,595

Query Match
16.9%; Score 66; DB 4; Length 232;
Best Local Similarity 28.6%; Pred. No. 3.6;
Matches 10; Conservative 11; Mismatches 14; Indels

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166 GSGLPPMESOFOGEDRKFAPSDKSOPPTTEREOVP 200

26 GAGOPPKRKEFSTEEEQHVPTPESEEKSEEKKPIP

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Peter R

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                                                                                                                                   RESULT 6
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Best Local Similarity
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                                                                                      Sequence 9, Applic
Patent No. 5916758
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                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50:
TELECOMMUNICATION INFORMATION:
TELEPHONE: .610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                        GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION NUMBER: (
                         APPLICANT:
APPLICANT:
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                                                                                                                                                                                273 LPRGTAKEGOGPGPKR----GTEPKVKLP-PKSQPPEKTEESPSAPDAPTCP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-NOV-1995
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                                                                                                                                                                                                             18 IPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESE--EKSEEKKPIPGAVKLP 66
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19406
                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                     Application US/08839008
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McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
Young, Peter R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young, romo
                                                                                                                                                                                                                                                                                                                                                                               449 amino acids
                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hurle, Mark R
                                         McDonnell, Peter C
                                                                                                                                                                                                                                             Conservative
           McNulty, Dean E
Rosen, Craig A
                                                         Hurle, Mark R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1997
                                                                                                                                                                                                                                                        16.7%;
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                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                            Score 65; DB 2
Pred. No. 11;
7; Mismatches
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                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                          Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                  US-09-095-443-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION UMBER: 08/563,697
PILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0.
FILING DATE: 23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Baumeister Kirk
REGISTRATION NUMBER: 3,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yue, Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF ALP RELATED DISORDERS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                   APPLICANT: Plowman, Gr
APPLICANT: Peles, Eior
                                                                                                                                                                                                                                                                                                                                                                                                                                                273 LPRGTAKEGQGPGPKR---GTEPKVKLP-PKSQPPEKTEESPSAPDAPTCP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U:
ZIP: 19406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 IPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESE--EKSEEKKPIPGAVKLP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                 STREET:
                                                                                                                     ZIP:
                                                                                                                                                                                   STREET:
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                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                 90071-2066
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                                                                                                                                                                                                  E: Lyon & Lyon
633 West Fifth
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    SmithKline Beecham Corporation
709 Swedeland Road

                                                                                                                                                                                   Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                            IBM Compatible
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50384
                                                                                  1.44 Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
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RESULT 9
5487709-6
;Patent No. 5482709
; Patent No. 5482709
; APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF, MICHAEL D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
5273901-7
;PATENT NO. 5273901
;PATENT NO. 5273901
; APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILSON,
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;SUSAN D.;POPE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
;SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 180
5273901-7
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Best Local Similarity 42.1%;
Matches 16; Conservative
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Best Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/581,693
PRICING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1132 PISSIQATIAKLSIRPPGGLESPVASLPGPAEPPGLPPASLPESTPIPSSSPPPLSSPLP 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/0
FILING DATE: June 12, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                              11 KREE---EEBEREERGEEEEKEEERAAAPAAATAAAPA 45
                                                                                                                                                                                              32 KRKEFSTEEEQHVPTPESEEKSEEKKPIPGAVKLPGPA 69
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESBEKSEEKKPIPGAVKLPGPAFNL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                          Score 63.5; DB 6; Length 180; Pred. No. 5.1; Indels
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Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1274;
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RESULT 10
US-07-757-022B-14
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; TITLE OF INVENTION: BIMERIA ANTIGENIC COMPOSITION WHICH; BLICITS, ANTIBODIES AGAINST AVIAN COCCIDIOSIS; NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:6
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COMPUTER: IM PC COMPATIBLE
COMPUTER: IM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
- PRIOR APPLICATION NUMBER: US 07/457,196
- PRIOR APPLICATION NUMBER: US 07/457,196
- PRIOR NUMBER: US 07/457,196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hewick, Rodney M.
INTLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 KREE---EEEEREERGEEEEKEEERAAAPAATAAAPA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/07/757,022B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.3%;
Best Local Similarity 28.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 84, Application US/07757022B
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990
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                                                TELEFAX: (617)8
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                                                                                                                                                                            FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      FILING DATE: 29-JUN-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. ARPPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                   SEQUENCE CHARACTERISTICS:
                                                                                                     REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 KEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPT 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 19910910
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                                       TELEPHONE:
                ENGTH:
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: 1022 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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(617)876-5851
OR SEQ ID NO: 14:
                                              (617)876-5851
TD NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics Institute,
                                                                                       (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                JMBER: US 07/390,901
08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Megakaryocyte Stimulating Factors
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-07-757-022B-74
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino aci
                                                                                                                                                                                                                 PILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                  REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AVKLPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 19910:
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                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                 AMINO ACID
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Y: U.S.A.
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87 CambridgePark Drive
                                                                  1038 amino acids
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                                                                                                  (617)876-5851
TO NO: 74:
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Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                      UMBER: US 07/390,901
08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
              protein
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                                                                                                                                                                                     31,822
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Pred. No. 44
                                                                                                                                                                       5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
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Query Match Best Local Similarity

16.3%;

Score 63.5; Pred. No. 45;

DB 4;

Length 1038;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
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                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: CBGIT, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)876-1170
                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                429 KEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 TPKEPAP 452
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                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachus
COUNTRY: U.S.A.
                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                  KQPA-SNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPIPG 61
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Cambridge
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                                                                                                                                                                                                                                                                                        (617)876-5851
                                                                                              Conservative
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Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gesner, Thomas G.
Clark, Stephen C.
                                                                                                                                                                                  protein
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                                                                                                             16.3%;
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                                                                                                                                                                                                                                                                       58:
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                                                                                         Score 63.5; DE
Pred. No. 45;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                            GI 5190
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                                                                                                                          DB 4;
                                                                                         40;
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                                                                                                                          Length 1049;
                                                                                         Indels
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COMPUTER: IBM PC COMPARTIBLE
COMPARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILLING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILLING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILLING DATE: 29-JUN-1990
PRIOR DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-922-635-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: COLYPECTED SEQUENCE LISTING
PATEENT NO. 6033871
CURRENT APPLICATION NUMBER: US/08/922,635A
CURRENT FILING DATE: 1997-09-03
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER APPLICATION NUMBER: 60/012,600
EARLIER APPLICATION NUMBER: 60/012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PILETZ, John E. APPLICANT: IVANOV, Tina R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1070
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 POGSF--ADGOPAERRASNDORPOEVP-----AEALAPAPVEVPAPAPA 630
                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 02140
                                                                                                                                                                                                                                                                                                           STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
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Pred. No. 4
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APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-DIG-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GIS 5190

TELECOMMUNICATION INFORMATION:
TELEPAX: (617)876-5851
LOCKET NUMBER: GIS 5190
TELECOMONICATION NUMBER: GIS 5190
TELECOMONICATION NUMBER: GIS 5190
TELECOMONICATION NUMBER: GIS 5190
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Maximum Match 100%
Listing first 45 so
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                  Score
                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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Match Length
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390
1 MSKQPASNIRSIQANINIPM......KKPIPGAVKLPGPAFNLSET
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118.6
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10 US-09-904-065-8
10 US-09-904-065-8
10 US-10-113-7948-1
9 US-10-113-7948-1
9 US-10-278-173-34
10 US-09-904-065-16
10 US-09-904-065-17
9 US-09-904-065-17
9 US-09-809-391-623
10 US-09-919-497-89
10 US-09-918-497-89
10 US-09-918-497-89
           US-09-864-761-34248
US-10-149-819-6
US-09-904-065-10
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    Sequence 705, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli Sequence 14, Appli Sequence 16, Appli Sequence 16, Appli Sequence 62, Appli Sequence 623, Appli Sequence 189, Appli Sequence 189, Appli Sequence 189, Appli Sequence 4, Appli Sequence 4, Appli Sequence 36182, Appli Sequence 34248, ASequence 34248, ASequence 34248, ASequence 34248, ASequence 10, Appli Sequence 10, Appli
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RESULT 2
US-09-904-065-8
; Sequence 8, Application US/09904065
; Patent No. US20020076789A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
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Matches , 2 112 46	RESULT 1 Sequence 70 Patent No. GENERAL INF APPLICANT: TITLE OF I FILE REFER CURRENT AP CURRENT AP CURRENT AP CURRENT FI I FILE REFER CURRENT FE I CURRENT FE I CURRENT PP I CURRENT PP I CURRENT AP I FI I FI I OUMBER OF SOFTWARE: SEQ ID NO 7 I LENGTH: 6 TYPE: PRT ORGANISM: FEATURE: I NAME/KEY: I OCATION: OTHER INF US-09-764-868 Query Match Best Local	44444444444444444444444444444444444444
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25; Conserva SKOPASNIRSIOANI	ULT 1 09-764-868-705 09-764-868-705 Q9-764-868-705 Applicat atent NO. US200201687 ENERAL INFORMATION: APPLICANT: ROSEN et a TITLE OF INVENTION IN FILE REFERENCE: PTZ32 CURRENT APPLICATION IN CURRENT APPLICATION IN CURRENT FILING DATE: PTIOT application dat NUMBER OF SEQ ID NOS: SOFTWARE: PATENTIN VE EQ ID NO 705 LENGTH: 603 TYPE: PRT ORGANISM: Homo Sapie. PEATURE: LENGTH: SITE LCCATION: (163) OTHER INFORMATION: X 09-764-868-705 usry Match est Local Similarity	16.3 16.3 16.3 16.3 16.3 16.3 16.3 16.3
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Mismatches 35; AGQPPKRKEFST GSYHPGRKRSKTQTPQQRSV KPIPGAVKLPGPAFNLS 73	164868 109/764,868 17 refer to PALM or fi	US-09-904-065-18 US-09-789-054A-40 US-10-124-557-84 US-10-124-557-74 US-10-124-557-104 US-10-124-557-104 US-10-124-557-142 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 US-10-124-557-60 US-10-124-557-62 US-10-124-557-62 US-10-124-557-62 US-10-124-557-62 US-09-932-145-7 US-09-98-2331-16 US-09-98-2331-16 US-09-98-2331-287 US-09-98-2331-287 US-09-98-2338-287
Indels 30; Gaps 3;EEEGHVP 45	lle wrapper occurring L-amino acids	Sequence 18, Appl Sequence 40, Appl Sequence 84, Appl Sequence 84, Appl Sequence 58, Appl Sequence 104, Appl Sequence 142, Appl Sequence 42, Appl Sequence 42, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 7, Appl Sequence 62, Appl Sequence 62, Appl Sequence 61, Appl Sequence 164, Appl Sequence 17, Appl Sequence 167, Appl Sequence 287, App

APPLICANT:

Hopkins, Wathen, Michael

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CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/904,065
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.6%;
Best Local Similarity 34.8%;
Matches 16; Conservative
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                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Flanagan et al.
TITLE OF INVENTION: B EPHRAIN REGULATION OF G-PROTEIN COUPLED
TITLE OF INVENTION: CHEMOATTRACTION
                                                                                                                                                                                                                                                                        Sequence 1, Application US/10113794A Publication No. US20030022202A1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 930
TYPE: PRT
ORGANISM: Mus musculus
S-10-113-79¶A.1
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APPLICANT: Thomsen, Darrell
TITLE OF INVENTION: A Method for Treating Herpes Virus
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APPLICANT: Wathe
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APPLICANT: Thomsen, Darrell
TITLE OF INVENTION: A Method for Treating Herpes Virus
                                                                                                                  CURRENT APPLICATION NUMBER: US/10/113,794A CURRENT FILING DATE: 2002-04-01 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 00221
                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 GRENGGGGEAPKREAAAREDEER---PEEEGEDEDEREEGGGEREF 683
                                                                                                                                                                                                                                                                                                                                                                                          641 GRFRGGGGEAPKRPAAAREDEER---PEEEGEDEDEREEGGGEREP 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72.5; DB 10;
Pred. No. 22;
9; Mismatches 18;
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-07
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SE0 ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
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Publication No
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Publication No. US20030061637A1
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NAME/KEY: SITE
LOCATION: (69)
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TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PA103P1C1
                 FILE REFERENCE: MBI-009
CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                           APPLICANT: Jiang, Cai-Zhong APPLICANT: Brown, Pierre
PRIOR APPLICATION NUMBER: US/09/533,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 260
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 AAPPTERKMFETEADEKEMPLVEGKGPGAEEPAPSKNPSPGQELPPG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 LNESEEEEE 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 QPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEE-QHVPTP------
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                    P: Samaha, Raymond
INVENTION: POLYNUCLECTIDES FOR ROOT TRAIT ALTERATION
                                                                                                                                                                                                                  Riechmann, Jose-Luis
Pineda, Omaira
Zhang, James
Yu, Guo-Liang
                                                                                                     Reuber, Lynne
Ratcliffe, Oliver
Adam, Luc
                                                                                                                                                                              Keddie,
                                                                                                                                                                                  Pilgrim, Marsha
Keddie, James
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5. US20030054421A1
                                                                                                                                                               Heard, Jacqueline
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38.3%;
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Pred. No.
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Pred. No. 11;
8; Mismatches 2
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Best Local Similarity
Matches 15; Conserve
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PRIOR APPLICATION NUMBER: 60/125,
PRIOR FILING DATE: 199-03-23
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 34
LENGTH: 300
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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US-10-278-173-34
CURRENT APPLICATION NUMBER: US/09/904,065
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 1235
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SOPTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 1335
TYPE: PRT
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APPLICANT: Wather
APPLICANT: Hopki
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 16, Application US/09904065 Patent No. US20020076789A1
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Patent No. US20020076789A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: Hopkins, Todd
APPLICANT: Thomsen, Darrell
TITLE OF INVENTION: A Method for Treating Herpes Virus
FILE REFERENCE: 00221
                                                                                                                                          APPLICANT: Homa, Fred
APPLICANT: Wathen, Michael
APPLICANT: Hopkins, Todd
APPLICANT: Thomsen, Darrel
                                                                                                        FILE REFERENCE: 00221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/904,065
CURRENT FILING DATE: 2001-07-12
                                                                                                          PPLICANT: Hopkins, Todd
PPLICANT: Thomsen, Darrell
ITLE OF INVENTION: A Method for Treating Herpes Virus
                                                                                                                                                                                                                                                                                                                                   641 GRFRGAGGEAPKRPAAAREDEER---PEEEGEDEDEREEGGGEREP 683
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Pred. No. 89;
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US-09-904-065-17
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; ORGANISM: herpes simplex
US-09-904-065-17
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Best Local Similarity 32.6
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SEQ ID NO 623
LENGTH: 232
TYPE: PRT
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SEQ ID NO 17
LENGTH: 1235
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Wather
APPLICANT: Hopkir
APPLICANT: Thomse
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
                                                                                                                                                 NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: :
NAME/KEY: SITE
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APPLICANT: Thomsen, Darrell
TITLE OF INVENTION: A Method for Treating Herpes Virus
FILE REFERENCE: 00221
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CURRENT FILING DATE: 2001-07-12
                                                                                          LOCATION: (9)
OTHER INFORMATION:
NAME/KEY: SITE
                            NAME/KEY: SITE
LOCATION: (11)
                                                            OTHER INFORMATION:
                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: herpes simplex
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                               LOCATION: (10)
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Wathen, Michael
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                                                                                                         Xaa equals any of the naturally occurring L-amino acids
                                                      Xaa equals any of the naturally occurring L-amino
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32.6%;
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32.6%;
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Pred. No. 89;
9; Mismatches
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Pred. No. 89;
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; LENGTH: 1690
; TYPE: PRT
; ORGANISM: human
US-09-788-043C-5
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; OTHER INFORMATION: Xaa equals any of the nature
; NAME/KEY: SITE
; LOCATION: (232)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-623
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US-09-788-043C-5
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US-09-919-497-89
US-09-919-497-89
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CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/184,152
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                              Sequence 89, Application U Patent No. US20020106662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09788043C Patent No. US20020107361A1
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                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 89
                                                                                                                                                  APPLICANT: MUTTER, GEORGE L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: BO801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR PILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zuo, Fengrong
APPLICANT: Klonowski, Paul
TITLE OF INVENTION: No. US20020107361A1el Metalloproteases Having
TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
TITLE OF INVENTION: Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ROCH-004
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                                                                                                                                 NUMBER OF SEQ ID NOS: 100
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                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1044 TMGNAIEEEAP---ELDLPGPVF 1063
                                                               ENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    984 AQQPASEVTCSLPLCRWPLGTLGPEGSGSGSSSHELFNEADFIPHHLAPRPSPASSPKPG 1043
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Local Similarity 28.6%;
nes 10; Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SKQPASNIRSIQANINIPMGAFRP-GAGQPPKRKEFSTEEE---QHV---PTPESEEKS- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EEKKPIPGAVKLPGPAF 70
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; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: SITE
; LOCATION: (249)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1282
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US-09-925-301-1282
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                                                                                ; TYPE: PRT; ORGANISM: Homo sapiens US-09-906-779-4
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Shi et al.
APPLICANT: Shi et al.
TITLE OF INVENTION: Human Protein Tyrosine Phosphatase Polynucleotides, Polypeptides
TITLE OF INVENTION: Antibodies
FILE REPERENCE: PT040P1
CURRENT APPLICATION NUMBER: US/09/906,779
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US01/01563
PRIOR APPLICATION NUMBER: 60/176,306
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1282
LENGTH: 458
TYPE: PRT
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                                                                                                                                                                  SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09906779 Patent No. US20020064844A1
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Best Local Similarity 37.3%;
Matches 19; Conservative
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Best Local
Matches
                 Query Match 16.7%;
Best Local Similarity 28.2%;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                              ENGTH: 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 LPRGTAKEGOGPGPKR---GTEPKVKLP-PKSOPPEKTEESPSAPDAPTCP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 LPRGTAKEGOGPGPKR---GTEPKVKLP-PKSOPPEKTEESPSAPDAPTCP 319
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24;
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Similarity 37.3%;
19; Conservative
Conservative
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7; Mismatches
13; Mismatches
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Pred. No.
                     Score 65; DB 10;
Pred. No. 57;
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30; Indels
                                         Length 603;
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SOPTHARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36182
LENGTH: 617
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005529.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN HEALO, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN HEALT LIVER, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN BOALT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BOALT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.0
OTHER INFORMATION: SYPRESSED IN BRAIN SYPRESSED SYPRESSED IN BRAIN SYPRESSED SYPRESSED SYPRESSED SYPRESSED SYPRESSED SYPRESSED SYPRE
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION UNMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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US-09-864-761-36182
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Patent No. US20020048763A1
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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     ED IN HELA, SIGNAL = 1.3
ED IN HELAT, SIGNAL = 0.94
ED IN HEART, SIGNAL = 1.3
ED IN ADULT LIVER, SIGNAL = 1.1
ED IN FETAL LIVER, SIGNAL = 1.3
ED IN BRAIN, SIGNAL = 5.6
OT HIT: P12036, EVALUE 2.00e-33
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; OTHER INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22 US-09-864-761-36182
Query Match
Best Local Similarity
Matches 15; Conserva
               16.7%;
37.5%;
               Score 65;
Pred. No.
                 DB 10; Length 617, 58;
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Search completed: April Job time : 18.6331 secs

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Maximum Match 100%
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Perfect score:
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390
1 MSKQPASNIRSIQANINIPM......KKPIPGAVKLPGPAFNLSET 75
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1: /SIDS2/gcgdata/
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
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AAY28834 AAY28651 AAE16632 AAY28650 ABG11263 ABG23750 AAU873044 AAU93023 AAU93023 AAU93023 AAU93023	ID
Xenopus chisel (Csl) Human chisel (Csl) Human 66214 protei Murine chisel (Csl) Novel human diagno Novel human diagno Novel central nerv Arabidopsis transc Arabidopsis thalia Drosophila melanog	Description

Drosophila melanog	ABB58529	22	771	17.4	ď	Ü	
	29	23	280	17.4	6 60	4	
ria	AAU72954	23	280	17.4	68	43	
t and ovari	AAB58795	21	260	•	68	42	
	AAM40893	22	746	٠	. 8	41	
	AAM40892	22	746	•		40	
polypeptide	AAM39106	22	739	•	68.5	39	
	AAB43147	21	712	•			
Human polypeptide	AAM39107	22	672			37	
phila mela	ABB63735	22	1557	•	6	36	
Φ	ABB57023	23	1072	17.7	69	35	
Novel human diagno	2	22	146		69	4	
ŏ	ABB66983	22	716	•	70	ω u	
human d	ABG20365	22	1098		71	32	
	AAM78535	22	907		71	31	
	AAM79519	22	893		71	30	
Human polypeptide	AAM40566	22	495	•	71	29	
polypept	AAM38780	22	356		71	28	
к	AAB33047	21	128		72	27	
00	AAE18865	23	1235		72.5	26	
s simple	AAE18856	23	1235		72.5	25	
	AAU17140	22	603		73	24	
centra	AAU87594	22	603		73	23	
Novel human secret	AAU33195	22	2153		73.5	22	
	AAU02976	22	517		•	21	
Human ovarian anti	ABP41705	23	513		74.5	20	
Recombinantly prod	AAW62026	19	482		•	19	
Human platelet der	AAR77531	17	482		•	18	
Placental derived	AAR20641	13	482		74.5	17	
Angiotensin conver	AAU02918	22	442		•	16	
Angiotensin conver	AAU02917	22	363			15	
Human protein semi	75	22	359	•		14	
Angiotensin conver	291	22	323	19.1	4	13	
ă	94	17	244	19.1	74.5	12	
Novel human diagno	ABG25362	22	167	19.1	4	11	

ALIGNMENTS

RESULT 1 AAY28834 17-JAN-2000 Xenopus chisel (Csl) protein. AAY28834 standard; Protein; 75 AA. (first entry)

Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; xenopus; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myogathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain. Xenopus sp.

WO9950410-A1.

07-OCT-1999.

26-MAR-1999; 99WO-AU00220.

27-MAR-1998; 98AU-0002634.

(CHAN-) CHANG CARDIAC RES INST VICTOR. (GEHO) GEN HOSPITAL CORP. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

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RESULT 2
AAY28651
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, skeletal myopathies such as Duchenne muscular dystrophy and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, myofiber atrophy, etc. The Csl gene sequence can also be used in gene therapy, for the production of transgenic animals and for drug screenir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the xenopus chisel protein (Csl), that is a member of the EF-Hand protein super family and is involved in signalling pathways. Csl protein is localised to the nucleus and does not show significant homology to any known protein. Structural homology between Csl and scallop regulatory myosin light chain is however detected. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                      Chisel protein; CS1; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; regulation; Xq21.3-q22; adaptive process; muscle homeostasis; cardiac hypertrophy; detection; diagnosis; prophylaxis; treatment; differentiation; nucleus; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; skeletal myopathy; Becker's myotonic dystrophy; heart failure; transgenic animal; drug screening; gene therapy; homology; scallop regulatory myosin light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chisel (Csl) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28651 standard; Protein; 88
(CHAN-) CHANG CARDIAC RES INST VICTOR. (GEHO) GEN HOSPITAL CORP.
                                                                                                                                26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                    98AU-0002634.
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Pred. No. 8.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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RESULT 3
AAE16632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the EF-Hand protein super family and is involved in signalling the protein super family and is involved in signalling to the mouse Csl protein is localised to the nucleus and has 86% homology ct to the mouse Csl. Structural homology between Csl and scallop regulatory cx myosin light chain is also detected. It is predominantly expressed in cycle art and skeletal muscles and is activated after the differentiation of coaltive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic ct treatment of diseases such as those involving aberrant muscle cell cc development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, skeletal myopathies such as Duchenne cmuscular dystrophy and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, myofiber atrophy, etc. The Csl gene cc sequence can also be used in gene therapy, for the production of transgenic animals and for drug screening.
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                                                                                                                                                                                                          Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 3; 157pp; English.
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                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                  Human 66214 protein
                                                                                                                                                                                                                                                                                                                                                                      09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE16632 standard; Protein; 88
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                                                                                                                        WO200192567-A2
                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is the human chisel protein (Csl), that is a member the EF-Hand protein super family and is involved in signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAKKLPGPAVNLSE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAVKLPGPAFNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSKQPVSNVRAIQANINIPMGAFRÞGAGQÞÞRRKECTÞEVEEGVÞ-ÞTSD---EEKKÞIÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiomyopathy,
                                                                                                                                                                                             sequence tag; EST; 66214 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 AA;
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Pred. No. 3.3e-22;
6; Mismatches 8;
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30-MAY-2000; 2000US-207400P 30-MAY-2001; 2001WO-EP06165

(MEDI-)

MEDIGENE

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method comethods for testing the predisposition of mammals and preferably humans comes for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, compathy, specific heart muscle disease, rhythm and conduction disorders, myopathy, specific heart muscle disease, rhythm and conduction disorders, compathy, specific heart muscle disease, rhythm and conduction disorders, compathy, specific heart muscle disease, rhythm and conduction disorders, compathy, specific heart disease, valvular compations, pulmonary heart disease, valvular compations, pulmonary heart disease, valvular condocarditis. Sequences of the invention are also used in gene therapy. Care useful for the development for medicaments for the treatments of heart diseases. The present sequence is 66214 protein encoded by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                       Chisel protein; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; nucleus; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; buchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; scallop regulatory myosin light chain.
              26-MAR-1999;
                                                07-OCT-1999
                                                                                                                                                                                                                                                                                                 Murine chisel (Csl) protein.
                                                                                                                                                                                                                                                                                                                                     17-JAN-2000 (first entry)
                                                                                WO9950410-A1
                                                                                                                                                                                                                                                                                                                                                                                                       AAY28650 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAVKLPGPAFNLSE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEEGVP-PTSD---EEKKPIP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAKKL PGPAVNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-122073/16
)B; AAD27216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reuner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence tag (EST) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9c;
          99WO-AU00220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.3%;
75.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 274; DB: Pred. No. 3.3e. 6; Mismatches
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.3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 52
           31-MAR-2000;
23-AUG-2000;
                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                    WO200175067-A2
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                Human; chromosome
                                                                                                                                                                                                                        Novel human diagnostic protein #11254.
                                                                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                                                                                                      ABG11263 standard; Protein; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids encoding chisel, used to develop products for treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610852/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harvey RP, Musaro A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHAN-)
(GEHO)
(HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKQPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVKLPGPAFNLSE 74
                                                                                                                                                                                                                                                                                                                                                                                                    GMKKFPGPVVNLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGAPT----TSEEKKPIP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANG CARDIAC RES INST VICTOR.
GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
           2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                          (first entry)
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70.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 262.5; DB
Pred. No. 5.5e-21
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                           forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) is useful in gene therapy techniques
CC (II), (II) is useful for generating amtibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Mote: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS75450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 41622; 103pp; English
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                                                                                                                                                                                                                       Novel human diagnostic protein #23741.
                                                                                                                                                                                                                                                                                                                        ABG23750 standard; Protein; 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
31-MAR-2000; 2000US-0540217
                                                                                                                                                                           food
                                                                                                                                                                                         Human; chromosome mapping;
                                                                                                                                                                                                                                                        18-FEB-2002
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                                             30-MAR-2001; 2001WO-US08631
                                                                                                             WO200175067-A2
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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                                                                                                                                                                                                                                                                                                                                                                                                                                    KSEEKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQIVHAIVCGLRMPLSGFPPWVGQVFLALIQPRRQSKTPSKKKEEEEEEEEEEEEEE 80
                                                                                                                                                                         supplement;
                                                                                                                                                                                                                                                                                                                                                                                                       HHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASNIRSIQANINIPMGAFRPGAGQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences.
                                                                                                                                                                             medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%;
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                                                                                                                                                                           imaging;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                         gene mapping; gene therapy;
maging; diagnostic; genetic c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 172; 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PPKRKEFSTEEEQHVPTPESEE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of mutations
                                                                                                                                                                             ; forensic; disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Query Match
                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                         The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 54109; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-2000; 2000US-0649167.
                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                              602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                              À,
                          20.6%;
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; Score 80.5; D; Pred. No. 2.2; 12; Mismatches
                                                   멂
                                                22;
                                                Length 602;
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RESULT AAU87304 Novel central nervous system protein #214. AAU87304 standard; Protein; 521 05-JUN-2002 (first entry)

Ś 밁 Ś

ESEEKSEEKK 57

443 48

VSROPSAELGLRPMOASQERKINFP---

-GPSPGFPPKRQNKTLSRREKKEEEKEEE 498

RKEFSTEEEQHVPTP 47

1 MSKQPAS--NIRSIQAN----INIPMGAFRPGAGQPPK-----

Matches

24; Similarity

Conservative

17;

Indels

17;

Gaps

4

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499

EEEEEGEEEK 508

Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; preservative; gene therapy

08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 112-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000	30-JUN-2000 07-JUL-2000 11-JUL-2000 11-JUL-2000 14-JUL-2000 26-JUL-2000 14-AUG-2000 15-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000	Homo @apiens. WC200155318-A2 02-AUG-2001. 17-JAN-2000; 2 31-JAN-2000; 2 24-FEB-2000; 2 24-FEB-2000; 2 17-MAR-2000; 2 18-APR-2000; 2 19-APR-2000; 2 19-APR-2000; 2 19-APR-2000; 2 28-JUN-2000; 2
2000US-0231243 2000US-02311414 2000US-0231413 2000US-0231414 2000US-0232080 2000US-0232081 2000US-0232081 2000US-023298 2000US-023298 2000US-023298 2000US-023298 2000US-023298 2000US-023290 2000US-023290 2000US-0233063 2000US-023401 2000US-023401 2000US-023401 2000US-023401 2000US-023401 2000US-02340998	2000US-0215135 2000US-0216867 2000US-0217487 2000US-0217496 2000US-0217496 2000US-0229964 2000US-0225213 2000US-0225214 2000US-0225213 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225757 2000US-0225757 2000US-0225759 2000US-0225759 2000US-0225759 2000US-0225757 2000US-0225759	A2. A2. A2. A2. A2. A2. A2. A2.
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X P P P P P P P P P P P P P P P P P P P	7 R R R R R R R R R R R R R R R R R R R	
17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000;	20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 00-NOV-2000 00-NOV-2000 08-NOV-2000	26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 01-OCT-2000 01-OCT-2000 01-OCT-2000 01-OCT-2000 01-OCT-2000
000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0 000008-0	2000US-0244786 2000US-0241889 2000US-024481787 2000US-0244817 2000US-0244817 2000US-0244817 2000US-0244874 2000US-0244876 2000US-0244876 2000US-0244876 2000US-0244523 2000US-0246524 2000US-0246524 2000US-0246527 2000US-0246527 2000US-0246528 2000US-0246528 2000US-0246610 2000US-0246611 2000US-0246611 2000US-0249210 2000US-0249210 2000US-0249211 2000US-0249216	2000US - 200

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RESULT 8
AAU93023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, cc angiogenesis, nervous system disorders e.g. Alzheimer's disease and cc amylotrophic lateral sclerosis, infections caused by bacteria, viruses ce.g. Acquired immundeficiency virus (AIDS) and fungi, ocular disorders ce.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cc disorders and irritable bowel syndrome, reproductive system cc disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes cd and pituitary dwarfism, cancers and disorders at the cellular level e.g. cleukaemia, disorders involving neovascularisation e.g. malignancies, cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cc acute kidney failure and blood related disorders e.g. myocardial cc infarction. The polypsptides can also be used to aid wound healing and cc pithelial cell proliferation, to prevent skin aging due to sumburn, to cmintain organs before transplantation, for supporting cell culture of cc maintain can also he used as a food additive or preservative to
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein, (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders e.g. neoplasms of the breast or liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing, treating or ametion food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                microbial disease resistance; herbicide resistance; seed yie: fruit yield; growth rate; leaf senescence; flower senescence plant; transcription factor; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                          Agriculture; metabolic chemical; environmental stress;
                                                                                                                                                                                                                                                               Arabidopsis transcription factor
                                                                                                                                                                                                                                                                                                     02-JUL-2002
                                                                                                                                                                                                                                                                                                                                          AAU93023;
                                                                                                                                                                                                                                                                                                                                                                              AAU93023 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increase or decrease storage capabilities, fat content,
                                                                                                                            Arabidopsis thaliana
                 22-AUG-2001; 2001WO-US26189
                                                       28-FEB-2002
                                                                                           WO200215675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKRTPMPDKTATPERPPAPENAPSSKKIPAPDKVPSPEKTLT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKQPASNIRSIQANINIPMGAFRPGAG-----QPPKRKEFSTEEEQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VPTPE---SEEKSEEKKPIPGAVKLPGPAFNLS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRTPSRDSQKLTSRDSGPNGGFQSGGSYHPGRKRSKTQTPQQRSVSSQEEEHSSPVKAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; SEQ ID No 822; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC
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Pred. No. 2.1;
18; Mismatches
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                                                                                                                                                                                                                                                                 #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disorders
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                                                                                                                                                                                                                            drought;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein,
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RESULT 9 AAG49497

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382 SVKTPAP 388

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322

SQWPASKWRSLQVQWDEPTTVQRPDKVSPWEIEPFLATSPISTPAQQPQSKCKRSRPIEP 38: SKOPASNIRSIQANINIPMGAFRPGAGOPPKRKEFSTEEEOHVPTPESEEKSEEKKPIPG 61

N

62

AVKLPGP 68

Query Match Best Local S Matches 20

Similarity

20.5%;

Score 80; DB Pred. No. 2.5; 10; Mismatches

DB 2.5; 23; 37;

Length 602; Indels

0

0

20;

Conservative

10;

Sequence

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che will Type of Island, or the plant of phenotype as compared to a wild-type or reference plant, or the plant of cexhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included or readable medium having stored sequence information, and identifying a computer or recombinant polymucleotide information, and identifying a computer or compose comprising inputting sequence information. The isolated or compiled trait, the method comprising selecting a plant having a composited trait, the method comprising selecting a plant having a composited trait, the method comprising selecting a polymucleotide that or an expression vector, or introducing the vector into a plant or a cell of a plant to overexpress complant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased producing a modified composition of agriculturally useful proteins or metabolic chemicals, pest tolerance, herbicide resistance, seed and fruit yield, growth of sease resistance, herbicide resistance, seed and fruit yield, growth of secification). The present sequence is one of the 232 proteins which are contained transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                           encoding an Arabidopsis thaliana transcription factor, their varian complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as cout a wild-type or reference plant, or the plant exhibits an altered to a wild-type or reference plant, or the plant exhibits an altered to a wild-type or reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK65209.
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Adam L, Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated or recombinant polynucleotide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-292022/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PILG/)
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RATCLIFF O.
REUBER J L.
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JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIECHMANN J L.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MENDEL BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 290-293; 941pp; English.
   602
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2000US-0713994.
2001US-0837944.
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Reuber JL, Riechmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang C,
,, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to produce a transgenic
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MAG4997 standard, Protein 222 A). 10-007-2000 ((Irst entry) Archidopale thelians protein Esginen SQD ID No. 62625. Protein Administration, cipral transduction pathway, matabolic pathway, variantical engages. 20-009-2001, 100028-010139. 20-009-
and: Protein; 222 AA. Potein; 222 AA.
DAO: 62625. PRILATIVE 1999 99US-0113946; PRILATIVE 1999 99US-0114092; PRILATIVE 1999 99US-011
18-JUN-1999; 99US-013946; 18-JUN-1999; 99US-013946; 18-JUN-1999; 99US-01396; 18-JUN-1999; 99US-01396; 18-JUN-1999; 99US-01396; 18-JUN-1999; 99US-01406; 18-JUN-1999; 99US-014035; 21-JUN-1999; 99US-014035; 22-JUN-1999; 99US-014128; 22-JUN-1999; 99US-014128; 23-JUN-1999; 99US-014128; 24-JUN-1999; 99US-01428; 26-JUL-1999; 99US-01428; 26-JUL-1999; 99US-01428; 26-JUL-1999; 99US-014406; 16-JUL-1999; 99US-014432; 16-JUL-1999; 99US-014432; 16-JUL-1999; 99US-014432; 19-JUL-1999; 99US-014433; 19-JUL-1999; 99US-014433; 19-JUL-1999; 99US-014433; 19-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUL-1999; 99US-014433; 20-JUG-1999; 99US-014433;
18-JUN-1999; 99US-0139463 18-JUN-1999; 99US-0139463 18-JUN-1999; 99US-013963 18-JUN-1999; 99US-013963 18-JUN-1999; 99US-0143963 18-JUN-1999; 99US-0140353 21-JUN-1999; 99US-0140353 22-JUN-1999; 99US-0140323 23-JUN-1999; 99US-0141842 01-JUL-1999; 99US-0142803 02-JUL-1999; 99US-0142803 02-JUL-1999; 99US-0142803 03-JUL-1999; 99US-0144005 16-JUL-1999; 99US-01
11999; 99US-013946; 11999; 99US-013946; 11999; 99US-013976; 11999; 99US-013976; 11999; 99US-0140352; 11999; 99US-0140352; 11999; 99US-014082; 11999; 99US-014280; 11999; 99US-014328; 11999; 99US-014408; 11999; 99US-014408; 11999; 99US-014432; 11999; 99US-014432; 11999; 99US-014432; 11999; 99US-014433; 11999; 99US-0145214; 11999; 99US-0145214; 11999; 99US-014730; 11
0.0139461 0.0139462 0.0139462 0.0139812 0.0140393 0.0140393 0.014129 0.014129 0.014293 0.0142

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RESULT 10
ABB68168
ID ABB68
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AC ABB68
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Best Local S
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12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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ABB68168;
          ABB68168 standard;
                                    106 TKLPEAFÉEEÉESE 119
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                                             44 VPTPESEEKSEEKK 57
                                                                 1 MSKQPASNIRSIQANINIPMGAFRPGAGQPPKRKE------
                                                        LSPAPAPGL--AQANGRLGNGSFGPGSGMIPQTKESWPSSSTTTDEEFEKLMATFDEEKN 105
                                                                            21;
                                                                                 Similarity
                                                                            Conservative
                                                                                                                                                                                                                                                                                                    99US-0153070.
99US-0153758.
99US-0154018.
99US-0154039.
99US-0154779.
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99US-0150566.
99US-0150884.
99US-0151065.
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99US-0158369.
99US-0159293.
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99US-0158029.
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99US-0156596.
99US-0157117.
99US-0157753.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0155659.
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                                                                                                                         S-0161406.
S-0161359.
S-0161360.
          Protein; 1469 AA.
                                                                                                                3-0161361.
3-0161920.
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-0159584.
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-0160770.
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                                                                                 19.4%;
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                                                                            13;
                                                                            Score 75.5; DE
Pred. No. 2.6;
13; Mismatches
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                                                                                       В
                                                                                      21;
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                                                                                     Length 222;
                                                                  -----FSTEEEQH 43
                                                                             Indels
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RESULT 11
ABG25362
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL9737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                    1044 QKPTSPVKKLKMPNININVHALLPGSGSVPKLIRKQESSSSER--DEPQATVQTEAEAPS 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published oct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL12271.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 31296; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE
Homo sapiens
                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                         Novel human
                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                        ABG25362 standard; Protein; 167 AA.
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                                                                                                                                                                                               ABG25362;
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                                                                                                         diagnostic protein #25353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75.5; Di
Pred. No. 21;
16; Mismatches
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RESULT 12
AAR99451
ID AAR99
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AC AAR99
XT 17-FE
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Thymi
XX
Thymi
KW Thymi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore mormal activity of (II) or to treat disease states involving CC (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of eltes expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascoult-Ascou
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Best Local S
Matches 24
    Thymidine phosphorylase; endothelial cell growth factor; PD-ECGF; human platelet; vascular tissue; monoclonal antibody; MAb; immunc
                                                                    Thymidine phosphorylase
                                                                                                                    17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                      AAR99451 etandard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and gene mapping, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (II) sequences. (I) is useful au polymerase chain reaction (PCR) primers, ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ
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                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                                                                   THG
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                                                                                                                                                                                                                                                                                                                                                         SET 75
                                                                                                                                                                                                                                                                                                                                                                                                                                     MGAFRPGAGQPPKRKE-FSTEEEQHV--PTPESEEKS----EEKKPIPGAVKLPGPAFNL
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2000US-0649167
                                                                                                               (first entry)
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                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%;
38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in recombinant production of (II).
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                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74.5; DB Pred. No. 2.4; 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         `;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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  MAD;
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immunoassay;
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17-NOV-2000; 2000WO-IL00766

25-MAY-2001.

Homo sapiens.

disorder;

Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon, hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosie; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; monarcoidotic pulmonary granulomatous disease; endothelial abnormality;

Angiotensin converting enzyme (ACEV) splice variant protein #19.

12-SEP-2001 AAU02919

(first entry)

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RESULT 13
AAU02919
                                                                                                                                                                           * ARXSOXEX EXEXEXEXEX SOUDDOUGH
                                                                                                                      Matches
                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                            are derived from human platelets and vascular tissue. A monoclonal antibody against these two sequences may be used in an immunoassay. The antibody may be used in the diagnosis and treatment of malignant tumours, metastasis, rheumatoid arthritis, diabetic cataract,
 AAU02919 standard;
                                                                                                                                                                         Sequence
                                                                                                                                                                                                   premature
                                                                                                                                                                                                                                                      and
are
                                                                                                                                                                                                                                                                                                         Claim 1; Page 14-15;
                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody against PD-ECGF derived peptide(s) - used in immunoassay of human platelet derived-PD-ECGF, for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                               Akiyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAIH ) TAIHO PHARM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 premature cataract; senile macular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malignant tumour; metastasis; rheumatoid arthritis; diabetic cataract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9620217-A1
                                                                                      25 PGAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPIPGAVKLPGPAFNLSE 74
                                                                   ь
                                                                                                                                                                                                                                                  sequences given in AAR99451-52 represent thymidine phosphorylase endothelial cell growth factor, respectively. These sequences derived from human platelets and vascular tissue. A monoclonal
                                                            PGTGAPPAPGDPSGEGSQGLPDP----SPEPKQLPELIRMKRDGGRLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                      18;
                                                                                                                                   Similarity
                                                                                                                                                                                                  cataract,
                                                                                                                                                                        244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Miyadera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94JP-0327328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-JP02661
Protein;
                                                                                                                                19.1%;
                                                                                                                                                                                                 and senile macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>,
                                                                                                                                                                                                                                                                                                     27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HTD.
                                                                                                                                                                                                                                                                                                                                                                                                              Takebayashi Y,
323
                                                                                                                  Score 74.5; D
Pred. No. 3.6;
6; Mismatches
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                                                                                                                   Indels
                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, mycoardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases with as hypertrophy, improved the molecules of the property and the seases with as hypertrophy, improved the molecules of the property and the seases when as the participants of the property and the property and
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                                                                                                                              anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiuleer; osteopathic; eczema; dermatological; antiallergic; antiathmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antiense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 19; 519pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                             neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                          Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGAGOPPKRKEFSTEEEOHVPTPESEEKSEEKKPIPGAVKLPGPAFNLSE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.1%;
llarity 36.0%;
Conservative
                                                                                                       disease; Parkinson's disease; neurodegenerative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence SEQ ID NO:1274.
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99IL-0133455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vein thrombosis.
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Pred. No. 5;
6; Mismatches
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OmoH

sapiens

RESULT 15 AAU02917

AAU02917 standard; Protein;

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AAU02917

Angiotensin 12-SEP-2001

converting enzyme

(ACEV) splice variant protein #17.

(first entry)

Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

arteriosclerosis; cancer;

disease;

multiple sclerosis; immune

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                                  S
                                                                          Query Match
Best Local S
Matches 18
                                                                                                                                                                                                         antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polymucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thromboorytopaemia, wounds, burns, uccers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, alzenier's disease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH99166 to AAH99904 encode the human proteins given in AAM2525 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer,
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                                                                                                                                                                                           neurological disorders.
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larity 36.0%;
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Search completed: April Job time: 28.9153 secs
                                                                                                                                                                                                                      CC The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor, receptor, glucagon, interleukin 6, cc platelet-derived endothelial cell growth factor, receptor, intestinal ccl polypeptide receptor 2. The polypeptides and vasoactive intestinal ccl polypeptide receptor 2. The polypeptides and their associated mucleic cardis are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various cc disorders including cardiovascular diseases such as arctiosclerosis, cc myocardial infarction and coronary arterial thrombosis, renal diseases cc immune disorders such as immune complex nephritis, multiple sclerosis, cc cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as abestosis and vascular pathologies involving an endothelial cc abnormality such as deep vein thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel alternative aplicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
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N-PSDB; AAS06017.
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10-DEC-1999;
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ilarity 36.0%;
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Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-647-019-5 390 1 MSKQPASNIRSIQANINIPM......KKPIPGAVKLPGPAFNLSET 75

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 . Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swimmerot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pfam; PF00944; Alpha_E2_glycop; 1.
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Pfam; PF01589; Alpha_E1_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
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"Nucleotide sequence of the genome region encoding the 26S mRNA of
eastern equine encephalomyelitis virus and the deduced amino acid
sequence of the viral structural proteins.";

J. Gen. Virol. 68:2129-2142(1987).

-i- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
-i- PTM. SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-i- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
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NCBI_TaxID=11021;
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16-OCT-2001 (Re
Myosin-binding
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         Immunoglobulin on Repeat.

DOMAIN 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved immunoglobulin C2 and fibronectin type II motifs J. Biol. Chem. 268:3670-3676 (1993).
-i- FUNCTION: BINDS TO MYOSIN; PROBABLY INVOLVED IN INTERACTIVICK MYOFILAMENTS IN THE A-BAND.
-i- TISSUB SPECIFICITY: SKELETAL MUSCIE. SEEMS TO BE ALSO INTERECTION TOOL ALD MUSCLE. NOT DETECTED IN GIZZARD OR INTERECTION TO BE ALSO INTERECTION OF THE SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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15-JUL-1999
                                                                            SMART;
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Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pectoralis muscle;
MEDLINE=93155224; PubMed=7679114;
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                                                                                             SMART;
                                                                                                             Pfam; PF00041; fn3; 2
Pfam; PF00047; ig; 2.
PRINTS; PR00014; FNTY
                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
Pfam; PP00041; fn3; 2.
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                                                              SMART;
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InterPro; IPR003006;
InterPro; IPR003598;
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InterPro; IPR003961;
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; SM00410; IG lik
; SM00408; IGC2;
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22; Conser
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(Rel. 40, Last annotation update)
ing protein H (MyBP-H) (H-protein)
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                                           adhesion; Muscle protein;
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N-LINKED (GLCNAC...)
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NW; 8C7664A405D2D41C C
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            FIBRONECTIN TYPE-III 1.
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; Galliformes; Phasianidae; Phasianinae;
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                            Miyamoto T., Kato T.;
"Neurotrophic action of gliostatin on cortical gliostatin and platelet-derived endothelial cel J. Biol. Chem. 267:20311-20316 (1992).
                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Kerlavage A.R., Fuldner R.A., Phillips C.A., v "Complete sequence of a chromosome 22q subtelomeric BAC.", Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Finnis C., Goodey A.R., Courtney M., Sleep I Finnis C., Goodey A.R., Courtney M., Sleep I Expression of recombinant platelet-derived Saccharomyces correvisiae.";
Submitted (JUL-1991) to the EMBL/GenBank/DDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;

MEDLINE=89181955; PubMed=2467210;

Ishikawa F., Miyazono K., Hellman U., Drexler H., Wernstedt Hagiwara K., Usuki K., Takaku F., Risau W., Heldin C.-H.;

"Identification of angiogenic activity and the cloning and of platelet-derived endothelial cell growth factor.";

Nature 338:557-562(1989).
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MEDLINE=93015908; PubMed=1400349;
MEDLINE=93015908; PubMed=1400349;
Median K., Nakanishi K., Isobe I.,
                                                                                                                                                                                                 Nature
[5]
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Adams M.D., Kerlav
"Complete sequence
                                                                                                                                                                                                                                                            Furukawa T., Yoshimu
Fukui K., Yamada Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPH HUMAN STANDARD; PRT; 482 AA.
P19971, Q13390;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thymidine phosphorylase precursor (EC 2.4.2.4) (TdrPase) (TP)
(Platelet-derived endothelial cell growth factor) (PD-ECGF)
                                                                                                                                                                                                                                    "Angiogenic factor.";
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nilarity 30.4%;
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FIBRONECTIN TYPE-III 2.
IG-LIKE C2-TYPE DOMAIN 2.
T -> G (IN REF. 1; AA SEQUENCE).
A -> P (IN REF. 1; AA SEQUENCE).
A -> K (IN REF. 1; AA SEQUENCE).
M; 06C4CF0EFEIDD233 CRC64;
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                                 d endothelial cell (1992).
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                                                                                                                      Eksioglu Y.Z., Hirano
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InterPro; IPR000312; Glycos_transf 3.
InterPro; IPR000053; Thymid_phosphIs.
Pfam; PP00591; Glycos_transf 3; 1.
Pfam; PF00591; Glycos_transf 3N; 1.
ProDom; PD001864; Glycos_transf 3; 1.
ProDom; PD005916; Thymid_phosphIs; 1.
ProDom; PD005916; Thymid_phosphIs; 1.
PROSITE; PS0064/; THYMID_PHOSPHORYLASE; 1.
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EMBL; U62317; AAB03344.2; -.
PIR; S03904; S03904.
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See)
     VARIANT
                                                                                                                                             Angiogenesis;
PROPEP
                                                                                                                                                                                                                                                                                                                 MIM; 131222;
MIM; 603041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usuki K., Saras J., Waltenberger J., Miyazono K., Pierce G.,
Thomason A., Heldin C.-H.;
"Platelet-derived endothelial cell growth factor has thymidine
                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:3148; ECGF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 283:689-692(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishino I., Spinazzola A., Hirano M., "Thymidine phosphorylase gene mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS MNGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99123033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92272724; PubMed=1590793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYOPATHY.

SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES FAMILY.

DATABASE: NAME=R&D Systems.com/asp/g_sitebuilder.asp?bodyId=219".

WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=219".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: DEFECTS IN ECGF1 ARE THE CAUSE OF MITOCHONDRIAL BISTROGRASTROINTESTINAL ENCEPHALOMYOPATHY (MUGIE) (ALSO KNOWN AS MYCNIEUROGRASTROINTESTINAL ENCEPHALOMYOPATHY); AN AUTOSOMAL RECESSIVE HUMAN DISEASE ASSOCIATED WITH MULTIPLE DELETIONS OF SKELETAL MUSCLE MITOCHONDRIAL DNA (MTDNA). IT IS CLINICALLY CHARACTERIZED BY ONSET BETWEEN THE SECOND AND FIFTH DECADES OF LIFE, PTOSIS, PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA, GASTROINTESTINAL DYSMOTILITY (OFTEN PSEUDOOBSTRUCTION), DIFFUSI LEKKOENCEPHALOPATHY, THIN BODY HABITUS, PERIFHERAL NEUROPATHY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribose 1-phosphate.
PATHWAY: Nucleotide and deoxys
SUBUNIT: HOMODIMER.
DISEASE: DEFECTS IN ECGF1 ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANOTHELIA CELLS IN VITRO.
ENDOTHELIAL CELLS IN VITRO.
FUNCTION: CATALYSES THE REVERSIBLE PHOSPHOROLYSIS OF THYMIDINE.
FUNCTION: CATALYSES THE REVERSIBLE PHOSPHOROLYSIS OF THYMIDINE.
THE PRODUCED MOLECULES ARE THEN UTILIZED AS CARBON AND ENERGY
SOURCES OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MAY HAVE A ROLE IN MAINTAINING THE INTEGRITY OF TH BLOOD VESSELS, HAS GROWTH PROMOTING ACTIVITY ON ENDOTHELIAL ANGIOGENIC ACTIVITY IN VIVO AND CHEMOTACTIC ACTIVITY ON ENDOTHELIAL CELLS IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                    P77836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23033; PubMed=9924029;
Spinazzola A., Hirano
     153
                                                                                                                                                           Repeat
                                    10
482
279
342
401
461
145
     153
                                                                                                                                                         Polymorphism; Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Commun. 184:1311-1316(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and deoxyribonucleotide catabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thymidine + phosphate = thymine + 2-deoxy-D-
R-V-A-A-A-L-X(5,6)-L-G-R.
R-V-A-A-A-L-X(5,6)-L-G-R.
R-A-L-X-X-A-L-V-L.
R-A-L-X-A-L-V-L.
G->R (IN MNGIE).
/FTId=VAR 007643.
G->S (IN MNGIE).
                                                                                                                         THYMIDINE PHOSPHORYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    í'n
                                                                                                                                                                           factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNGIE,
                                                                                                                                                       mutation.
                                                                                                                                                                           Chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                      TRANSFAC; T03881;
MGD; MGI:9948; Atbfl.
MGD; MGI:9948; Atbfl.
InterPro; IPR001356; Homeobox.
InterPro; IPR000822; Znf_C2H2.
InterPro; IPR003604; Znf_U1.
Pfam; PF00046; Jomeobox; 4.
Pfam; PF00096; zf-C2H2; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABF1 MOUSE
Q61329;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Alpha-fetoprotein enhancer binding protein (ACT-binding transcription factor 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
ProDom; PD000010; Homeobox; 4.

SMART; SM00389; HOX; 4.

SMART; SM00355; ZnF_C2H2; 22.

SMART; SM00451; ZnF_U1; 7.

SMART; SM00451; ZnF_U1; 7.

PROSITE; PS00027; HOMEOBOX_1; 2.

PROSITE; PS00027; HOMEOBOX_2; 4.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 9.

Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/MK X ICR; TISSUE-Brain;
MEDLINE=96194902; PubMed=8654949;
Ido A., Miura Y., Watanabe M., Sakai M., Inoue Y., Miki T.,
Hashimoto T., Morinaga T., Nishi S., Tamaoki T.;
"Cloning of the cDNA encoding the mouse ATBF1 transcription
Gene 168:227-231(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D26046; BAA05046.1;
HSSP; P20263; 10CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Transcriptional activator that binds to the AT-rich core sequence of the enhancer element of the AFP gene.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATBF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 PGAGOPPKRKEFSTEEEQHVPTPESEEKSEEKKPIPGAVKLPGPAFNLSE
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36.0%;
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/FTId=VAR 007645.

E -> A (IN MNGIE).

/FTId=VAR 007646.

MISSING (IN MNGIE).
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Pred. No. 4.8;
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0652FA132C3BDE28
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K -> R (IN MNGIE)
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions
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tions on its
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Best Local (
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ZN FING

                                                                                                                                                                                                                                                                                          BAT2 HUMAN
P48634;
01-FEB-1996
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Large proline-rich protein BAT2 (HLA-B-associated BAT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
DNA_BIND
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BAT2_F
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Mammalia; Eutheria;
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MEDLINE-90192810; PubMed=2156268;
Banerji J., Sands J., Strominger J.L., Spies T.;
Banerji J., Sands J., Strominger D.L., Spies T.;
"A gene pair from the human major histocompatibility complex encodes
large proline-rich proteins with multiple repeated motifs and a
                                                                                      SEQUENCE FROM N.A.
TISSUE=T-cell;
                                                                                                                                                              NCBI
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Genew; HGNC:13918; BAT2.
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EMBL; M33518; AAA35586.1; -.
EMBL; M33512; AAA35586.1; JOJ
EMBL; Z15025; CAA78744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93272029; PubMed-8499947;
Iris F.J.M., Bougueleret L., Prieur
Perrot V., Jurka J., Rodriguez-Tome
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MIM; 142580;
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Proc. Natl. Acad. Sci. U.S.A. 8
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                                                                                                                                                       TYPE A REPEATS
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Claverie J.-M.,
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                                                                                      1;
                                            34;
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                                                                                   Length 2142;
                                                                                                                                    CRC64;
                                            Indels
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M., Dausset J.,
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RESULT 7
Y429_HUMAN
SCCOREDERA
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Best Local
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O43312;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                              PLE1_HUMAN STANDARD; PRT; 4(
Q15149; Q16640; Q15148;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
16-OCT-2001 (Rel. 40, Last annotation
Plectin 1 (PLTN) (PCN) (Hemidesmosomal
                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02205; WH2; 1.
SMART; SM00246; WH2; 1.
Hypothetical protein.
SEQUENCE 356 AA; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outer the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98116655; PubMed=9455477;
Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
78 new cDNA clones from brain which code for large proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; /
           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                     PLEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB007889; BAA24859.1; -. InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
KIAA0429.
                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 4:307-313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                263
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                                                                                                                                                                                                         <u>ດ</u>-
                                                                                                                                                                                                                                    G 67
                                                                                                                                                                                                                                                           SMMSGQASVNPPL----PG----PKP---SIPEEHRQAIPESEAEDQEREP-PSATVSP 310
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                                                                                                                                                                                                                                                                                                                  23;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
L protein KIAA0429.
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          Chordata;
Primates;
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Primates;
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37.7%;
                                                                 (Hemidesmosomal
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                                                                                                                                                                                                                                                                                                                                 Score 71;
Pred. No.
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           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO DESMOSOMES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STRABILIZATION OF CYTOSKELETAL INTERMEDIATE FILMMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.

-!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.

-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- PRODUCED BY ALTERNATIVE SPLICING.

-!- DISABLE, HEART, PLACENTA AND SPINAL CORD.

-!- DOMAIN: THE N-TERMINUS INTERACTS WITH HIGHEST LEVELS IN MUSCLE, HEART, PLACENTA AND SPINAL CORD.

-!- DOMAIN: THE N-TERMINUS CAN BIND INTEGRIN BETA-4.

-!- DISABLE: DEFECTS IN PLEC1 ARE THE CAUSE OF THE REMIDESMOSOME AND ASSOCIATED AND STROPHY (MD-EBS OR EB-MD), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY EPIDERMAL BLISTER FORMATION AT THE LEVEL OF THE HEMIDESMOSOME AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.

-!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.

-!- SIMILARITY: CONTAINS 3 PLECTIN REPEATS.

-!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.

-!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.

-!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.

-!- SIMILARITY: BELONGS TO THE DLAKIN OR CYTOLINKER FAMILY.
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MEDLINE=21090821; PubMed=11159198;
Bauer J.W., Rouan F., Kofler B., Rezniczek G.A., Kornacker I.,

Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,

Wiche G., Uitto J., Hintner H.;

"A compound heterozygous one amino-acid insertion/nonsense mutation

"he plectin gene causes epidermolysis bullosa simplex with plectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uitto J.;
"Loss of plectin causes epidermolysis bullosa with muscular dystrophy: "CDNA cloning and genomic organization.";
Genes Dev. 10:1724-1735(1996).
                                                                                               This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deficiency.";
Am. J. Pathol. 158:617-625(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C.-G., Maercker C., Castanon M.J., Hau "Human plectin: organization of the gene, chromosome localization (8q24) ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscular dystrophy.";
Hum. Mol. Genet. 5:1539-1546(1996).
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TISSUE=Placenta;
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Z54367; CAA91196.1; -. U53204; AAB05427.1; -.
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ch F., Burgeson R.E., Amano
h J.A., McMillan J.R., Eady
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PubMed=8698233;
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Eady R.A.J., Le:
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son D.L., Owaribe K.,
Leigh I.M., Christiano A.M.,
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Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 19.
Pfam; PF03501; S10 plectin; 1
SMART; SM00033; CH; 2.
SMART; SM00250; PLEC; 33.
SMART; SM00150; SPEC; 5.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U63610; AAB05428.1; 
EMBL; U63609; AAB05428.1; U63609; AAB054765.1; 
EMBL; X97053; CAA65765.1; 
HSSP; Q01082; 1BKR. 
Genew; HGNC:9069; PLEC1.
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                                                                                                                                                            REPEAT
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InterPro;
                       DOMAIN
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MIM; 226670;
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                                                                                                                                                                                                                                                                                           mutation.
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IPR001715; Calponin-like.
IPR0011015; Plectin repeat.
IPR005326; S10 plectin.
IPR002017; Spectrin.
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PLECTIN 33.
BINDING TO INTERI
SIMILARITY).
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PHOSPHORYLATION
SIMILARITY).
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SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
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P41073; Q9VVJ3; Q9VVJ4;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Zinc finger protein on ecdysone puffs.
PEP OR CGG143.
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                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  SEQUENCE
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GSPPKRGPLPTEEQRLYRKELLEEVSPETPVVPATTQRTLA
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EVAR 011337.

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RA George R.A., Lewis S.E., ELLEW, HORKING R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.M., Radell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Predictor B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklog G.L.G., RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannboch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessly R.M., Ballew R.M., Glasser K.M., Glas
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MEDLINE=91138953; PubMed=1899840;
Amero S.A., Elgin S.C.R., Beyer A.L.;
"A unique zinc finger protein is associated preferentially with active ecdysone-responsive loci in Drosophila.";
Genes Dev. 5:188-200(1991).
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Amanatides P.G.,
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the European Bioinformatics Institute. There ...

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Pfam; PF00096; zf-C2H2; 3 SMART; SM00355; ZnF_C2H2;

PIR; S26759; S26759. FlyBase; FBgn0004401; Pep. InterPro; IPR000822; Znf_C2H2 InterPro; IPR000690; Znf_matr:

matrin.

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STRAIN=JAL-1 / DSM 2661 / AILC -.....
STRAIN=JAL-1 / DSM 2661 / AILC -.....
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Reich C.I., Serlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidmanf J.F., Fuhrmann J.L., Nguyen D., Scott J.L., Geoghagen N.S.M., Weidmanf J.F., Fuhrmann J.L., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Commisse geneme sequence of the methanogenic archaeon, Methanococcus
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
Zinc_finger; DNA-binding; Nuclear protein; Metal-binding.
DOMAIN 7 166 ASN/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
01-NOV-1997
      between
the Euro
                                                                                                    jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Metr
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii.
                This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                 -!- PATHWAY: Thiamine biosynthesis.
                                                    -!- SUBCELLULAR LOCATION: Cytoplasmic (Pot
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European
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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ASP/GLU-RICH (ACIDIC)
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104K_THEPA
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P15711;
                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                        MEDLINE-90158697; PubMed=1689460;
Iams K.P., Young J.R., Nene V., Desai J., Webster
Ole-Moiyoi O.K., Musoke A.J.;
"Characterisation of the gene encoding a 104-kilod
rhoptry protein of Theileria parva.";
Mol. Biochem. Parasitol. 39:47-60(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02568; ThiI; 1.
Pfam; PF02956; THUMP; 1.
TIGRFAMS; TIGR00342; ThiI; 1.
Thiamine biosynthesis; Complete
SEQUENCE 381 AA; 43436 MW; C
                                                                                                           Antigen;
                                                                                                                                             EMBL;
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-AUG-1992
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                                                                                                                                    PIR; A44945; A44945.
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PGA-GQPPKRKEFSTEEEQHV-PTPESEEKSEEKKPIPGAVKLPGPA
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1 19
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924 AA;
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32.9%;
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Pred. No. 31;
                                    Pred. No. 31;
3; Mismatches
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OA31F1069DA3357B CRC64;
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01-NOV-1990 (Rel. 16, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet H protein (200 kDa neurofilament protein)
                                                                                                               EMBL;
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PIR;
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MEDLINE-89089138; PubMed=3145094;
Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.;

"The structure of the largest murine neurofilament protein (NF-H)
revealed by CDNA and genomic sequences.";
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SEQUENCE FROM N.A.
MEDLINE=89121513; PubMed=3220257;
Cote F., Beaudet L.,
                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no resume by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carden
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[2]
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NEFH OR NFH.
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                                                                         BL; M24496; AAA39813.1;

M23349; AAA39813.1;

BL; M24494; AAA39813.1;

BL; M24495; AAA39813.1;

BL; M35131; AAA39813.1;

BL; M35131; AAA39813.1;

BL; M35131; AAA39809.1; F

BL; M35131; AAA3778.
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OF AKONAL CALIBER.

OF AKONAL CALIBER.

THE PROSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534

TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NE-H HAS AN IMPORTANT KUNCILOW AND THE TRIPEPTIDE K-S-P, SUBSERVED BY THE TWO SMALLER NF PROTEINS.

SUBSERVED BY THE TWO SMALLER NF PROTEINS.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATIC THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATIC THOUGHT THAT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINT
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PE
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURO
NE-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT
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С.
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01-NOV-1990
01-AUG-1992
                                                                                                                                                            TISSUE-Oocyte;

MEDLINB-87161764; PubMed-3549279;

Kleinschmidt J.A., Dingwall C., Maier G., Frank

"Molecular characterization of a karyophilic, h

protein: cDNA cloning, amino acid sequence and

protein NI/N2 of Xenopus laevis.";

EMBO J. 5:3547-3552(1986).
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                                       This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatically and this statement is not removed.
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                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                      -1- FUNCTION: THIS PROTEIN IS INVOLVED IN NUCLEOSOME ASSEMBLY. IT IS BOUND TO H3 AND H4 IN THE ABSENCE OF DNA, BUT RELEASED FR.
H3 AND H4 IN THE PRESENCE OF DNA.
-1- SUBCELLULAR LOCATION: NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
-1- SIMILARITY: WITH RABBIT NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                              Histone-binding protein N1/N2.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                               Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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    Last sequence update)
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37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K -> QA (IN REF. 2 AND 3).
A -> AR (IN REF. 2 AND 3).
S -> T (IN REF. 2 AND 3).
L -> G (IN REF. 2 AND 3).
P -> PREAKSP (IN REF. 3).
MISSING (IN REF. 3).
G -> A (IN REF. 3 AND 3).
T -> N (IN REF. 2 AND 3).
T -> N (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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50 X 6 AA TANDEM F
GLU/LYS-RICH.
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                              (See http://www.isb-sib.
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                                                  There are no restrictions ong as its content is in
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                                                                                                                                                                                     Franke W.W.;
lic, histone-binding
e and expression of
                                      Usage
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                                                                          collaboration -
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                                        commercia.
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RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Bates K.N., Beasley O.P.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Clamp M.E., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortinore B.J.C.T.,
RA Mclaren S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Mcman A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyana S.,
RA Manda J., Lewis S., Lin S.-P., Loh P., Malaj E., Mguyen T., Pan H.,
RA Manda J., Lewis S., Lin S.-P., Loh P.,
RA Manda J., Kanga T., Walliamson H., Man
                        REPARED BY A PARED BY 
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GTSE_HUMAN
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Matches 18
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15-JUN-2002 (Re
15-JUN-2002 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 254:229-236(2000).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20432105; PubMed=10974554; Monte M., Collavin L., Lazarevic D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GISE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SKQPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTDES-EEKSEEKK ::: |:::|| : | |:|| | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologue of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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002 (Rel. 41, Last sequence update)
002 (Rel. 41, Last annotation update)
002 (Rel. 41, Last annotation update)
phase expressed protein 1 (B99 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome mapping and ologue of murine Gtse-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; CatarrHīni; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64897
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31.6%;
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ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68.5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 functional (B99) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Utrera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R., Dragani T.A.,
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                                                                                                          Query Match
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Matches 16
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A Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
ACOrdes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
AL, Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
AScheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
AKORÍ I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
AL Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarí M.L.,
AMCDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
AMCDERMID J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.
AN Seroussi E., Fransson I., Tapla I., Bruder C.E., O'Brien K.P.,
AN Seroussi E., Franseon I., Tapla I., Bruder C.E., O'Brien K.P.,
AN Hikinsbn P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
AN Wilkinsbn P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
AN Tilahun Y., Wright H.;
ATT Tha DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature [3]
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                        Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + +
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230
                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            progression.
SUBCELLULAR LOCATION: Cytoplasmic.
SUBCELLULAR LOCATION: Expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: May be involved in p53-induced cell cycle aphase by interfering with microtubule rearrangements required to enter mitosis. Overexpression delays G2/N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quiescent cells. Phosphorylated in mitosis (By similarity)
                                                  PGAGQPPKRKEFSTEEEQHVPT-PESEEKSEEKKPIPGAVKLPGPAFNLSE
PGAAEKPKKEIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQ
                                                                                                                                                                                                                                                                                                                                                               AF223408; AAF31459.1; -. AL031588; CAB38415.1; -. AL022325; CAB63079.1; -. BC006325; AAH06325.1; -.
                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                          h 17.6%;
Similarity 31.4%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APR-2001)
                                                                                                                                                                                                                                                                                                          Phosphorylation.
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          MW;
                                                                                                          Score 68:5; D
Pred. No. 27;
9; Mismatches
                                                                                                             9;
                                                                                                                                                                                                              POLY-SER.
V -> I (IN REF. 1).
R -> W (IN REF. 2; CAB38415)
R -> W (TOURD CONTROL CARSELLE CONTROL CARSELLE CARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Associated G2/M phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                  BB
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gements that a
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RARRA PRANCE
                                                                                                                                                                                                         RESULT
                                                                                                     TRX2 HUMAN STANDARD; PRT; 2715 AA.

Q9UMM6; Q9UK25; O95836; Q9Y669; Q9Y668; O1502:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trithorax homolog 2 (Mixed lineage leukemia gy
TRX2 OR HRX2 OR MLL2 OR MIL14 OR KIAA0304.
                                                                                                                                                                                              HUMAN
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
            Angrand P.O., Valva
                                    SEQUENCE
                                                                                               Homo sapiens
                                     FROM N.A.
                                                                                  Metazoa;
                                                                                               (Human)
            Valvatne H.
n F., Olsen
                                     (LONG ISOFORM).
                                                                       Chordata;
Primates;
            Jeanmougin ., Tekotte F
                                                                       Craniata; Vertebrata; Euteleostomi Catarrhini; Hominidae; Homo.
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015022;
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Huang N.,
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                                                                                                                      homolog
           Poch
₽0
                                                                                                                                                                      Q96IP3;
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Losson R.,

Stewart A.,

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FEARE & & & & EARE & SEE FEARE & SEE FEARE
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L Genomics 59:187-192(1999).

C -!- FUNCTION: POSSIBLY ARC'S AS A TRANSCRIPTIONAL REGULATORY FACTOR.

C -!- SUBCELLULAR LOCATION: Nuclear (By Similarity).

C -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS IN TESTIS.

C -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS IN TESTIS.

C ALSO FOUND IN BRAIN, BONE MARROW, HEART, MUSCLE, KIDNEY, PANCREAS,

CC SPLEEN, THYMUS, PROSTATE, OVARY, INTESTINE, COLON, PERIPHERAL

CC BLOOD LYMPHOCYTES, AND PLACEBYRA.

C -!- SIMILARITY: CONTAINS 1 SET DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 CXXC.-TYPE ZINC FINGERS.

CC -!- SIMILARITY: CONTAINS 1 CXXC.-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement, (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            code for DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta, and Bone marrow, MEDLINE=99339983, PubMed=10409430 FitzGerald K.T., Diaz M.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1918-2715 FROM N.A. TISSUE-Brain, and Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Ishikawa K.-I., Nakajima p., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntsman D.G., Chin S.-F., Mileris M., Batley S.J., Collins V.P., Wiedemann L.M., Aparicio S., Caldas C., "MLL2, the second human homolog of the Drosophila trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines."; Oncogene 18:7975-7984(1999).
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Lamerain J.E., McCready P.M., Adam
Garcia E., Kyle A., Ramirez M., St
Bruce R., Quan G., Montgomery M.,
Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97349984; PubMed=9205841;
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MEDLINE=20105772; PubMed=10637508;
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                           AJ007041;
AD000671;
AB002302;
AF186605;
AF104918;
AF105279;
BC009337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     large proteins in vitro.";
4:141-150(1997).
                                                 ; -; NOT ANNOTATED ; BAA20763.2; - . ; AAD56420.1; - . ; AAD17932.1; - . ; AAD26113.1; - .
                                                                                                                                                                                              CAB45385.1;
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EMBL/GenBank/DDBJ
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M., Ow D., Kobayashi A., Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LONG ISOFORM).
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Pfam; PF02008; zf-CXXC; 1.
SMART; SM00384; AT hook; 1.
SMART; SM00542; FYRC; 1.
SMART; SM00542; FYRC; 1.
SMART; SM00549; PHD; 4.
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PROSITE; PS01359; ZF_PHD_1; 3.
PROSITE; PS50016; ZF_PHD_2; 3.
DNA-binding; Bromodomain; Nucl:
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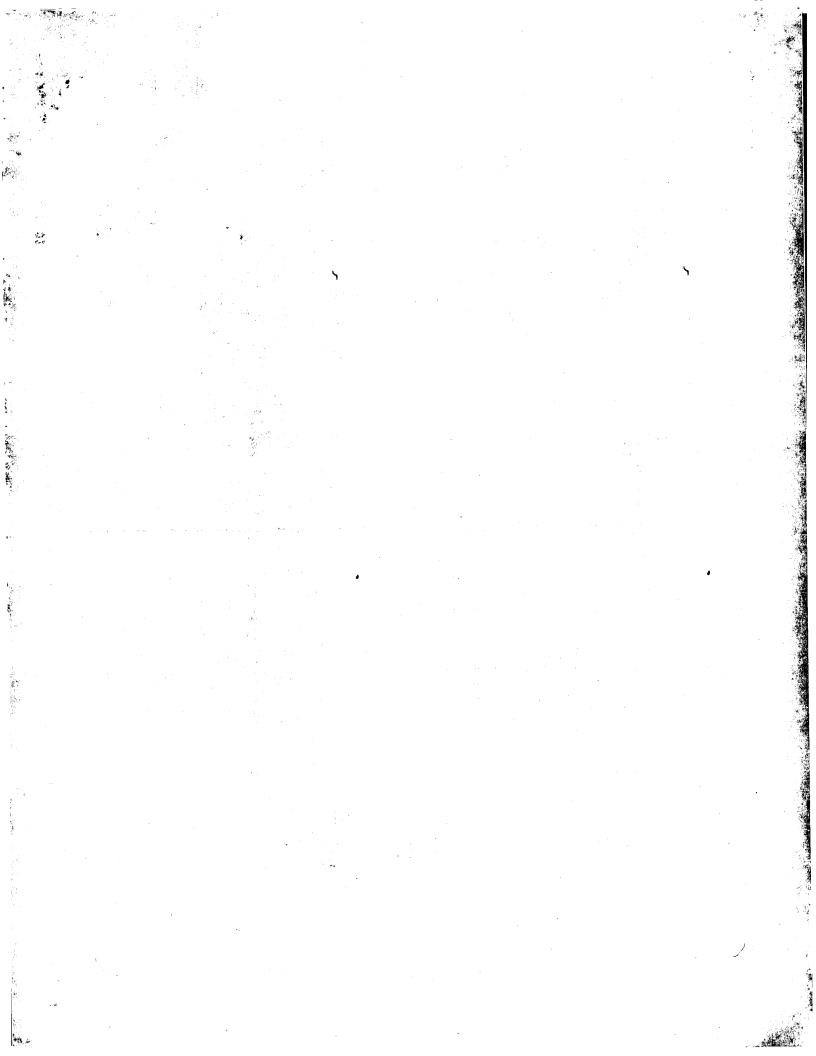
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Compugen_Ltd.
Q90258 xenopus lae
Q9e798 mus musculu
Q92569 rattus norv
Q98qh0 mycoplasma
Q9c5w9 arabidopsis
Q9m355 arabidopsis
Q9m355 arabidopsis
Q21980 caenorhabdi
Q1741 aedes aegyp
Q95125 macaca fasc
Q86653 streptomyce
Q9zwa4 arabidopsis
Q91749 xenopus lae
Q9v953 drosophila
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Q9v953 drosophila
Q9v954 mus musculu
Q8wvb7 homo sapien
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Q9u010 drosophila	Q95jc9 aua acrofa	Q960k6 drosophila	Q26033 plasmodium	neur	Q9bre0 homo sapien	homo			Q8sy35 drosophila	Q9v513 drosophila			Q8z1l3 salmonella	0	Q8txa4 methanopyru	3	Q41733 zea mays (m	O97770 oryctolagus	Q94ht8 oryza sativ	6 rati	homo	homo	3	agr	_			Q9et80 mus musculu

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OC MEDILINE=2127:
RA MEDILINE=2127:
RA MEDILINE=1127:
RA MONUN T.J.;
RT "THE SMAIL MI
PTOMOTES MYOC
RT MANNET.";
RL J. Cell Biol.
DR EQUENCE 9:
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Matches 74
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J. Cell Biol. 153:985-998(2001).

EMBL; AF343894; AAK71068.1; -.
SEQUENCE 91 AA; 10006 MW; BD2BA90B82B3846C CRC64;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=21275706; PubMed=11381084;

Palmer S., Groves N., Schindeler A., Yeoh T., Biben C., Wang C.-C.,

Palmer S., Groves N., Schindeler A., Yeoh T., Biben C., Wang C.-C.,

Sparrow D.B., Barnett L., Jenkins N.A., Copeland N.G., Koentgen F.,

Mohun T.J., Harvey R.P.;

"The Small Muscle-specific Protein Csl Modifies Cell Shape and

"The Small Muscle-specific Protein Csl Modifies Cell Shape and

"The Small Muscle-specific Protein Csl Modifies Cell Shape and

"The Small Muscle-specific Protein Csl Modifies Cell Shape and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
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Local Similarity 100.0%; Pred. No. 8.1
hes 74; Conservative 0; Mismatches
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    GAVKLPGPAFNLSE
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Q925F0;
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Q1-DEC-2001
Q1-JUN-2002
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MGD; MGI:1913356; Smpx.
MGD; MGI:1913356; Smpx.
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MEDIJINE=20065879; PubMed=10598820;
Patzak D., Zhuchenko O., Lee C.C., Wehnert M.;
"Identification, mapping, and genomic structure chromosomal human gene (SMPX) encoding a small hum. Genet. 105:506-512(1999).
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Q9ER98;
Q9ER98;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Stretch responsive muscle (X-chromosome) (SMPX protents)
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STRAIN=CS7BL/10; TISSUE=SKELETAL M
MEDLINE=21295047; PubMed=11401441;
Kemp T.J., Sadusky T.J., Simon M.,
Sassoon D.A., Coulton G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21275706; PubMed=11381084; Palmer S., Groves N., Schindeler A., Yeosparrow D.B., Barnett L., Jenkins N.A.,
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               SMPX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promotes Myocyte Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Small Muscle-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mohun
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                              (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                   PRELIMINARY;
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Sciurognathi; Muridae;
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A., Copeland N.G.,
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y a small muscular prote
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                                                                                                                                                                                                                 PRINTS; PR01217; PRICHEXTENSN. Hypothetical protein; Complete SEQUENCE 757 AA; 86350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S.,
Moszer I., Dybvig K., Wroblewski H
                                                                                                                                                                                                                                                                                                MYPUList; MYPU 3930; -.
                                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
                                                                                                                                                                                                                                                                                                                                                                                                           Moszer I., Dy Blanchard A.;
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Mycoplasma
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Patzak D., Zhuchenko O., Lee C.C., Wehnert M.;
"Identification, mapping, and genomic structure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasmataceae;
NCBI_TaxID=2107;
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Hum. Genet. 105:506-512(1999).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome
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    TPESEEKSEEKKPIPGAVKLPGPA
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1 protein MYPU_3930.
                                                                                                                                Conservative
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(., Wroblewski H.,
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                                                                                                                                                                                                                                                                            rich extensn.
                                                                                                                                10;
                                                                                                                          Score 92.5; DI
Pred. No. 0.05
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244.5; DB 1
Pred. No. 4.2e-20,
5; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
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    69
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                                                                                                                                                                                                               proteome.
BBD9FC7CD714238C
                                                                                                                                                                                                                                                                                                                                                                                                                            Barbe V., S., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                     murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757
                                                                                                                                                .054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                respiratory pathogen
                                                                                                                                                                     16;
                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Samson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                              Rocha
                                                                                                                                                                                                               CRC64;
                                                                                     ---RKEFSTEEEOHVP
                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galisson
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                                                                                                                              19;
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                                             85
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98

KPEPEKPKEEPKPAPPPVVIPAPA 109

RESULT Q9C5W9

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PRELIMINARY;

602

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AP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Wu H.C.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,

RA Ecker J.R., Theologis A.;

"Full Length cDNA of gene At3g61830 (GI:15228619).";

"whmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                  Vamada K., Bahh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
A Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Carninci P., Chen H., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayushizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Maria T., Satou M., Shinn P., Southwick A., Shinnozaki K.,
A Davis R. W., Ecker J.R., Theologis A.,
Theologis A.,
Thabidopsis Open Reading Frame (ORF) Clones.";
"Arabidopsis Open Reading Frame (ORF) Clones.";
"Arabidopsis Open Reading Frame (ORF) Clones.";
"Arabidopsis Open Reading Frame (ORF) Clones.";
"BMBL; AR934717; AAG50095.1; -.
REMBL; AY059746; AAL24094.1; -.
REMBL; AY059746; AAL49129.1; -.
REM
Greny
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9C5W9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yemada K., Liu S.X., Sakano H., Pham P.K., I
Goldsmith A.D., Lee J.M., Toriumi M., Yu G.,
Chen H., Karlin-Neumann G., Kim C., Lam B.,
Palm C.J., Shinn P., Southwick A., Davis R.!
Theologis A.;
"Pull Length cDNA of gene P15G16.220 (GI:68)
Submitted (JAN-2001) to the EMBL/GenBank/DDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted [2]
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F15G16.220 OR AT3G61830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamura Y., Yu G.,
Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis cDNA clones.";
Submitted (DEC-2001) to the
  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene F15G16.220 (GI:6850874).";
to the EMBL/GenBank/DDBJ databa
20
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Score
80;
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Yu G., Brooks S., Chao
m B., Miranda M., Nguye
DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.W.,
10;
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Length
  602;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                      Q21980;
Q21980;
01-NOV-1996
01-OCT-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9M355
Q9M355;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing pr
Submitted (JAN-2000) to the
EMBL; AL132959; CAB71113.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viriddiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddiotyledons; core e:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                 Hypothetical R13F6.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
De Haan M., Maarse A.C
Mayer K.F.X., Quetier
                                                                                                                  Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                   MEDLINE=99069613;
                                                                                             NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AVKLPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKOPASNIRSIQANINIPMGAFRPGAGOPPKRKEFSTEEEOHVPTPESEEKSEEKKPIPG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVKTPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                   SVKTPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQWPASKWRSLQVQWDEPTTVQRPDKVSPWEIEPFLATSPISTPAQQPQSKCKRSRPIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02309;
PF02362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | IPR003311; AUX IAA.
| IPR003340; TF B3.
| 102309; AUX IAA; 1.
| 102362; B3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                      (TrEMBLrel. 01,
(TrEMBLrel. 18,
(TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                       282.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽3;
                     PubMed=9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.C., Grivell L.A.,
ier F., Salanoubat M.
                                                                                                                                                                                                       kDa
                                                                                                                                          Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                project;
                                                                                                                       ›da; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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Last
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Pred. No. 1.1;
10; Mismatches
                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                 Created)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E253AAABAB90E045 CRC64;
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annotation update
                                                                                                                                                                                                                                              sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                             8
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R InterPro; IPR001579; Chitin bind PerA.
R InterPro; IPR002557; Chitin bind PerA.
R InterPro; IPR001223; Glyco_Nydro_18.
R Pfam; PF001607; CBM 14; 1.
R Pfam; PF00704; Glyco hydro_18; 1.
R Pfam; PF001574; TUBEYPROTEIN.
R PRINTS; PR01574; TUBEYPROTEIN.
R ProDom; PD000471; Glyco_hydro_18; 1.
R ProDom; PD000491; ChtBD2; 1.
R RMART; SM00494; ChtBD2; 1.
R PROSITE; PS01095; CHITINASE_18; 1.
W Hydrolase; Glycosidase; Chitin degradation; Glycoprotein;
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de la Vega H., Specht C.A., Liu Y., ACCOUNTY
"Chitinasses are a multi-gene family in Aedes, Anopheles and
Drosophila.";
Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY; HDROLYSIS OF THE 1,4-BETA-LINKAGES
N-ACETYI-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       017411;
01-JAN-1998
01-JAN-1998
01-JUN-2002
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Pfam; PF01436; NHL; 5.
PRAINTS; PR00011; EGFLAMININ.
SMART; SM00181; EGF; 6.
PROSITE; PS001022; EGF 1; UNKNOWN 7.
PROSITE; PS01186; EGF 2; 7.
EGF-like domain; Glycoprotein; Hypothetical protein.
SEQUENCE 2560 AA; 282782 MW; DOCE8ED49183CF4F CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98324849; PubMed-9662472;
MEDLINE-98324849; PubMed-9662472;
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Eukaryota; Metazoa; Arthropoda; Trach
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InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001258; NHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7159;
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Submitted (SEP-2001) to the
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STRAIN=BRISTOL N2;
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STRAIN=BRISTOL N2;
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itted (APR-1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          998 (TrEMBLrel. 05, Created)
998 (TrEMBLrel. 05, Last sequence update)
902 (TrEMBLrel. 21, Last annotation update)
chitinase 1 precursor (EC 3.2.1.14).
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Pred. No. 6.9;
8; Mismatches
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EMBL/GenBank/DDBJ
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Matches 27
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Best Local
                     086653 PRELIMINARY;

08653; PRELIMINARY;

01-NOV-1998 (TrEMBLrel. 08, I

01-NOV-1998 (TrEMBLrel. 21, I

01-UN-2002 (TrEMBLrel. 21, I

ATP/GTP binding protein.

SC05734 OR SC3C3.20C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95LZ5;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                   TISSUE=TESTIS;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hi
Terao K., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque
libraries.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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CHAIN
DOMAIN
ACT SITE
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 98.6 kDa protein.
            Streptomyces coelicolor
                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 8
                                                                                                                                                                                                                                                                                                    InterPro; IPR001440; TI
Pfam; PF00515; TPR; 7.
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27; Conserv
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1 15
16 574
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175 175
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Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                               872 AA;
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31.3%;
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Pred. No. 3.9;
7; Mismatches
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Pred. No.
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N-LINKED (GLCNAC ) (POTE

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Matches 21
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Nature 417:141-147(2002).
EMBL; AL031231; CAA20269.1;
InterPro; IPR002543; FtsK SpoIIIE.
Pfam, PF01580; FtsK_SpoIIIE; 3.
SEQUENCE 1321 AA; 143529 MW; 65C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
STRAIN=A3(2);
STRAIN=A3(2);
STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A.
Redenbach H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic ar
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
     SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Federspiel N.A., Palm C.J.,
Altafi H., Araujo R., Huiza
                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids_II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                               Q9ZWA4
                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
P11MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=A3[2] / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.P., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Cronin A., Fraser A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                         NCBI_TaxID=3702,
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Submitted (AUG-1998)
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Parkhill J.,
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Murphy L., Harris D.
Submitted (AUG-1998)
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NCBI_TaxID=1902;
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33.9%;
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r L., Rowley !
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e EMBL/GenBank/DDBJ
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Pred. No. 6.2;
8; Mismatches
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  D., Buehler
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RESULT 13
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Q9V953;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAY-2000
                                                                                                                          CG16742 protein.
CG16742 protein.
CG16742.
CG16742.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Q91749; Q91750;
01-NOV-1996 (Tri
      STRAIN=BERKELEY;
MEDLINE=20196006;
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"Structural and functional characterization and cloning FOSP-1 (frog oviduct-specific protein-1) genes.";
Eur. J. Biochem. 229:224-232(1995).
EMBL; X81569; CAA57265.1; -.
EMBL; X81571; CAA57267.1; -.
EMBL; X81571; CAA57267.1; -.
SEQUENCE 480 AA; 53182 MW; 191204199FD13A65 CRC64;
                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; C
Amphibia; Batrachia;
Xenopodinae; Xenopus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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01-NOV-1996 (TrEMBLrel. 01,
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07-iduct specific protein-1A.
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MEDLINE=95262671; PubMed=7744034;
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LAUYOS S., Schwartz J., Shinn P., Toriumi M., Vysotskaia
Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003027, AAD10686.1; -.
SEQUENCE 222 AA; 25205 MW; 4EBA390B6611E468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373
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17; Conser
                                                                     FROM N.A.
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21; Conservative
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PubMed=10731132;
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Pred. No. 2.6;
6; Mismatches
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a V.S.,
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RA Ballew R.M. Basu A., Am H. "J., Amurews Frammood, C., Denard R. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Bestix K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Perrar C., Ferras S., Pleischmann W., RA Dodson K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Fosler C., Gabrielian A., E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glaster K.A., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. L., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Menus J., Welson K.A., Nison K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weinsenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., D., Scheeler F., Shen H., RA Wang Z.-Y., Wassarman D.A., Reinstock G.M., D., Yang S., Yao Q.A., RA Wang Z.-Y., Wassarman D.A., Reinstock G.M., D., Santh H.O., RA Gibbs R.A., Myers E.W., Elong W., Zhou X., Zhang G., Zhao Q., Zheng L., Palasco F., Shon H., Wang X., Ra Mang Z.-Y., Wassarman D.A., Rabin G.M., Venter J.C.; Shon M., Smith H.O., Ra Gibbs R.A., Myers E.W., Elong W., Zhou X., Smith H.O., Ra Gibbs R.A., Myers E.W., Long W., Zhou X., Smith H.O., Ra Gibbs R.A., Marg Z.-Shoo S.,
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Q99LB3;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to KIAA0429 gene product (Fragment).
Mus musculus (Mouse)
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Strausberg R.;
Sybmitted (FBB-2001) to the EMBL; BC003483; AAH03483.1;
InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Pred. No. 9.1;
16; Mismatches
                                                                                                                         EMBL/GenBank/DDBJ databases.
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X., Smith H.O.,
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SMART; SM00246; WH2; 1.
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SEQUENCE 231 AA; 245
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Q8R1S4;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC024131; AAH24131.1; -
SEQUENCE 759 AA; 82408 MW; 3E9008065FF78439 CRC64;
                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                  Similar to metastasis suppressor
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                    TISSUE=LIVER;
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                                                                                                                  4 QPASNIRSI----QANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKSEEKKPI 59
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                                                  PSATVSPGP 715
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                                                                                             QGVSNIPSSLWSGQAPVNPPL---
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CarD protein - Myx conserved hypothet probable exported 104K microneme-rho neurofilament trip nuclear histone-bi hypothetical prote variant-specific s TonB protein NMA19 TonB protein NMB17
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oviduct-specific p
myosin-binding pro
platelet-derived e
MHC Class III hist
MHC Class III hist
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structural polypro
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66.5	67	67	67	67	67	67	67	67	67.5	67.5	67.5	67.5	. 68	68	89
17.1	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.3	17.3	17.3	17.3	17.4	17.4	17.4
227	1242	1242	1240	1236	1140	961	300	249	1235	880	687	332	5037	1655	1107
N	N	N	_	۲	N	N	N	N	r	N	N	N	N	N	N
B87802	A56605	S72350	VHWVEV	VHWVWE	D88690	G90053	T52020	I67637	DJBE16	B87222	T29220	B43427	B35041	T13998	S61667
protein Cl0G11.10	structural polypro	structural polypro	structural polypro	structural polypro	protein F41H10.3 [hypothetical prote	ethylene responsiv	proteasome activat	DNA-directed DNA p	probable iron-sulp	hypothetical prote	neurofilament prot	ryanodine receptor	gene mastermind pr	probable membrane

ALIGNMENTS

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auxin response factor-like protein - Arabidopsis thaliana
N;Alternate names: protein F15G16.220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47975
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quesubmitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-757 <KUR>
A,Residues: 1-757 <KUR>
A,Cross-references: GB:AL445566; PID:gl4089807; PIDN:CAC13566.1; GSPDB:GN00153
A,Experimental source: strain UAB CTIP
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C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A99561
R;Chambaud, I:, Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
R;Chambaud, I:, Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pull
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                 A/Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,FESIdus: 1-613 <DEH>
A,Cross-references: EMBL:AL132959
A,Experimental source: cultivar Columbia; BAC clone F15G16
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A; Genetic code: S(
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                                                               Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 PKNNLDYSBANISNTDFNLPEIPKPLPKPEPPKPPQEDPIIKIPPQPEPEKPKEEPKPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 TPESEEKSEEKKPIPGAVKLPGPA 69
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16/1; 54/3; 87/3; 106/3; 157/3; 186/1; 216/2; 271/2; 309/2; 344/3; 504/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 31.0
26; Conservative
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31.0%; Pred. No. 0.3;
vative 10; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-1239 CCHA>
A; Residues: 1-1239 CCHA>
A; Residues: 1-1239 CCHA>
A; Cross-references: EMBL:X05816; NID:g62074; PIDN:CAA29261.1; PID:g62075
C; Superfamily: togavirus structural polyprotein
C; Koywords: coat protein; glycoprotein; transmembrane protein
C; Koywords: coat protein; G #status predicted cCPC>
F; 260-322/Product: membrane glycoprotein E3 #status predicted <MG3>
F; 261-277/Domain: transmembrane #status predicted <TN1>
F; 323-742/Product: membrane glycoprotein E2 #status predicted <MG2>
F; 684-701/Domain: transmembrane #status predicted <TN3>
F; 741-798/Product: GK protein #status predicted <TN3>
F; 741-798/Product: GK protein #status predicted <TN4>
F; 777-798/Domain: transmembrane #status predicted <TN4>
F; 777-798/Domain: transmembrane #status predicted <TN4>
F; 777-798/Domain: transmembrane #status predicted <TN4>
F; 741-798/Product: GK protein #status predicted <TN4>
F; 741-798/Product: Transmembrane #status predicted <TN4-
F; 741-798/Produ
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T16743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chang, G.J.J.; Trent, D.W.
J. Gen. Virol. 66, 2129-2142, 1987
J. Gen. Wirol. 66, 2129-2142, 1987
A;Title: Nucleotide sequence of the genome region encoding A;Reference number: A26816; MUID:87282265; PMID:2886548
A;Accession: A26816
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A;Introns: 52/2; 113/1; 170/2; 594/1; 1009/1; 1181/1; 1547/3; 1672/3; 1890/1; 2278/1; 2: C;Superfamily: unassigned EGF-related proteins; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C;Species: eastern equine encephalomyelitis virus
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Best Local S
Matches 20
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              799-1239/Product:
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Pred. No. 22;
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Pred. No. 4;
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cosmid R13F6.
       E1 #status predicted
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C;Accession: G88168
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Reference number: Z17215
A;Accession: T10929
                                                                                                                                     A; Map position:
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-222 < S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1-1321 < PAR >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C3.20c protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                Cross-references: GB:AE005172; NID:g4204305; PIDN:AAD10686.1; GSPDB:GN00141
                                                                                                                                                                                                                                                    Status: preliminary
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1 MSKQPASNIRSIQANINIPMGAFRPGAGQPPKRKE--
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Similarity 33.9%;
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                                          13;
                                          Score 75.5; D. Pred. No. 3.8; 13; Mismatches
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Pred. No. 19;
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                                                                                           222;
-FSTEEEQH 43
                                              19;
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A/Reference number: A46611; MUID:93155224; A/Accession: A46611
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-537 <VAU>
A/Residues: 1-537 <VAU>
A/Residues: Destoralis muscle
A/Resperimental source: pectoralis muscle
A/Note: sequence extracted from NCBI backbo
                                                                                                                                                                                                                                                          myosin-binding protein H - chicken
C/Species: Gallus gallus (chicken)
C/Date: 21-Sep-1993 #Bequence_revision
C/Accession: A46611
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A/Gene:
                                                                                                                                                                                          R.Vaughan, K.T.; Weber, F.E.; Einheber, J. Biol. Chem. 268, 3670-3676, 1993 A;Title: Molecular cloning of chicken my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X81571; NID:g587593; PIDN:CAA57
A;Note: the nucleotide sequence was submitted to the EME
R;Lerivray, H.; Smith, J.A.; Tatta, J.R.
Mol. Cell. Endocrinol. 59, 241-248, 1988
A;Title: POSP-1 (frog oviduct-specific protein-1) gene:
A;Reference number: A60880; MUID:89031654; PMID:2846384
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R;Mehta, R.J.; Tata, J.R.
Eur. J. Biochem. 229, 224-232, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oviduct-specific protein 1A - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
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A; Residues: 1-480 < MEH>
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A, Residues: 1-182 <MEW>
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Best Local Similarity
Matches 17; Conserv
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Comment: This mRNA is expressed
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                                                                                                                                                                                        of chicken myosin-binding protein
                               from NCBI backbone
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Pred. No. 8.4;
6; Mismatches
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                                                                                                                                                        PMID: 7679114
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to the EMBL Data
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R;Bougueleret, L.
submitted to the EMBL Data
A;Reference number: S37671
                                                               C; Accession: S37671
                                                                   MHC class III histocompatibility antigen HLA-B-associated protein 2 [similarity] C;Datecies: Homo sapiens (man) C;Datecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Sep-2000
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                                                                                                                                                S37671
                                                                                                                                                                   RESULT 10
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A;Map position: 22q13-22q13
C;Superfamily: thymidine phosphorylase
C;Superfamily: thymidine phosphorylase
C;Keywords: angiogenesis; glycosyltransferase; growth factor; mitogen; pentosyltransfera
F;6-482/Product: platelet-derived endothelial cell growth factor, placental form #status
F;11-482/Product: platelet-derived endothelial cell growth factor, platelet form #status
F;63/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A60966; MUID:91175877; PMID:2078568 A;Accession: A60966
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Thymidine phosphorylase activity associated with | A;Reference number: JX0275; MUID:94012588; PMID:8407883 A;Accession: JX0275 mRNA A;Residues: 125-244 <SUM> A;Residues: 125-244 <SUM> A;Experimental source: placenta A;Experimental source: placenta R;Usuki, K.; Norberg, L.; Larsson, E.; Miyazono, K.; Hellm. Cell Regul. 1, 577-596, 1990 cell Regul. 1, 577-596, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: part of this sequence, including the amino end of the mature pa;Note: 471-Ser was also found R;Sumizawa, T.; Furukawa, T.; Haraguchi, M.; Yoshimura, A.; Takeyasu, J., Blochem. 114, 9-14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 23-Oct-1998 #sequence revision 23-Oct-1998 #text_change
C;Accession: S03904; JX0275; A60966
R;Ishikawa, F.; Miyazono, K.; Hellman, U.; Drexler, H.; Wernsted
Nature 338, 557-562, 1989
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S03904
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C;Genetics:
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A;Residues: 6-14 <USU>
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A; Residues: 1-482 <ISH>
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PGTGAPPAPGDFSGEGSQGLPDP----SPEPKQLPELIRMKRDGGRLSE
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Pred. No. 9.4;
6; Mismatches
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                                                                                                             Score 74.5;
Pred. No. 10
                                                                                    Mismatches
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Library,

August 1992

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Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within A;Reference number: 836152; MUID:93272029; PMID:8499947
A;Accession: 836152
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C;Date: 06-Jun-1995 #sequence_revision
C;Accession: S36152
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C;Genetics:
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1870 <BOU>
                                                                                                                                                                                                   MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported] C;Species: Homo sapiens (man) C;Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 24-Aug-2001 C;Accession: B35098
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A;Note: in the authors' translation residues
A;Note: the authors translated the codon AAT
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                                                                                                 R;Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T. Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A;Title: A gene pair from the human major histocompatibility A;Reference number: A35098; MUID:90192810; PMID:2156268
A;Accession: B35998
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A;MOJecule type: mRNA
A;Residues: 1-2142 <BAN>
A;Cross references: GB:M33509;
A;Note: the authors translated
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                                                                                   A;Status: preliminary
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      NID:g179338; PIDN:AAA35585.1; PID:g179339; the codon AGT for residue 97 as Gly
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Pred. No. 53;
LO; Mismatches
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Pred. No. 53;
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46 RSI-ANLTIKQRAPNPPAGPPAKRKKPAPSISIRRKKKRPPPPA--KKOKRKPKPG 10 RSIQANINIPMGAFRPGAGQPPKRKE----FSTEEEQHVPTPESEEKSEEKKPIPG

86 61 Gaps

2

Query Match Best Local S Matches 21

Similarity

18.6%;

Score 72.5; Pred. No. 4

DB 2;

Length 1241; Indels

Conservative

9

Mismatches 43;

19;

7;

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1241 <VOL>
A;Rresidues: 1-1241 <VOL>
A;Rresidues: 1-1241 <VOL>
A;Rross-references: EMBL:X63135; NID:g59185; PIDN:CAA44845.1; PID:g59186
A;Rote: sequence could not be checked because of bad print in paper
C;Superfamily: togavirus structural polyprotein
C;Keywords: capsid protein; envelope protein; glycoprotein; polyprotein
F;1-260/Product: capsid protein C #status predicted <CAP>
F;261-323/Product: envelope protein E3 #status predicted <EP3>
F;344-300/Product: envelope protein #status predicted <EP1>
F;344-800/Product: envelope protein #status predicted <EP1>

A; Accession: S26373

gen

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R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus
A;Reference number: S26369; MUID:91375524; PMID:1896061
                                                     C; Accession: Szba.
                                                                                         genome polyprotein - eastern equine encephalomyelitis virus N;Contains: 6K protein; capsid protein C; envelope protein l C;Species: eastern equine encephalomyelitis virus C;Species: eastern equine encephalomyelitis virus C;Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_ch
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                                                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                              P---GAVKLPGPAFNLSE
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                                                                                                                                                                                                                                                                                                                                                   KQPASNIRSIQANINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKS---EEKKPI 59
                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         18.8%;
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Pred. No. 61;
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                                                                                                                                 envelope protein
                                                                                             26-Aug-1999
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Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A90575
                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein MYPU_5050 [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A90575
                                                                                                             A;Gene:
                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-833 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                    A;Genetic
                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            R;Chambaud,
                                                                                                                                                                                                                                                                                                                                                                                 C; Accession:
                                                                                                                                                          A;Experimental source: strain
                                                                                                                                                          Cross-references: GB:AL445566; PID:g14089919; PIDN:CAC13678.1; Experimental source: strain UAB CTIP
                                          Query Match
                     Local
                                                                                                             MYPU_5050
                                                                                        code:
                                                                                                                                                                                                                                                                                                                                    I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, is Res. 29, 2145-2153, 2001
                     Similarity
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                                                                                        SGC3
                     18.5%;
Score 72; DB Pred. No. 32; 7; Mismatches
                                            2;
                                            Length 833
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                                                                                                                                                                                   GSPDB:GN00153
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5 PASNIRSIQA---NINIPMGAFRPGAGQPPKRKEFSTEEEQHVPTPESEEKSBEK-KPIP

29;

Indels

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Gaps

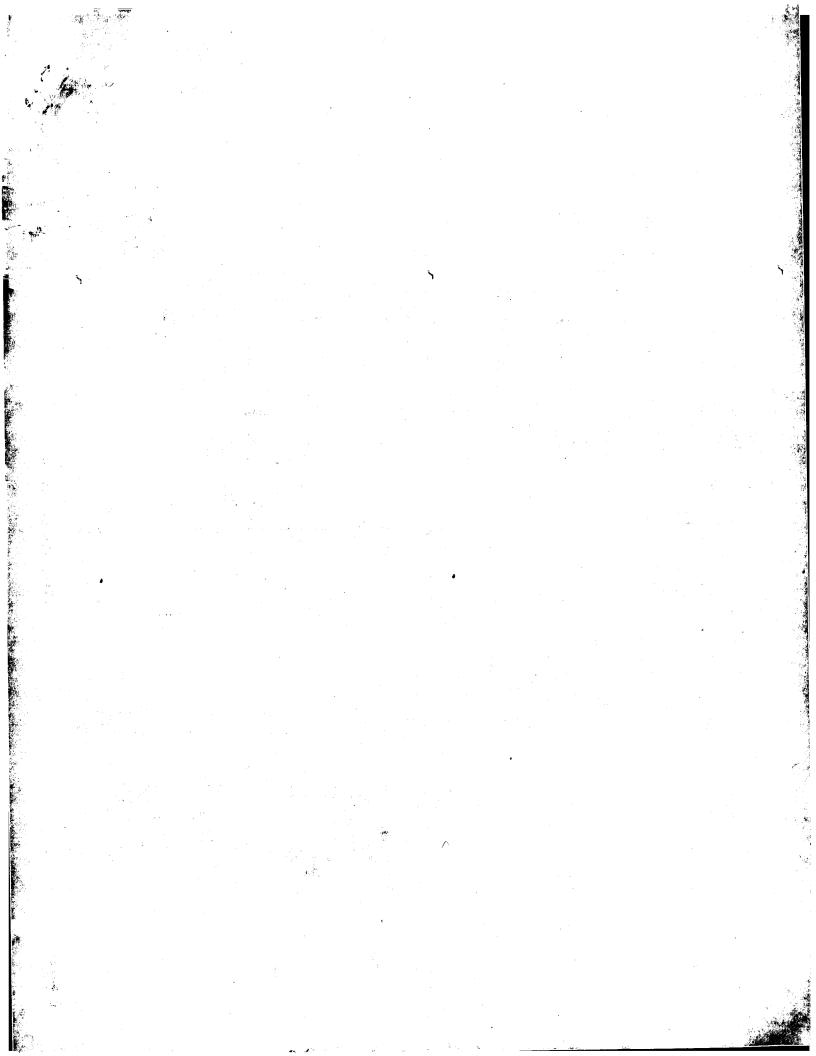
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Matches

Conservative

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Search completed: April 9, 2003, 12:39:43 Job time : 22:0524 Becs
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A;Molecule type: DNA
A;Molecule type: DNA
A;Gresiduse: 1-307 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK85984.1; PID:g15155045; GSPDB:GN00169
C;Genetics:
C;Genetics: AGR C_267
A;Gene: AGR C_267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AGR_C_267 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C.) Species: Agrobacterium tumefaciens C.) Species: Agrobacterium tumefaciens C.) Species: Agrobacterium tumefaciens C.) Accession: G97378 R. Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Lilu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-3328, 2001 Science 294, 2323-3328, 2001 Science 294, 2323-3328, 2001 A;Filtle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume, A, Cecession: G97378
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Best Local S:
Matches 18
                                                                                                                                                                     114 KPAPLPKP 121
                                                                                                                                                                                                                                                                     y Match
Local Similarity 28.1%; Pred. No. 13;
Local Similarity 28.1%; Pred. No. 13;
hee 18; Conservative 12; Mismatches 19; Indels 19
                                                                                                                                         57 KPIP 60
                                                                                                                                                                                                                4 QPASNIRSIQ-----ANINIPMGAPRPGAGQPPKRKEFSTEBEQHVPTPESEEKSEEK 56
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Maximum Match 100%
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Maximum DB
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    No. 18 the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

  seq length: 0
seq length: 2000000000
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172
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 US-09-484-970B-111
US-08-464-342-1
US-08-355-520-1
US-08-464-604A-1
US-08-875-272-1
US-08-866-663A-1
US-08-995-601-4
US-08-995-601-4
US-08-995-601-4
US-08-895-601-4
US-08-895-601-8
US-08-484-970B-119
US-08-484-970B-119
US-08-839-00B-8
US-09-484-970B-119
US-08-839-00B-9
US-08-839-00B-9
US-08-839-00B-9
US-08-680-506-6
US-09-133-861-73
US-09-127-946-9
US-08-680-506-8
US-08-680-506-8
US-08-680-506-6
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Compugen_Ltd.
Sequence 111, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 119, Appli Sequence 119, Appli Sequence 73, Appli Sequence 9, Appli Sequence 6, Appli Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                     Description
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GENERAL INFORMATION:

APPLICANT: Jones, Karen A.

APPLICANT: Volkmuth, Wayne

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOPTWARE: PERL Program

SEQ ID NO 111

LENGTH: 000-01-11

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	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2
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	US-09-060-694-19	US-08-487-811A-19	US-07-928-611-19	US-08-056-051-3	PCT-US93-07370-17	US-09-378-074-17	US-09-060-694-17	US-08-487-811A-17	US-07-928-611-17	US-08-056-051-1	US-08-475-742-3	US-08-434-877-2	US-08-086-439C-2	PCT-US93-07370-1	US-09-378-074-1	US-09-060-694-1	US-08-487-811A-1	US-08-333-977-1
,	Sequence 19, Appl	Sequence 19, Appl		Sequence 3, Appli	•	Sequence 17, Appl	•	Sequence 17, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	GENERAL INFORMA	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

US-09-484-970B-111

Sequence 111, Application Patent No. 6426186 K

US/09484970B

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RESULT 2
US-08-464-342-1/c
US-08-464-342-1/c
; Sequence 1, Application US/08;
; Patent No. 5650313
; GENERAL INFORMATION: TAL.
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: 'Ubiqu'
; TITLE OF INVENTION: '7, 8;
; NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NC
US-09-484-970B-111
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Best Local (
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                      96 GATCGCAGCTCAGAGGACACCGGGGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT
                                                                                                                                                                                                                                                                                                                                          36 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA 95
                                                                                                                                                                                                                                                                                                          62 GATCGCAGCTCAGAGGACACC-GGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT 120
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Similarity 98.8%;
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                                                                                                                   US/08464342
                                Ubiquitin Conjugating 7, 8 and 9
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 4;
Pred. No. 7.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 909
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GILFILLAN,

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US-08-305-520-1/c
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08305520 Patent No. 5744343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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          ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: ASCII(text)

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-464-342-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                       APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
                                                                                                                                                                                                                                                          APPLICANT: Guillaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01250
FILING DATE: 31 JAN 95
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258800-373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 337
APPLICATION NUMBER:
                                                                                                                                        COUNTRY:
                                                                                                                                                            STATE:
                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ATCGCAGCTCAGAGGACACCGGG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                         60 State Street
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                                                                                                                                        USA
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CECCHI, STEWART & OLSTEIN
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60.2%;
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US/08/305,520
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Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08464604A Patent No. 5849286
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                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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REGISTRATION NUMBER: M11--
REFERENCE/DOCKET NUMBER: M11--
REFERENCE/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKET/DOCKE
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                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/464,604A
FILING DATE: 05-UN-1995
CLASSIFICATION: 514
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STREET: NOSELAND
CITY: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GENTZ, REINER APPLICANT: ADAMS, MARK D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 ATCACACAACAGAGAACAGATGG 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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   STRANDEDNESS:
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                                                                     ENGTH:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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nucleic acid EDNESS: double
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                                                                                                                                                                                                    TELEPHONE: 201-994-1744
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 BASE PAIRS
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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                                                                                                           Matches
                                                                                                                                      Query Match
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Patent No. 5945321
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,272
FILING DATE: Concurrently
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                STRANDEDNESS: SIN
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                               NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
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NAME/KEY:
LOCATION:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER PARM ROAD
                                        396 TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 337
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63 ATCGCAGCTCAGAGGACACCGGG 85
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                                                                                                                       Local
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STATE: NEW JERSEY
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nes 50; Conservative
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                                                               TTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
                                                                                                      17.6%;
1 Similarity 60.2%;
50; Conservation
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60.2%;
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                                                                                                   Score 30.2; DB
Pred. No. 0.25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                               325800-244
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Pred, No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                               DB 2; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,
                                                                                                      33;
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                                                                                                   Indels
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                                                                                                Gaps
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                                                                                                  0,
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RESULT 7
US-08-903-396-1/c
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*Gequence 1, Application US/08903396
Patent No. 5968797
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Ubiquitin C
TITLE OF INVENTION: 7, 8 and 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-486-663A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS LOCATION: 1..441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MITELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COMPUTER: PC COMPUTER: PC
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APPLICANT: Draetta, Giulio
APPLICANT: Guillaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                         336 ATCACACAACAGAGAACAGATGG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 TTCTCTATCTGTTTGGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: US
ZIP: 02109
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STRANDEDNESS: both
TOPOLOGY: linear
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milarity 60.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
   Ubiquitin Conjugating Enzymes 7, 8 and 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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Gaps

NUMBER OF SEQUENCES:

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US-08-247-904B-1/c
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COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,396

FILING DATE: 22-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/464,342

APPLICATION NUMBER: 9CT/US95/0125

APPLICATION NUMBER: PCT/US95/0125

APPLICATION NUMBER: 31-JAN-1995

ATTORNEY/ACENT INFORMATION:

NAME: MULLINS, J.G.

REGESTRATION NUMBER: 33,073

REGESTRATION NUMBER: 33,073
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                      APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 ATCACACAACAGAGAACAGATGG 314
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CITY: ROSELAND
STATE: NEW JERS
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
ZIP: 02109
OMPUTER READABLE FORM:
DMEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAŢING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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One Post Office Square
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Patent No. 6060262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 50; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                          ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-096.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION, TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 ATCACACACAGAGAACAGATGG 314
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                                                                                                                                                                                                                                                                                                                                            STREET: One P
CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                            APPLICATION NUMBER: US/08/895,601 FILING DATE: 16-JUL-1997
                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                               02109-2170
                                                                                                                                                                                                                                                                                                                                                                                    B: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strack, Peter J.
Glass, Susan J.
Rolfe, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 base pairs
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                   617-832-7000
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                                                   US-08-767-942A-1
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 Query Match
Best Local Similarity
                                                                                                                                                   TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                      ZIP: 02109-2170

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIAN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6068982
GENERAL INFORMATION:
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Best Local Similarity 60.2%;
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LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
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ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                      FEATURE:
                                                                                                                     MOLECULE TYPE:
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LOCATION:
                                                                     NAME/KEY:
LOCATION:
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                                                                                                                                      STRANDEDNESS:
TOPOLOGY: 111
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Chiu, M. Isabel
Berlin, Vivian
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Score 30.2; DB 3; Pred. No. 0.25;
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RESULT 12
US-09-535-008-50/c
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/425,299A
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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                                                                                                                                 345 ATCACACAACAGAGAACAGATGG 323
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                                                                                                                                                                                                       63 ATCGCAGCTCAGAGGACACCGGG 85
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                     3 TTCTCAATACCGGGAGAGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
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                                                                                                                                                                                                                                                               TTCTCTATCTGTTTGGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 346
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King, Randall W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.2; DB 1;
Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 452;
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; LOCATION: 2323, 2332, 2337
; OTHER INFORMATION: a, t, c,
US-09-484-970B-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-535-008-50
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Progra
SEQ ID NO 119
LENGTH: 2343
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 119,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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LENGTH: 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
TITLE OF INVENTION: AND OTHER CANCER TYPES
FILE REFERENCE: 2318-259
CURRENT APPLICATION NUMBER: US/09/535,008
CURRENT FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09535008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: U.S. 60/125,806 EARLIER FILING DATE: 1999-03-23 NUMBER OF SEQ ID NOS: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jones, APPLICANT: Volkmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
954 GACGGCTGTCTATGCCCCTGTTCTCTTGGCCTGGGTGGGCGTGGGGCATGCGTCTAGCTTCC 1013
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                                        74 GAGGACACCGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCC 133
                                                                                                                        14 GGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 CAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCT 126
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                                                                                                                                                                Conservative
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62.2%;
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Pred. No. 0.72;
0; Mismatches 28; Indels
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Patent No. 5916758
                                                                                                      Patent No.
                                                                                                         Sequence 1, Application US/08839008 Patent No. 5916758
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                         GENERAL INFORMATION:
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                                                           APPLICANT:
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                                                                                                                                                                                                                                                     1272
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APPLICATION NUMBER: 08/50
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
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                                             APPLICANT:
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ADDRESSEE: SmithKline Beecham Corporation
                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 23-APF
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Baumeister, Kirk REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                             CCAGGAC 1338
                                                                                                                                                                                                                                                     AGAAGAAACAGAAGCCCCCGTCCTTCCTAGAAGAGCTTTGTGGTTCTCCACCGGCCCAA 1331
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                                      McDonnell, Peter C
                                                                                                                                                                                                                                                                                                                                                                                                                                            1480 base pairs
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McNulty, Dean E
Rosen, Craig A
                                                                                                                                                                                                                                                                                                             Conservative
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                            McNulty, Dear
Rosen, Craig
Siemens, Ivo R
Young, Peter R
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Young, Peter R
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62.7%;
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Pred. No. 5.6;
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                                                                                                                                                                                                                                                                                                                                          DB 2;
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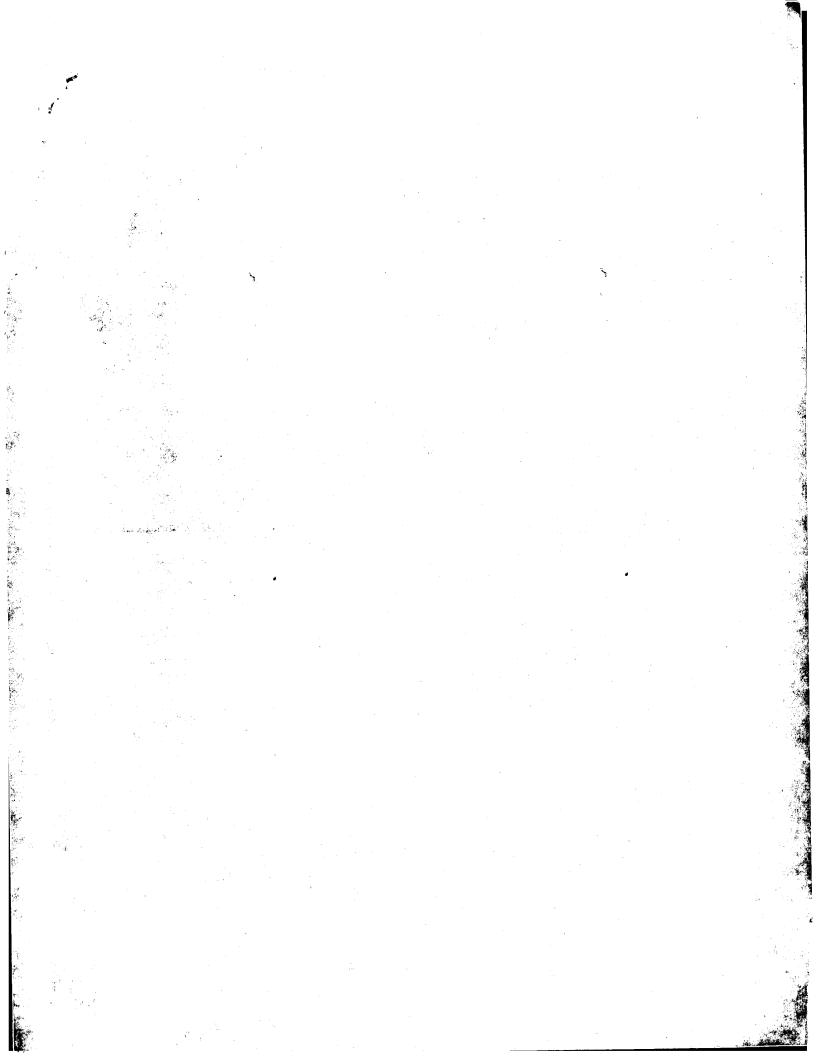
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25

ICURENT APPLICATION UNMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION UMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION NUMBER: 08/563,697
FRICAR APPLICATION NATA:
APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumedster, Kirk
REGISTRATION NUMBER: P50384
TELEPHONE: 610-270-5096
TELEPHONE: 610-270-5096
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
Search completed: April 15, 2003, 22:46:48 Job time: 13.1771 secs
                                                                                                                                                                                                                                                                       Ouery Match 15.7%; Score 27; DB 2; Length 1537; Best Local Similarity 62.7%; Pred. No. 5.7; Matches 42; Conservative 0; Mismatches 25; Indels
                                                                                               1365 CCAGGÁC 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
                                                                                                                                         133 СТОССАС 139
                                                                                                                                                                                                         73 AGAGGACACCGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGC 132
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ZIP: 19406
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Maximum Match 100%
Listing first 45 s
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seq length: 2000000000
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1: /cgn2_6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptcdata/2/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*

13: /cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*

14: /cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*
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10 US-09-960-352-5216
10 US-10-043-487-198
10 US-09-833-381-896
10 US-10-026-188-3
10 US-10-026-188-3
     0 US-09-770-445-525

0 US-09-917-800A-1389

0 US-09-917-805-27-12958

0 US-09-878-574-12958

0 US-09-819-497-39

0 US-09-880-107-2196

0 US-09-822-849A-273

0 US-09-825-301-440

US-10-121-049-79

US-10-121-049-79

US-10-123-904-79

US-10-175-746-79

US-10-175-746-79
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Sequence 198, App
Sequence 3, Aph
Sequence 3, Aph
Sequence 525, App
Sequence 139, App
Sequence 12958, A
Sequence 12958, A
Sequence 239, Aph
Sequence 2196, App
Sequence 273, App
Sequence 79, Appl
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Sequence 5216, Ap
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	26.2	26.2	26.2	26.2	26.2	26.2	26.2	26.4	26.4	26.4	26.4	26.8	26.8	26.8	27	27	27	27	27	27	27	27	27	27	27	27
			15.2		15.2	15.2	15.2	15.3	15.3	15.3	15.3	O	15.6	15.6	15.7	15.7	15.7	15.7	15.7	15.7	15.7		15.7	15.7	15.7	15.7
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ALIGNMENTS	US-09-874-923-105	US-09-991-496-105	US-09-874-923-73	US-09-991-496-73	US-09-925-301-736	US-09-864-761-5490	US-09-728-446-732	US-09-923-684-1	US-09-923-684-2	US-09-822-849A-341	US-09-925-300-736	US-09-738-626-1	US-09-974-300-1841	US-09-738-626-3175	US-10-143-032-79	-10-141-755	-050	US-10-142-423-79	US-10-123-262-79	-10-142-419	-10-140-002	US-10-143-114-79	-10-142-431	US-10-140-474-79	US-10-137-865-79	US-10-176-921-79
	e 105,	105,	e 73	3,	736, 1	Ç	732	٢		341	736	٢		317		79,		79,	79,		79,	79,	79,		79,	Sequence 79, Appl

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GENERAL INFORMATION:

APPLICANT: Walker, Michael G.

APPLICANT: Volkmuth, Wayne
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYMUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
CURRENT FILING DATE: 2001-06-12
INUMBER OF SEQ ID NOS: 62
SOFTWARE: PERL PROGram
SEQ ID NO 4
LENGTH: 824
TYPE: DNA
ORGANISM: Homo Bapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1
US-09-880-192-4
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US-09-880-192-4
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Best Local Similarity 100.
Matches 171; Conservative
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Patent No. US20020077470A1
                                            122
155
                                                                                      95
                                                                                                                                 62
                                                                                                                                                                           35 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA 94
                                                                                                                                                                                                   2 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA 61
                         CATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                      GATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTG
                                                                                                                          GATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCAACCTTCCAAGGAGCTTTGTATTCTTG 121
CATCTGGCTGCGTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAG
                                                                                                                                                                                                                                                                h 99.4%; Score 171; DB 10; Length 824; Similarity 100.0%; Pred. No. 1e-56; 71; Conservative 0; Mismatches 0; Indels
205
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RESULT 2

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CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILLING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
SEQ ID NO 198
LENGTH: 433
RESULT 4

US-09-33-381-896/c

; Sequence 896, Application US/09833381

; Parent No. US20020132090A1
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                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Shigella Flexneri
US-10-043-487-198
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US-10-043-487-198/c
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Publication No. US20030055220A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Warren, I
APPLICANT: Tao, Ne.
APPLICANT: Byatt,
APPLICANT: Mathial
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                         Query Match
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SEQ ID NO 5216
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Patent No. US20020137139A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptic
TITLE OF INVENTION: mammalian polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: B4778A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HYBRIGENICS APPLICANT: Pierre, LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 23-BOVMS1-014-Q1-E1-F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 TCCCTTAGGCAGTAAAACAAATACATAAAAGCA 171
                                                                                                                                                                                                385 TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 320
                                                                                                                                                        63 ATCGCAGCTCAGAGGACACCGGG 85
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 CCGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 67; Conserv
                                                                                                                                                                                                                                       3 TTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCGGCGTCCCTTCCACTCACTGATGAGCCTTG--TTCATGTACCTGACTGCCTGCGACT 58
                                                                                                                    ATCACACAGAGAGAACAGATGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCTCAGGCATGAAACATGTGCATATAGCA 89
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60.2%;
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73.6%;
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Pred. No. 0.094;
0; Mismatches
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Pred. No. 2.8e-06;
D; Mismatches 22
                                                                                                                                                                                                                                                                                                                  DB 9;
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                                                                                                                                                                                                                                                                               33;
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                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 249487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1946
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1946)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                       Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10026188 Patent No. US20020164645A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 896
                                                                                                                                                                                           Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zuker, Charles S.

APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: Ion Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Robison, Keith E.

TITLE OF INVENTION: NO. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: US 60/259,379 PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                        OTHER INFORMATION: mouse genomic region containing ltrpc5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 840 TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCÁGGCÁCTAAÁGGATCÁTCTGGÁTTGGG
                                                                                                                         35 CAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACACCGGGCGCCCCTTC 94
                                       95 CACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACTTCCCTTAGGCAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ATCGCAGCTCAGAGGACACCGGG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TTCTCAATACCGGGAGAGCCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
CCAAACCAGTGTGAGTGACAATGGCAGCTTCAGGCGGCCCGTGACTCCCCCAAGTCAG 127004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCACACAACAGAGAACAGATGG
                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 17.6%;
Similarity 60.2%;
                                                                                                                                                                  17.4%; ilarity 53.4%; Conservative
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                                                                                                                                                                  Score 30; DB
Pred. No. 1.7;
0; Mismatches
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                                                                                                                                                                       Indels
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US-09-770-445-525/c

Patent No. Usec. Patent No. Usec. Corresponding Correction:

Gorlach, Jorn

525, Application US/09770445 o. US20020023281A1

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Sequence 1389, Application US/09917800A

Patent No. US2002011946ZA1

PAPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Archur
APPLICANT: Castle, Archur
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION DATE: 2000-01-0-31
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US-09-917-800A-1389/c
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; ORGANISM: Arabidopsis thaliana
US-09-770-445-525
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Matches
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012FRV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 TCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTCTGCTTTCTCTTCCTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAAGGCGAGAAGCGGAGATAGTTCATCTGCTCGCTACGCTTACGAATGGCGTTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGCCTGGGGACTTCCCT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 4.0
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Allen, Keith
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Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
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Rameaka, Joshua G.
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50.7%;
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; ORGANISM: Homo sapiens
US-09-877-065-2
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US-09-877-065-2
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APPLICANT: HEARD, CHERYL J.

TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF OVARIAN CARCINOMAS
FILE REFERENCE: 037003-0280631
CURRENT APPLICATION NUMBER: USO/09/877,065
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,451
PRIOR APPLICATION NUMBER: 60/210,451
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
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Best Local Similarity
Matches 39; Conserv
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SEQ ID NO 1389
LENGTH: 952
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LENGTH: 1257
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                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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1159
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                                      156
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OR FILING DATE: 2001-05-11
OR APPLICATION NUMBER: US 60/290,645
OR FILING DATE: 2001-05-15
OR APPLICATION NUMBER: US 60/292,336
OR APPLICATION NUMBER: US 60/292,336
OR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                             36 AGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCC 95
                                                                                                                           96
                                      ACAAATACATAA 167
                                                                                                                                                                      AGCCAGAAGAAGCACTGGATTCCTCAGTCCACCAGCTCAGACAGCACCCGCCCCCC 1098
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                                                                                                                        ACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACTTCCCTTAGGCAGTAA 155
                                                                                  ACCCATCAAGCCCTTTTATATTATTTATAAAGTGACTTTTTTATTACTTTAATTTTTTTA 1158
                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                             Conservative
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50.8%;
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Pred. No. 1.1;
0; Mismatches
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US-09-880-107-2196
; Sequence 2196, Application US/09880107
; Patent No. US20020142981A1
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US-09-919-497-39
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                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT PILING DATE: 2001-12-21
CURRENT PILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701066451H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1480
                                                                                                                          1332 CCAGGÁC 1338
                                                                                                                                                                                                 1272 AGAAGAGAACAGAGGCCCCGTCCTTCCTCCAGAGAGCTTTGTGGTTCTCCACCGGCCCAA 1331
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                                                                                                                                                             133 CTGGGAC 139
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                                                                                                                                                                                                                                       73 AGAGGACACCGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGC 132
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                                                                                                                                                                                                                                                                               42;
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                                                                                                                                                                                                                                                                                                 15.7%;
62.7%;
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57.5%;
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                                                                                                                                                                                                                                                                           Score 27; DB 10;
Pred. No. 2.8;
0; Mismatches 25
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US-09-822-849A-273
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                                                                                                                                                                                                                  SEQ ID NO 273
LENGTH: 1542
TYPE: DNA
                                                                                                                                                                                                                                                                   FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                             Query Match
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 2001-06-14
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Genbank Accession No. US20020142981A1 L33799
                                   1327 AGAAGAGAACAGAGGCCCCGTCCTTCCAGAGAGCTTTGTGGTTCTCCACCGGCCCAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1272 AGAAGAGAACAGAGGCCCCGTCCTTCCTCCAGAGAGCTTTGTGGTTCTCCACCGGCCCAA 1331
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133 CTGGGAC 139
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                                                                                                       / Match 15.7%;
Local Similarity 62.7%;
nes 42; Conservative
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                                                                     73 AGAGGACACCGGGCGCCCTTCCAACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGC 132
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Graham, James R.
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Agostino, Michael J
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Scherf, Uwe
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                                                                                                       Score 27; DB 1
Pred. No. 2.9;
0; Mismatches
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Pred. No. 2.8;
0; Mismatches
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                                                                                                                                           DB 10; Length 1542;
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US-09-925-301-440
US-09-925-301-440
; Sequence 440, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26
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Publication No.
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Best Local Similarity
Matches 42; Conserv
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SEQ ID NO 440
LENGTH: 1580
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10028072
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Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                  Stewart, Timothy A.
                                                                                                                                                                                                                                    Smith, Victoria
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Pred. No. 2.9;
0; Mismatches 25; Indels
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PRIOR PRIOR PRIOR FILING DATE: 1997-09-17 PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059113 OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066453
OR FILING DATE: 1997-11-24
OR FILING DATE: 1997-11-24 DR APPLICATION NUMBER: 60/066511
DR FILING DATE: 1997-11-24
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/069212
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DR APPLICATION NUMBER: 60/069278
DR APPLICATION NUMBER: 60/069278
DR APPLICATION NUMBER: 60/069278
DR APPLICATION NUMBER: 60/069278 APPLICATION NUMBER: 60/064248
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/064809 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
FILING DATE: 1997-10-17 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063733
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063735 APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063082
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/059836 FILING DATE: 1997-09-24 APPLICATION NUMBER: 60/062250 APPLICATION NUMBER: 60/063550 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063327 FILING DATE: 1997-10-27 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063045 APPLICATION NUMBER: 60/062814 FILING DATE: 1997-10-24 FILING DATE: 1997-09-19 APPLICATION NUMBER: 60/059588 FILING DATE: 1997-09-18 APPLICATION NUMBER: 60/059352 APPLICATION NUMBER: 60/059184 APPLICATION NUMBER: 60/059122 FILING DATE: 1997-09-APPLICATION NUMBER: 60/059115 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-17 FILING DATE: 1997-09-17 APPLICATION NUMBER: 60/062816 FILING DATE: 1997-09-19

NUMBER: 60/069334

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RESULT 15
US-10-121-049-79
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                                            Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 79
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Best Local
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                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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LENGTH: 2714
TYPE: DNA
ORGANISM: Homo Sapien
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090538
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089532
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DeForge, Laura
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Pred. No. 3.7;
0; Mismatches 4
                                                                            See File Wrapper or Palm
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                                                                                                                                                              POLYPEPTIDES
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60/085697 60/085579 60/085339

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APPLICATION NUMBER: 60/088741 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810

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60/088730

APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04

APPLICATION NUMBER: 60/086430 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28

PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: FILING DATE: 1998-0 APPLICATION NUMBER:

1998-05-12

60/085149

APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 APPLICATION NUMBER: FILING DATE: 1998-04

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APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627

1998-05-07

APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28

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1998-04-24 1998-04-1

60/082999

APPLICATION NUMBER:

60/081818

APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-14 APPLICATION NUMBER: 60/081695

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APPLICATION NUMBER: 60/085323 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-13

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APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09

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FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-03-31

APPLICATION NUMBER: 60/079728 FILING DATE: 1998-02-27 APPLICATION NUMBER:

3

PRIOR PRIOR PRIOR

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APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-APPLICATION NUMBER:

60/078910 60/077791

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APPLICATION NUMBER: 60/074086

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APPLICATION NUMBER: 60/073612

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APPLICATION NUMBER: 60/074092 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/ FILING DATE: 1998-01-23

60/072320

DATE: 1997-12-DATE: 1997-12-11

NUMBER: 60/069694

FILING

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	Db 2264 ACATGGAGCTCCCAAGCAGGT 2294 Search completed: April 16, 2003, 01:14:11 Job time: 80.1865 secs	20 GGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGAC 79	Query Match 15.7%; Score 27; DB 9; Length 2714; Best Local Similarity 56.0%; Pred. No. 3.7; Matches 51; Conservative 0; Mismatches 40; Indels 0: Gans 0.	US-10-121-049-79
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Minimum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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cDNA encoding huma	AAT79814	18	444	17.6	30.2	4	
Ubiquitin conjugat	AAT39695	17	444	17.6	30.2		
Human ubiquitin-co	AAQ97831	16	444	17.6	30.2	0 ~	
Human secreted pro	AAA26372	21	1563	17.9	30.8	0	
Human cDNA differe	ABK83560	24	86574	18.1	31.2		
cDNA encoding muri	AAX90903	20	778	55.3	95.2		
Human 66214 EST cl	AAD27216	24	988	99.4	1/1		
Human secreted pro	AAC01483	21	428	99.4	17.1	, V	
cDNA encoding huma	AAX90904	20	887	100.0	172	, _	
Description	IB	- BB	Length	Match	score	20	
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1314 23 2818 23 6101 23		1522 24 1522 24 2631 23 7889 23 27289 22 27289 22		50526 22 5076 22 5076 22 19487 24 1098 23 1529 21 6288 22 881 24 948 21	444 444 20 444 20 444 20 444 21 452 17 452 17 24 24 24 26 27 27 27 27 27 27 27 27 27 27 27 27 27
400	w ~ ~ ~ ~ ~	ABL57467 ABL67467 ABL03923 ABL03922 ABL039821 AAS34624	AAC4455 AAL07039 AAL62717 ABN22475 AAC58894	AAH14290 ABA14699 ABA14700 ABN85733 AAS70200 AAC59838 AAS45090 ABN98757 AAC50935	AAZ25304 AAZ27558 AAX78496 AAV82865 AAA61613 AAT41769 ABK4311 AAH14153 ABI99458
כסס	numan secreted pro Eosinophil activat Human inflammation Human GTPase activ Human DeltaT-atero	Human nervous syst Human protein phos Drosophila melanog Drosophila melanog Human DNA for a no	dopsis reprod breast ORFX p tumour	3 17 12 14 12 12 12	n ⊷.

ALIGNMENTS

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CDS	exon				exon	Key	ייכווס פמטיכוום.		gene therapy;	Becker's myoto	muscular and r	detection; dia	Xq21.3-q22; ac	heart/skeleta	Chisel gene; (cDNA encoding		17-JAN-2000		AAX90904;		AAX90904 stan	AAX90904	RESULT 1
/*tag= b /label= Exon_2 /note= "Corresponds to residues 15687-15631 of human cosmid clone U228D4" 185451	173229	/note= "Corresponds to residues 19497-19327 of	/label= Exon_1	/*tag= a	1172	Location/Qualifiers			gene therapy; transgenic animal; drug screening; ss.	Becker's myotonic dystrophy; heart failure; differentiation; exon;	myotonic dystrophy; Duchenne muscular dystrophy; therapy;	detection; diagnosis; prophylaxis; treatment; cardiac hypertronby;	Xq21.3-q22; adaptive process; muscle homeostasis; skeletal myonarhy;	heart/skeletal muscle cell development; signalling pathway; regulation;	gene; Csl; EF-Hand protein super family: muscle development.	90000	cDNA encoding human chisel (Csl) gene	•	(first entry)				AAX90904 standard; cDNA; 887 BP.		

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                                                                                                                                                                                                                                   Best Local Similarity Matches 172; Conserv
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating muscular
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                                                                                                                                                                                                                                                                                                                              Sequence
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  121
                                    ~61
                                                                                          61
GCATCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                                                                                                             GGTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTG 60
                                                                                                                                                                                                                                                                                                                                                                          screening.
                                              AGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT 120
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human cosmid clone U112E8"
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numan cosmid clone U112E8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan
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/product= "Chisel
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                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                              Score 172; DB 20;
Pred. No. 1.8e-51;
0; Mismatches 0;
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predominantly in heart muscles"
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST; expressed sequence tag; gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45.
P-PSDB; AAG01477.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 1481; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic, forensic, gene therapy and chromosome mapping procedures
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               122
                                                                        125
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CATCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                                                GATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTG 121
                                                                        GATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCAACCTTCCAAGGAGCTTTGTATTC
                                                                                                                                                                                         GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA
                                                                                                                                                                                                                                                GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGA
                                                                                                                                                                                                                                                                                                             171;
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 123
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                                                                                                                                                                                                                                                                                                                                                                   99.4%;
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                                                                                                                                                                                                                                                                                                                                        3e-51;
                                                                                                                                                                                                                                                                                                                                                                   DB 21;
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RESULT 3
AAD27216
                                                                                              The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary heart disease, valvular heart disease, congenital heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy.
                                 A transgenic non-human mammal comprising the sequences of the invention are also used in gene therapy. As transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present DNA sequence is expressed sequence tag (EST) 66214 clone.
   Sequence
                                                                                                                                                                                                                                                                                                                        Claim 2a; Fig
                                                                                                                                                                                                                                                                                                                                                                  Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-207400P
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     886
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     BP;
                                                                                                                                                                                                                                                                                                                        9b;
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/note= "66214 cDNA fragment"
857..862
/*tag= c
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     278
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                                                                                                                                                                                                                                                                                                                      154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beck
 A.
   172
C; 191 G; 245
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Query Match

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Length 886;

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The present sequence is the CDNA encoding the murine chisel gene (Csl) that is mapped to the mouse X chromosome. It is a member of the EF-Hand protein super family and is involved in signalling pathways. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those
                                                                                                                                                          Isolated nucleic acids encoding c treating cardiomyopathy, cardiac muscular myopathies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chisel gene; C81; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasls; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; ss.
                                                                                                                                                                                                                      WPI; 1999-610852/52.
P-PSDB; AAY28650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                    Claim
                                                                                                                                                                                                                                                               Harvey
                                                                                                                                                                                                                                                                                                        (CHAN-)
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                                                                                                                                                                                                                                                                                           (HALL-)
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                                                                                                                               3; Page 148; 157pp; English.
                                                                                                                                                                                                                                                               RP,
                                                                                                                                                                                                                                                                                        CHANG CARDIAC RES INST VICTOR GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER
                                                                                                                                                                                                                                                              Musaro A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Chisel
/note= "Expre-
                                                                                                                                                                                                                                                                                                                                                98AU-0002634.
                                                                                                                                                                                                                                                                                                                                                                            99WO-AU00220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ct= "Chisel (CSL) protein"
   "Expressed especially in heart muscles"
                                                                                                                                                                                                                                                              Palmer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Csl) gene.
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                                                                                                                                                                        chisel, used to develop products c hypertrophy, heart failure and
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                                                                                                                                                                                                                                                              Rosenthal NA;
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ARESULT 5
ABK83560/c
ID ABK835
XX ABK835
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XX Human;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                       The invention relates to detecting (M1) granulocyte (GC) active (GCA), by detecting the level of expression of gene(s) (Gs) to NA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002
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                                                                                                                                                                                                                                                  Detecting granulocyte activation of genes associated with granuloc diagnostic markers that is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000;
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                                                                                                                                                                      Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-435328/46
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                                                                                                                                                                      No 131; 114pp; English.
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76.5%;
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                                                                                                                                                                                                                                                  ctivation by detecting differential expression h granulocyte activation, which serves as is useful for monitoring disease states and
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Pred. No. 6.8e
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s) identified
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CC. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (CC an allergic response in a subject, exposure of a cor sterile inflammatory disease, by contacting a tissue having CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for cor sterile inflammatory disease, by contacting a tissue having CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for creponse in a subject, exposure of a subject to a pathogen of the detecting an inflammation (especially chronic) in a tissue, an allergic cresponse in a subject to a subject to a pathogen or creponse in a subject to a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, cor creponse in a subject, exposure of a subject to a pathogen or sterile conflammatory bowel disease, Crohn's disease, ulcerative colitis, cor parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present conditions are part of the printed specification, but was obtained in electronic format directly from WIPO at this patent did not form part conditions and make the printed specification, but was obtained in electronic format directly from WIPO at
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30-JUL-1998;
05-AUG-1998;
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 98US-0094657.
98US-0095486.
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                                                                                                                                                                                                                                                                            protein; diagnosis; cytostatic;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                 corresponding secreted proteins are useful for preventing, treating or can meliorating medical conditions, e.g. by protein or gene therapy. Also conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the collectives, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, cantoimmune diseases, hepatic and renal diseases, inflammation, caltergies, Alzheimer's and behaviourzi disorders, schizophrenia, cord cransplant rejection, disbetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal cord disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. Chaptels are also useful for identifying their bridging partners. Chaptels are also useful for identifying their binding partners.
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Best Local S
Matches 74
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06-AUG-1998;
12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive; antiHIV; antiInflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polynuclectide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreptoceins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they enco useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
               06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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DB; AAY91477.
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98US-0095455.
98US-0096319.
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04-JAN-1994;
23-MAY-1994;
27-MAY-1994;
Ubiquitin conjugating enzyme; UCE7; mammal; proteolytic pathway; therapy; ubiquitin-protein conjugation; DNA repair; cell viability; antagonist; heat shock resistance; cell cycle progression; protein degradation; AIDS; inhibitor; cell proliferation; malignant cell; immunological disorder;
                                                                                                                                                                                                                                                                                                                                        cDNA encoding the human ubiquitin-conjugating enzyme was cloned i HeLa cells using the PCR primers given in AAQ97835-38. The gene subsequently cloned into expression vectors to allow prepn. of recombinant hUDCE in bacterial or insect cells. The gene can be also be used in antisense or gene therapy of e.g. cancer, fibrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating e.g. cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubiquitin-conjugating enzyme; cell proliferation; cancer; pr
                                                                            03-APR-1997
                                                                                                                      AAT39695 standard;
                                                                                                                                                                                                                                                                                                             Sequence 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense;
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                                                                                                AAT39695
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 85; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-1995;
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                                                     Ubiquitin
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                                                                                                                                                                                                                                                                             Local
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DB; AAR79648.
                                                                                                                                                                            ATCACACAACAGAGAACAGATGG 314
                                                                                                                                                                                                ATCGCAGCTCAGAGGACACCGGG
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                                                                                                                                                                                                                                                                            Similarity
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                                                     conjugating
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                             BP, 132
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                                                                           (first
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94US-0176937.
94US-0247904.
94US-0250795.
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                                                                                                                      cDNA;
                                                                           entry)
                                                                                                                                                                                                                                                                         17.6%;
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                                                     enzyme
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рвогіавів; fibroвів; antagonist;
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                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                         Score
Pred.
                                                   7 coding sequence.
                                                                                                                      ΒP
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                                                                                                                                                                                                                                                                                                           91 G;
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                                                                                                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                             30.2;
No. 1
                                                                                                                                                                                                                                                                                                          122 T; 0 other;
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                                                                                                                                                                                                                                                                                      BG
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                                                                                                                                                                                                                                                                                      444;
                                                                                                                                                                                                                                                                                                                                                                                        cloned from
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                                                                                                                                                                                                                                                               Gaps
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0

protein degradation; AI immunological disorder;

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AAT79814/c
ID AAT798
XX
AC AAT798
XC AAT798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC conjugating enzymes (UCE) 7, 8, and 9 respectively. Mammalian cells conjugating enzymes (UCE) 7, 8, and 9 respectively. Mammalian cells contain two distinct proteolytic pathways, one of which is ubiquitin content of ubiquitin to the proteolytic pathway requires the post-translational catachment of ubiquitin to other proteins using UCEs, such as the encoded proteins. Ubiquitin-protein conjugation is highly selective and is required for a large variety of cellular functions, including DNA crepair, cell viability, heat shock resistance, and cell cycle progression. The UCEs 7, 8, and 9 may also play a role in selective protein degradation in human cells. The UCE proteins encoded by these sequences can be used to treat patients that require one of the UCEs, or need one of the UCEs inhibited. The three UCEs can also be used to treat immunosuppression related disorders, such as CL AlDS, or to regulate immunological disorders such as hymenoptera venom thypersensitivity or aspirin-induced asthma. Antagonists against the UCEs can be used to treat disorders such as Alzheimer's disease, catcophying skeletal muscle, African swine fever virus, and apoptotic cell
                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquitin Conjugating Enzyme 7, 8 and 9 polypeptide(s) - useful the treatment of e.g. the proliferation of malignant cells, Alzheimer's disease and immunological disorders
   Ubiquitin conjugating enzyme; UCE; lýmphocyte homing receptor;
                                         cDNA encoding
                                                                               12-NOV-1997
                                                                                                                                                      AAT79814 standard; cDNA; 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 52; 85pp; English.
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                                                                                                                                                                                                                                                                                                                     396 TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                      human ubiquitin conjugating enzyme
                                                                            (first entry)
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Pred. No. 1.
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Mismatches
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AAZ25304/c
ID AAZ253
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AC AAZ253
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                      AAZ25304;
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P-PSDB; AAW25114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
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growth hormone; viral infection; apoptosis inhibition; platelet; programmed cell death; AIDS; acquired immune deficiency syndrome
disorder; Alzheimer's disease; ss.
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Location/Qualifiers 1..444 /*tag= a

95US-0464342

95US-0464342

(HUMA-) HUMAN GENOME SCI INC

72

Ubiquitin conjugating enzyme-7, -8 and -9 and encoding DNA - used i

Example 1; Column 29-30; 32pp; English

CC (UCE) 7. UCE polypeptides were expressed intracellularly via gene CC therapy and can be used to provide a signal for the lymphocyte common receptor, thereby regulating lymphocyte trafficking. The growth common receptor is modified by ubiquitin and UCE polypeptides may be used to regulate growth hormone activity. UCE polypeptides can be used to overcome viral infection by suppressing programmed cell death, e.g. cc in the treatment of ADDS. They can also be used to inhibit the cytotoxic properties of platelets and the production of oxygen metabolites by cc platelets. They may be used to regulate immunological disorders in which cc platelets seem to be involved, e.g. hymenoptera venom hypersensitivity cc and aspirin-sensitive asthma. The UCE polypeptides may also be used to treat malignant transformation because proto-oncoproteins c-Mos and co v-Jun are degraded in a ubiquitin-dependent manner. UCE antagonists, care able to pass through the cell membrane and to the proteins catalyses the transfer of ubiquitin to a substrate and marks that common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that the common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that the common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that the common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that the common to the proteins catalyses the transfer of ubiquitin to a substrate and marks that the common to the proteins catalyses the transfer of ubiquitin to the proteins catalyses the transfer of ubiquitin to the proteins catalyses the transfer of ubiquitin to the AAT79814 is a cDNA sequence encoding human ubiquitin conjugating enzyme foliaceus.

Sequence 444 BP; 135 A; 95 C; 91 G; 123 T; 0 other;

TTCTCTATCTGTTTTGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 337 TTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG **ATCACACACAGAGAACAGATGG ATCGCAGCTCAGAGGACACCGGG** Similarity Conservative 17.6%; Score 30.2; DB Pred. No. 1.2; 0; Mismatches **,** 314 28 DB 18; 33; Length 444; Indels 0 Gaps 62 0

밁 S В S

AAZ25304 standard; cDNA; 444 ВP

16-DEC-1999

(first entry)

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                                                                                                                                                                                                                                                                                                                  RESULT 11
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Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis; cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosi proliferative disorder; cancer; restenosis; tissue connective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ubiquitin conjugating enzyme; UCE7; UCE8; UCE9; proliferation; Alzheimer's disease; atrophying skeletal muscle; diagnosis; African swine fever; apoptotic cell death; detection; cervical carcinoma; endemic pemphigus foliaceus; immunological disorder;
                                                                                               Human ubiquitin conjugating enzyme coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the polypeptides. UCE antagonists can be used in the treatment of atrophying skeletal muscle, cervical carcinoma, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes human ubiquitin conjugating enzyme (UCB) UCE enzymes and the DNA encoding them are useful for treating maligna transformations, immunological disorders, marking unwanted cells for death and to screen for agonists and antagonists which interact with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human ubiquitin transformations and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1995;
31-JAN-1995;
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                                                                                                                                                                                                                                                             standard;
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95WO-US01250.
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                                                                                                                                                                                                                                                          CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugating enzymes useful for treating immunological disorders -
                                                                                                                                                          entry)
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Pred. No. 1.2;
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                          atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a ubiquitin conjugating enzyme (UDCB). The CC invention relates to assays for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein cc ubiquitin-mediated proteolysis of a cell-cycle regulatory protein cc comprising contacting a candidate agent with an ubiquitin-conjugating system comprises: (a) a reconstituted protein mixture including a ubiquitin conjugating enzyme (UDCB) produced by the cxpression of a nucleic acid which hybridizes under high stringency conditions to human UDCE, Candida albicans UDCE, or Schizosaccharomyces CC conditions to human UDCE, Candida albicans UDCE, or Schizosaccharomyces CC pombe UDCE coding sequences; (b) a regulatory protein; and (c) ubiquitin. The polymucleotides are useful for identifying ubiquitination inhibitors. CC The polymucleotides polypeptides, antisense compounds and antibodies against them may also be useful for the treatment and/or diagnosis of creative disorders (e.g. cancer, atherosclerosis, or restenosis), ctissue connective disorders, controlling wound healing, and disorders characterized by fibrosis (e.g. rheumatoid arthibits, insulin dependent disorders feet and controlling wound healing).
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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23-MAY-1994;
27-MAY-1994;
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                                                             09-SEP-1999
                                                                                          AAX78496;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 444 BP; 132 A; 99 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 67-70; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma; insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
                              Human UBC4
                                                                                                                        AAX78496
                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes mellitus, glomerulonephritis, cirrhosis, and scleroderma).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying ubiquitination inhibitors using
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                                                                                                                                                                                                                                                                                         TTCTCAATACCGGGAGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
                                                                                                                                                                                                                               ATCGCAGCTCAGAGGACACCGG
                                                                                                                                                                                                                                                              TTCTCTATCTGTTTGGTAGATCCGAGCAATCTCAGGCACTAAAGGATCATCTGGATTGGG 337
                                                                                                                                                                                                  ATCACACAACAGAGAACAGATGG
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                                                                                                                        standard;
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                              CDNA
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94US-0247904.
94US-0250795.
94US-0305520.
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                                                                                                                        CDNA;
                                                           entry)
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Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       91 G; 122 T; 0 other;
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0

Inhibitor; ubiquitin-mediated proteolysis; IkappaB polypeptide; HECT;

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ubiquitin-conjugating system; Homologous to E6-Ap carboxyl terminus; ligase; whiquitin; ubiquitination; RSC ligase; KIAAN ligase; UBC4; MAD3; modulator; treatment; proliferative disorder; apoptosis; sepsis; differentiative disorder; viral infection; tissue wasting disorder; cachexia; malignancy; inflammatory disease; parasitic disease; tuberculosis; II-2 therapy; rheumatory distress syndrome; osteoarthritis; gouty arthritis; respiratory distress syndrome; cerebral malaria; chronic pulmonary inflammatory disease; silicosis; pulmonary sarcoidosis; bone resorption disease; reperfusion injury; graft versus host reaction; allograft rejection; Crohn's disease; ulcerative colitis, pyresis; multiple sclerosis; autoimmune diabetes;
      systemic
erythematosus; leprosy; AIDS; ds.
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Homo sapiens

WO9904033-A1 1..444 /*tag= Location/Qualifiers /product= "UBC4" עם

28-JAN-1999

16-JUL-1998; 98WO-US14638

16-JUL-1997; 97US-0895601

(MITO-) MITOTIX INC.

Beer-Romero P, Glass SJ, Rolfe Z, Strack PR;

Identifying modulators of I-kappa-B proteolysis - used to develop products for treating e.g. proliferative and/or differentiative disorders, infections, tissue wasting, cachexia or AIDS

Page 64-65; 79pp; English.

CC ligase and ubiquitin, to promote ubiquitination of the Ikappas CC polypeptide by the HECT ligase; (b) contacting the ubiquitin-conjugating CC system with a candidate agent; (c) measuring a level of ubiquitination of CC the polypeptide in the presence of the candidate agent and (d) comparing CC the measured level of ubiquitination in the presence of the candidate agent with ubiquitination of the IkappaB polypeptide in the absence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide in the presence of the CC modulate agent is indicative of an inhibitor of ubiquitination of the CC modulate binding and/or ubiquitinylation of an IkappaB (or other cellular CC or viral substrate) by a HECT ligase, such as RSC or KIAAN. Such CC modulators can be used e.g. in the treatment of proliferative and/or CC differentiative disorders, to modulate apoptosis, in the treatment of CC viral infections, and in the treatment of tissue wasting disorders e.g. CC cachexia secondary to infection or malignancy, cachexia secondary to infection or malignancy, cachexia secondary to the conditate and other arthritis, rheumatoid spondylitis, CC ostoratoritis, gouty arthritis and other arthritic conditions, sepsis, CC respiratory discress syndrome, cerebral malaria. Chronic milmonary respiratory distress syndrome, cerebral malaria, chronic pulmonary inflammatory disease, silicosis, pulmonary sarcoidosis, bone resorption diseases, reperfusion injury, graft versus host reaction, allograft rejections, Crohn's disease, ulcerative colitis, or pyresis, in addition to a number of autoimmune diseases such as multiple sclerosis, autoimmune diseases such as multiple sclerosis, autoimmune diseases, systemic lupus erythematosus; and ENL in leprosy, HIV, and This invention describes a novel assay identifying an inhibitor of ubiquitin-mediated proteolysis of a IkappaB polypeptide. The method comprises: (a) providing a ubiquitin-conjugating system including the IkappaB polypeptide and a HECT (Homologous to B6-Ap Carboxyl Terminus ligase and ubiquitin, to promote ubiquitination of the IkappaB This sequence encodes a human UBC4 protein which is used Terminus) ij autoimmune

to mark cells (particularly virus-infected) for death and to screen for agents (antagonists and agonists) that interact with them. The UCE products are also used to regulate lymphocyte trafficking or activity of the growth receptor, to treat many viral infections (by overcoming virus-induced suppression of apoptosis), for treating immune suppression (particularly acquired immune deficiency syndrome), to treat cytotoxic effects of platelets and their production of oxygenated metabolites. The

The present sequence encodes a human ubiquitin conjugating enzyme 7 (UCE7). The UCE products are used to treat malignant transformation (where associated with c-Mos and v-Jun proto-oncoproteins, since these undergo ubiquitin-dependent degradation) or immunological disorders (e.g. hypersensitivity to wasp/bee stings or aspirin-sensitive asthma),

(e.g. hy

Example 1;

Fig 1A-B; 34pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Ubiquitin conjugating enzyme; UCE; UCE7; malignant transformation; c-Mos; v-Jun proto-oncoprotein; ubiquitin-dependent degradation; immunological disorder; hypersensitivity; aspirin-sensitive asthma; lymphocyte trafficking; growth receptor; viral infection; acquired immune deficiency syndrome; skeletal muscle atrophy;
                                                                                                                                                      Human ubiquitin conjugating enzymes and related nucleic suseful for treating or diagnosing e.g. cancers, skeletal atrophy, immunonological diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                          acquired immune of cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 444 BP; 132 A; 99 C; 91 G; 122 T; 0 other;
                                                                                                                                                                                                            WPI; 1999-069655/06
                                                                                                                                                                                                                                                                         05-JUN-1995;
                                                                                                                                                                                                                                                                                            05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 cell death; ds.
                                                                                                                                                                                                                                Adams MD,
                                                                                                                                                                                                                                                                                                                  15-DEC-1998.
                                                                                                                                                                                                                                                                                                                                     US5849286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ubiquitin conjugating enzyme (UCE) 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV82865;
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                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                     HUMAN
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                                                                                                                                                                                                                               Gentz R,
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                                                                                                                                                                                                                                                     GENOME
                                                                                                                                                                                                                                                                         95US-0464604.
                                                                                                                                                                                                                                                                                             95US-0464604
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          /product= UCE7
                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                         endemic pemphigus foliaceus; African swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.6%;
60.2%;
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Pred. No. 1
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                                                                                                                                                                 muscle
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RESULT 14
AAA61613/c
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Best Local
                                                                                                                                                                                 04-JAN-1994;
23-MAY-1994;
27-MAY-1994;
13-SEP-1994;
                                     Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory protein for treating cancers involves measuring ubiquitination levels of the protein in the presence of candi
     Claim 1; Column 67-70; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              hUbCE; ubiquitin conjugating enzyme; ubiquitin mediated proteolysis; human; cellular protein half life; ubiquitination inhibitor; p53; cyclin; cell cycle regulator; myc deregulation; human papillomavirus; HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia; epidermal neoplasia; psoriasis; connective tissue disorder; wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic;
                                                                                                        WPI; 2000-410854/35.
                                                                                                                               Chiu MI,
                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                          17-DEC-1996;
                                                                                                                                                                                                                                                                                    30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UCE protein is used to raise antibodies, useful in diagnostic immunoassays and as a therapeutic inhibitor. Antagonists of the UCE protein are used to treat atrophy of skeletal muscle, cervical cancer (and some other tumours), endemic pemphigus foliaceus and African swine fever, or generally any condition in which UCE catalyses transfer of ubiquitin to a substrate, marking it for cell death.
                                                                                                                                                                                                                                                                                                           US6068982-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA61613 standard; cDNA; 444
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2000
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                                 eukaryotic cell
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                                                                                                                                                        MITOTIX INC.
                                                                                             AAB03169.
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                                                                                                                               Cottarel G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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94US-0176937.
94US-0247904.
94US-0250795.
94US-0305520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human ubiquitin-conjugating enzyme hUbCE
                                                                                                                                                                                                                                                          96US-0767942
                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /product= "hUbCE"
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60.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 444;
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                                       candidate agent
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RESULT 15
AAT41769/c
ID AAT417
XX AAT417
XX Human
XX Ubiqui
KW Ucrp;
XX CCRP;
XX Homo s
XX Homo 
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CC The ubiquitin-mediated protoclysis system is the major pathway for the selective, controlled degradation of intracellular proteins in cell cycle progression. Alterations in the ubiquitination of cc involved in cell cycle progression. Alterations in the ubiquitination of these proteins may therefore play a role in the development of cancers. For example, human papillomaviruses such as HPV-18 encode a transforming protein, Bc (AAB03177) to stimulate the ubiquitination of protein (Bc-AP, AAB03177) to stimulate the ubiquitination of post the method of the invention are useful for treatment of protein, Bc (AAB03176), which combines with a cellular Bc-associated corructal cancers and connective tissue disorders and for controlling the epidermal conditions such as spooriasis, neoplastic epidermal conditions, such as spooriasis, neoplastic proterm of hyperplasic epidermal conditions such as spooriasis, neoplastic epidermal conditions, such as spooriasis, neoplastic epidermal conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ubiquitin-conjugating enzyme UBC4 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquitin-conjugating enzyme; UBC4; cell cycle regulatory CCRP; inhibitor; apoptosis; cell differentiation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT41769;
                                                                                                                            20-APR-1995;
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                                                                                                                                                                                                                                                                                                                         WO9633286-A1
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                                                            (HARD ) HARVARD COLLEGE
                                                                                                                                                                                         19-APR-1996;
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                                                                                                                            95US-0425299
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No. 1.
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King RW,

Kirschner MW,

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                                                                                                                                                                                                                                                                               Query Match 17.6%; Score 30.2; DB 17; Length 452; Best Local Similarity 60.2%; Pred. No. 1.3; Matches 50; Conservative 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA sequence (AAT41769) comprises the coding region for human ubiquitin-conjugating enzyme UBC4 (AAW0352). It was obtd. from an HeIa cDNA library by PCR amplification (see also AAT41765-68). The cDNA was incorporated into a baculovirus vector and used to produce recombinant UBC4 in Spodoptera frugiperda 5:59 cells, and into a pGEX vector to allow UBC4 prodn. in E. coll. UBC4 can be used in a novel ubiquitin-conjugating system to identify inhibitors ubiquitin-mediated proteolysis of cell cycle regulatory proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting inhibitors of ubiquitin-mediated proteolysis of CCRPs - used in the treatment of proliferative and/or differentiation diseases, and in modulation of apoptosis
                                                                                                                                                                                                                                                                                                                                                                         Sequence 452 BP; 134 A; 101 C; 92 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 52; 63pp; English.
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P-PSDB; AAW00363.
                                                                                               345 ATCACACACAGAGAACAGATGG 323
                                                                                                                                                                                    405 Trictictarctgttttggtagatccgagcaarctcaggcactaaaggatcarctggariggg 346
                                                                                                                                           63 ATCGCAGCTCAGAGGACACCGGG 85
                                                                                                                                                                                                                              3 TTCTCAATACCGGGAAGCACACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAG 62
                                                                                                                                                                                                                                                                                   0; Gaps
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                   Score
     172
160
152
152
151
136
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172
1 ggttctcaataccg
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Match
     100.0
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87.8
79.1
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggttctcaataccgggagag.....taaacaaatacataaagcag 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2:*
gb_htc:*
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em_estfun:*
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  9 AA248485
12 BF790243
14 N86813
14 W07478
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AA248485 csh0287.8
BF790243 602249777
N86813 L1050F Huma
W07478 za96c10 r1
AI355905 3555-10R-
BF790636 602250354
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214 225 225 225 480 501	510 510 510 416 303	55 55 55 55 55 55 55 55 55 55 55 55 55	517 159 906 450 319 459 491	756 793 719 871 263 263 394
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BF672902 BF672902 AAA092554 AAA9531 N56276 AA214155 AA211521 AA033164	AI035961 AW918749 BQ554133 AK005857 AA800829 BB565182 AI153970	W97451 W97451 W29186 W13738 AN434782 AK003105 BF395391 AK0010172	BG224245 AA248067 BF672126 AA214147 N87511 AA800221 BF284896 AA763276	BF791178 BF671987 BM697544 BF693124 AA247872 N55839 N55839 AA389647 BF575112 BF395174
BF672902 602152759 BF672902 602152759 AA092554 115591.8e AA249531 JJ5502.8e A56276 JJ5502.8e N56276 JJ55022F Hum AA214155 zn58f10.r AA211521 zn55b01.r AA033164 mi37c11.r	A1035961 ub50b12.r AW918749 EST350053 BQ554133 H4026C08- AK009857 Mus muscu AA800829 EST190326 BB565182 BB565182 A1153970 ud49h02.r	W97451 m697c02.r1 W97451 m697c02.r1 W29186 mc22f02.r1 W13738 mb32a12.r1 AA434782 vc23c01.r AK003105 Mus muscu BF395391 UI-R-CM0- AK010172 Mus muscu	BG224245 IM0028F05 AA248067 cp1451.8e BF672126 602152580 AA214147 zn58F02.r N87511 LL1191F Hum AA800221 EST189718 BF284896 EST49484	BF791178 602251278 BF671987 602152408 BM697544 UI-E-DX0-BF693124 602080151 AA247872 3)3204 F Humma AA389647 M104 Feta BF575112 602134792 BF395174 UI-R-CM0-

ALIGNMENTS

FEATURES source		TITLE JOURNAL COMMENT	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AA248485 LOCUS DEFINITION
EMBALI: Cllew@rics.bwh.harvard.edu PCR PRimers PCR PRimers PCRWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3' BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3' Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'. Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'. 1280	Brigham and Women's Hospital Harvard Medical School 75 Francis St. Boston, MA 02115, USA Tel: 6177328915 Fax: 6179750995	LIEW, C.C. CDNAs from human fetal heart (1997) Unpublished (1997) Contact: Liew CC	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 280)	ด∌	AA248485 280 bp mRNA linear EST 11-MAR-1997 CBD0287.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens

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Query Match
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 909)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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BF790243.1
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602249777F1 NIH_MGC_81 Homo
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCCGGCCGACATG-dT(30) BN-3' (where B = A, C, Or G and N = A, C, O, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length
                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone=InhAGE:4328154"
/clone lib="NHH MGC 81"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db xref="taxon:9606"
/clone lib="Human fetal heart,
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .909
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Primates;
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                            CCGGGCGCCCCTTCCAACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACT 140
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Harvard Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liew, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 Francis St. Boston, MA 02115,
Tel: 6177328915
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                                                                                                                                                             Similarity
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                                                                                                                                                                                                                              /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor.primer. BcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

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Alto, CA)."
a 200 c 212 g 218 t
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/db_xref="taxon:9606"
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100.0%;
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No. 2.7e-41;
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TCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
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za96c10.r1 Soares fetal lung NbHL19W Homo
IMAGE:300402 5', mRNA sequence.
W07478
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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83 C 77 g 67 t 1 others
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin_resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI355905
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                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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142 CCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TCCCTTAGGCAGTAAACAAATACATAAAGCAG 153
                                               61
                                                                                       82
                                                                                                                                                                                    22
                                                                                                                                                               CACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACAC 81
                                                                         CGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACTT 141
                                          CGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACTT
                                                                                                                                  CACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACAC 60
                                                                                                                                                                                                                                 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single path sequence (manual checked and edited) with a vector primer of clone xh8H11. Sequence starts with base I following the determined vector sequence (ACCGGTGgCGTCgCGTC, small letters: NotI-site). ESTS 3055-L0R-8H11-2, 3055-10U-8H11-2 (with vector primers) and 8H11-R1-C8-OZ, 8H11-U1-C7-OZ (with gene specific primers) provide a contig of the whole insert of clone xh8H11. Insert Length: 850 Std Error: 10.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Molecular Human Genetics
Institut for Human Genetics
Fleischmannstr. 42/44, D-17487 Greifswald, Germany
Tel: +49 3834 8653-78(-74)
Fax: +49 3834 8653-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 8 row: H column: 11
Seq primer: 3055-10R (like M13 reverse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: 8H11-R1-C8-OZ, 8H11-F1-C7-OZ, 3(Contact: Patzak D., submitter; (Wehnert M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)
Zhuchenko,O., Patzak,D. and Wehnert,M.
ESTs of clone xh8H11 (human heart)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3055-10R-8H11-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: patzak@rz.uni-greifswald.de ( mwehnert@rz.uni-greifswald.de
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                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 360.
Location/Qualifiers
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="E. coli"
/lab_host="E. coli"
/lab_host="E. coli"
/note="Organ: heart; Vector: Lambda ZAP II, pKSII-;
/note="Organ: heart; Vector: Lambda ZAP II, pKSII-;
Site_1: NotI; Site 2: NotI; Human heart cDNA library was
constructed in Lambda ZAP II vectors using NotI linkers.
Clones from the primary cDNA library were deposited into
96-well trays for storage and retrieval. The 'Isolation of
chromosome-specific genes by reciprocal probing of arraed
cDNA and cosmid libraries (Human Molecular Genetics, 1995
, Vol. 4, No 8; pp1373-1380) provided cDNA-Clones as
plasmids (vector pKSII-, E. coli)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="xh8H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="heart muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Human heart cDNA (CCLee) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                                                                                                                                                                               0
                                                                                                                                                                                                                            Score 151; DB 9;
Pred. No. 2e-38;
0; Mismatches
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RESULT 6
BF790636
                            BF791178
LOCUS
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ORIGIN
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          DEFINITION
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Best Local S
Matches 169
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TITLE
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                                                                                                                                                                                                                                           AGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTT 120
                                                                                                                                                                                                                                                                                                    GTTCTCAATACCGGGAGAGCCACAGAGCTATTTCATGCCACATGAAAAGCATCGGAA-TG 112
                                                                                                                                                                                                                                                                                                                                 GTTCTCAATACCGGGAGAGGCACAGAGCTATTTCA-GCCACATGAAAAGCATCGGAATTG 60
                                                                                                                                                                                                                      AGATCGCAGCTCAGAGGACACCGGGCGCCCTTCCACCTTCCAAGGAGC-TTGTATTCTT
                            BF791178
                                                                                                                                   GCATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAAATACATAAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                       169;
*BF791178 756 bp r
602251278F1 NIH_MGC_81 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLCM1212 row: 1 column: 14
High quality sequence stop: 514.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M. http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ggapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, I
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria;
1 (bases 1 to 867)
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BF790636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                   79.1%; llarity 98.3%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30) EN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4337821"
/clone=lib="NHIMGC 84"
/clone_lib="NIH MGC 84"
/lab host="DHIOB (TI phage-resistant)"
/lab host="DHIOB (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: Sfil (ggccgcctcggcc); Site 2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used in cloning
(ggccattatggcc); 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism≃"Homo sapiens"
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                   Score 136; DB 12;
Pred. No. 1.7e-33;
D; Mismatches 0;
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    mRNA line
s cDNA clone
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                            linear
        IMAGE:4338594 5'
                                                                                                                                   223
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                          EST 12-JAN-2001
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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Best Local Similarity
                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACATAAAGCAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACATAAAGCAG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133;
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BF791178
BF791178.1 GI
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Tissue Procurement: CLONETECH Laboratories, Inc.

Tissue Procurement: CLONETECH Laboratories, Inc.

Therefore Preparation: CLONETECH Laboratories, Inc.

Therefore Preparation: CLONETECH Laboratories, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1214 row: 1 column: 19
High quality sequence stop: 619.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               BF671987.1
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                                                                                                                                                                                         mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
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/clone=lib="NMIH MGC 81"
/lab_nost="DH10B (TT phage-resistant)"
/lab_nost="DH10B (TT phage-resistant)
/lab_nost="DH1
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|db_xref="taxon:9606"
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Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                     1 (bases 1 to 719)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                    DM697544 719 bp mRNA linear | UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA UI-E-DXO-agn-i-12-0-UI 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov
                                                                                        discovery
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BM697544.1 GI:19010802
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/clone_lib="NIH_MGC_81"
/lab_host="DH10B (Ti phage-resistant)"
/not="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggcggcctgggc); Site_2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T), Average insert size
1.55 kb (range 1.0-4.0 kb): 15/15 colonies contained
inserts by PCN. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
                                                             Res. 6 (9), 791-806 (1996)
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Pred. No. 1.6e-32;
0; Mismatches 0;
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Best Local 9
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                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 871)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                        mRNA sequence.
BF693124
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602080151F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4244364 5'
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Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                             BF693124.1
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Tel: 319 335 8250
Fax: 319 335 9565
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/clone_lib="UI-E-DX0"
/tissue_type="fetal eyes"
/dev_stage="fetal"
/lab_bost="DH10B (Life Technologies) (T1 phage resistant)"
/lab_bost="DH10B (Life Technologies) (T2 phage resistant)"
/lab_bost="DH10B (Life Technologies) (T2 phage resistant)"
/lab_bost="DH10B (Life Technologies) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
/not="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
/UI-E-DX0 is a cDNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library as AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
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/db_xref="taxon:9606"
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Pred. No. 1.4e-30;
0; Mismatches 0;
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High quality sequence stop: 575.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
                        PCR PRimers
                                                                         Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
                                                                                                                                                              CDNAs from human fetal heart 
Unpublished (1997)
                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 263)
                                                                                                                                                                                                                                                                                                                                                                j3204.seq.F Human fetal heart,
5', mRNA semieron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                      Email: cliew@rics.bwh.harvard.edu
                                                           Fax: 6179750995
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                           AA247872.1 GI:1880264
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                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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|db_xref="taxon:9606"
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Pred. No. 4.3e-28;
0; Mismatches 1
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meart, Lambda ZAP Express
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGGACTTTCCCT 120
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Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                            Email: cliew@rics.bwh.harvard.edu
Seq primer: TCCAAAGAATTCGGCACGAG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                            Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                             75 Francis St. Boston, MA 02115,
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                    Harvard Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                          Brigham and Women's Hospital
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/lab host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

58 g 58 t
                 /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

58 g 58 t
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/db_xref="taxon:9606"
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/clone="J3204"
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Best Local Similarity
Matches 109; Conserv
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MEDLINE
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Best Local
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                                            TCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 109
                                                                       TCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biochemistry
The Chinese University of Hong Kong
Shatin, New Territories, Hong Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 394)

Hwang, D.M., Fung, Y.W., Wang, R.X., Laurenssen, C.M., Ng, S.H., Lam, W.Y., Tsui, K.W., Fung, K.P., Waye, M., Lee, C.Y. and Liew, C.C.

Analysis of expressed sequence tags from a fetal human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ldskok@spider.net.hk
Seq primer: Forward Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 30 (2), 293-298 (1995)
96163883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kok LDS
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                                                                                                                                                                                                                                                                          /note="Vector: Lambda ZAP; Site 1: EcoRI; Site 2: XhoI; The library is a gift from Prof. C.C. Liew, University of Toronto, Ontario, Canada. mRNA was purified from human fetal hearts (8-10 wks). cDNA was synthesized using a XhoI-Oligo dT adaptor primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lb="Fetal heart, Lambda ZAP Express"
/lab_host="E. col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                       63.4%; Dr/
100.0%; Pr/
0;
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                                                                                                                                                                                                            Score 109; DB 9;
Pred. No. 9.3e-25;
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Pred. No. 3.8e-26;
0; Mismatches 3
                                                                                                                                                                                               Mismatches
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Express Homo
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                                                                                                                                                                                                                              Length 394,
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                                                                                                                                                                                                                                                                    TCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGGGACTTCCCCTTAGGCAGTAAACAA 159
                                                                                                                                                                                                                                                                                                                                            ACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAGGACACCGGGCGCCCCTTCCACCT
                                          BR395174 542 bp mRNA UI-R-CM0-bjj-g-03-0-UI.81 UI-R-CM0 Rattus UI-R-CM0-bjj-g-03-0-UI 3', mRNA sequence.
             BF395174.1 GI:11380139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: CLONSTECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLCM1131 row: h column: High quality sequence stop: 595.
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:4289735"
/clone_lib="NIH MGC_8189"
/clone_lib="NIH MGC_8189"
/lab_host="PH108 (T] phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: SfiI (ggcggctcgggc); Site 2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
c', or G and N = A, C, G, or T). Average insert size
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 a
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Pred. No. 1e-24;
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                                                  linear EST 27-NOV-.
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Search completed: April 15, 2003, 22:02:30 Job time : 359.738 secs
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.9%; Score 106.4; DB 12; Best Local Similarity 80.1%; Pred. No. 6.8e-24; Matches 125; Conservative 0; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                     GACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                                                                                                      GACTGTCCTCAGGCAGTAAACAAATCCAGAGAGCAG
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The sequence contained an oligo-dT track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized heart library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 1-24, AT_rich#Low_complexity
Seq primer: M13 Forward
polyNa-yes.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction, two approaches to facilitate gene
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451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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Program for Rat Gene Discovery and Mapping
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/dev stage="ADDIT"
/lab host="DH10B (Life Technologies)"
/lab host="DH10B (Life Technolog
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/strain="Sprague-Dawley"
/db_xref="traxon:10116"
/clone="UJ-R-CMO-bjj-g-03-0-UI"
/clone_lib="UJ-R-CMO"
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Maximum Match 100%
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1: gb_ba:*
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Gapop 10.0 , Gapext 1.0
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(without alignments)
12845.099,Million cell updates/sec
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is the number of results predicted by chance to have a

KEYWORDS SOURCE ORGANISM

 $\mbox{Srmx gene}_i$ stretch responsive muscle (X-chromosome). human.

REFERENCE AUTHORS

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 885) Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Eastwood, M., Sassoon, D.A. and Coulton, G.R.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ACCESSION VERSION	RESULT 1 HSA250584 LOCUS DEFINITION			C 443		. 4.		c 38		·	C 34	• 2 2 3	υ 1 (1	30	2 0	27	N	C 25	223	22	0 20	, <u>,</u>	c 18	16		C 14	c 12	, ب	- -	> ω	7	4	Ω	ωι	у ப	Result No.	
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•)r stretch responsive	ALIGNMENTS	AC115802	AC087341	AC012469	BC0033	AC114732	AC073257	ACU98375 HS833B7	AC104671	AC113090	AC101909	AF	228	AC116286	AC108928	AC068959	AC026726	AC020963	AC027362	AC068953			AB080118	AC079954	AC110999	AP002022	1811	MMU245772		BC005948	AL772370	509	2950	HSA250584	ID	
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Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial College of Science Technology and Medicine, SAF Bldg, Level 2, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Related sequences: AJ245772, U73508 to U73509.
                                                                                         Bunk, D., Reuner, B., Beck, J. and Henkel, T. Novel target genes for diseases of the he Patent: WO 0192567-A 18 06-DEC-2001;
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/product="stretch
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Human Genetics, Fleischmannstr. 42/44, I
Location/Qualifiers
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MAPPING INFORMATION
                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                   restriction digest.
                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
                                                                                                                                                                                                                                                                          St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-JUL-1998)
University, 4444 Forest
5 (bases 1 to 47440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 47440)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence.
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens 
Unpublished (1999)
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cosmid clone U228D4 from Xp22.1-22.2, complete
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                                                                                                                                                                                                                                                                                                                                                                                                    Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomic 44:227-231 (1997). Genomics

FEATURES

GM07297-F, from Robert Nussbaum at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livermore Nation Laboratory at http://www-bio.llnl.gov/genome to obtain the clone. This clone The source of the chromosomes was a r Lawrist16 from Robert Nussbaum at the University of Pennsylvania Medicine. Please contact the Lawrence Livermore National was a human/hamster hybrid COSMID LIBRARY LLOXNCCO1

misc_feature repeat_region misc_feature repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature misc_feature misc_feature repeat_region repeat_region repeat_region source repeat_region /mote="match to EST AA092554 (NID:g1637327)"
/complement(5169. 5222)
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/note="match to EST AA24885 (NID:g1879506)"
complement (15622. .15689)
/note="match to EST W07478 (NID:g1281479) za complement (5133 . .5222)
/note="match to EST W07478 (NID:g1281479) za96c10.rl"
/complement (5148 . .5222) /rpt_family="MER1_type" 12770. .12961 complement(5131. .5222)
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misc_feature misc_feature misc_feature

complement (19314.

fami

ly="Retroviral"

family="Alu"

note="match to EST AA092554 (NID:g1637327)

misc_feature misc_feature

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.19497)

family="MIR"

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/note="match to EST AA248067 (NID:g1878536)"

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/note="match to EST AB2511 (NID:g1440713)"

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25920. .26860
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26867. .27210

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Homo sapiens chromosome X clone RP11-184B10, ***
PROGRESS ***, 2 unordered pieces.
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Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator ET-amersham; 0% of reads Consensus
quality: 149793 bases at least Q40
Consensus quality: 149914 bases at least Q20
Consensus quality: 150006 bases at least Q20
Insert size: 150219; sum-of-contigs
Insert size: 150219; sum-of-contigs
Quality coverage: 17.18x in Q20 bases; sum-of-contigs
Quality coverage: 17.58x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
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Web site: http:/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                         Similarity
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4860 4959: gap of 100 bp
4960 150319: contig of 145360 bp in length
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="X"
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Best Local Sim
Matches 125;
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                                          137 GACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG
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                                                                                         GACACCGGGGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGCCTGG
                                                                                                                                AGAGCACTCCAGCTATTCCAGCCACATGAAAAGCACTGGAATTGAGATCTCAGCTCAGAG
                                                                                                                                                         AGAGGCACAGAGCTATTTCAGCCACATGAAAAGCATCGGAATTGAGATCGCAGCTCAGAG 76
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                                                                         GACACCGGGAGTTCCTTCTACCCTGTAAAGCGTTTTCTGTTTTTTGCACCTGGCTGCCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patzak, D., Zhuchenko, O., Lee, C.C. an Identification, mapping, and genomic x-chromosomal human gene (SMEX) encc Hum. Genet. 105 (5), 506-512 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-MAR-2001) E.M.-Arndt-Uni, Inst. f. Humang., Fleischmannstr. 42-44, D.17487 Greifswald, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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892 bp mRNA
Rattus norvegicus SMPX protein (Smpx) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                             /gene="Smpx"
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862. .867
                                                                                                                                                                                                                                                                                                                                                                                /gene="Smpx"
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<1. .892</pre>
                                                                                                                                                                                                                                                                 /evidence=experimental
183 c 193 g
                                                                                                                                                                                                                                                                                               /gene="Smpx"
/note="alternate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Smpx"
190. .447
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                                                                                                                                                                                                         61.9%;
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                                                                                                                                                                                            0;
                                                                                                                                                                                         Score 106.4; DB 10;
Pred. No. 4.6e-27;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, C.C. and Wehnert, M.
and genomic structure of a novel
(SMPX) encoding a small muscular protein
                                                                                                                                                                                                                                                                    245
                  171
                                               172
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BC005948
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Best Local (
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TITLE
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                                         133
      61
                                                                                                                                                                              Local Similarity
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                                                                                               AGAGGACACCGGGCGCCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGC 132
                             CTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                          AGAGGACACCGGGCGCCCTTCCACCTTCCAAGGAGCTTTGTATTCTTGCATCTGGCTGC
                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6625 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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IMAGE:4246501,
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                                                                                                                                                                                                                                                             282
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                   /trānslation="MNMSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEE
GVPPTSDEEKKPIPGAKKLPGPAVNLSEIQNIKSELKYVPKAEQ"
1 155 c 171 g 227 t
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                                                                                                                                                                                                                                                                                                                                                                                                    113. .379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pDNR-LIB"
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mRNA, complete cds.
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                                                                                                                                                           <u>.</u>
                                                                                                                                                     Score 100; DB 9;
Pred. No. 9.2e-25;
0; Mismatches 0;
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X-linked, clone MGC:14584
100
                                                                                                                                                                                                                                                                                                                                                           X-linked"
                                                                                                                                                                                             Length 835
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                CTGGAGAGAGAGAGCACTCCAGCTATTTCAGCCACATGAAAAGCACTGGAATTGAGAT 77
                                                                                                                                                                                                      ACCTGGCCGCCTGGGACTGTCCTCAGGCAGTAAACCAATCCAGAGAGCAG
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Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang, (Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentg Mohun,T. and Harvey,R.P.
The small muscle-specific protein Csl modifies cell shape and promotes myocyte fusion in an insulin-like growth factor
 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY026524 787 Mus musculus muscle-specific AY026524
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Submitted (01-FEB-2001) Developmental Biology, Victor Chang Cardiac Submitted (1997) Submitted (1997) New Personnel Institute, 384 Victoria St, Darlinghurst, Sydney, New
                                                       Mus musculus SMPX protein
AF364070
AF364070.1 GI:13940507
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South Wales 2010, Australia
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Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,C.-C., Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentgen,F., Mohun,T. and Harvey,R.P.
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Mus musculus.
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167 c 185 g 202 t
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/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ortholog of Homo sapiens SMPX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="Csl"
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Pred. No. 4.9e-23;
D; Mismatches 38;
                                                                                                                  936
                                                                                           936 bp mRNA linear (Smpx) mRNA, complete cds
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protein CSL (Csl) mRD
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Sciurognathi; Muridae; Murinae; Mus.
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Koentgen, F.,
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REFERENCE
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AUTHORS
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MMU245772
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                                                                                                                                                                                                                                                                                                                                                                                                        ATCTGGCTGCCTGGGACTTCCCTTAGGCAGTAAACAAATACATAAAGCAG 172
                                                                                                                                                                                                                                                                                                                                                                               ACCTGGCCGCCTGGGACTGTCCTCAGGCAGTAAACCAATCCAGAGAGCAG
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2 (bases
Kemp, T.J.
                                                 Genomics
21295047
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Fleischmannstr. 42-44, D-17487 Greifswald, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                          Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Sassoon, D.A. and Coulton, G.R.
                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 943)
                                                                                                                                                                                      Mus musculus
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/db_xref="taxon:10090"
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187 c 203 g
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Pred. No. 5.1e-23
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responsive
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muscle (X
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Matches 130; Conserv
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                                                                                                                                                                                                    CTGGAGAGAGACACTCCAGCTATTTCAGCCACATGAAAAGCACTGGAATTGAGAT 86
                                                                                                                                            CCCCGCTCAGAGGACACCGGGAGTTCCTTCTATCCTGTAAAGCGCTTTTTGTGTTTTTTGC
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Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, SAF Building, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM
AL731811 239667 bp DNA Mus musculus chromosome X clone RP23-60A1,
                                                                                                                                                                                                                                                                                                                                      278
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/function="mRNA (
658. .662
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192 c
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943
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923. .928
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535. .539
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215. .472
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740. .744
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/db_xref="taxon:10090"
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function="mRNA
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(product="stretch responsive muscle (X-chromosome)"
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L. .943
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76.5%;
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ear HTG 12-AUG-2002
SEQUENCING IN
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AUTHORS
TITLE
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VERSION
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Assembly program: XGAP9; version 4.5
Chemistry: Dye-terminator; 96% of reads
Chemistry: Dye-terminator; 96% of reads
Chemistry: Dye-terminator Big Post 3% of reads
Consensus quality: 235503 bases at least Q40
Consensus quality: 236735 bases at least Q30
Consensus quality: 237530 bases at least Q20
Insert size: 24867; sum-of-contigs
Insert size: 24867; sum-of-contigs
Quality coverage: 7.58x in Q20 bases; sum-of-contigs Quality
coverage: 10.48x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 13, 2002 this sequence version replaced gi:21912698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 239667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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HTG; HTGS_PHASE1;
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AL731811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bM60A1
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                                                                                                                                                                                      231640 231739: gap of 100 bp 231740 236718: contig of 4979 br
                                                                                                                                                                                                                                                                           228885 228984: gap of
                                                                                                                                                                                                                                                                                                   221610 221709; gap of 100 bp 1221710 223856; contig of 2147 bp in length 223857 223956; gap of 100 bp 1223957 226508; contig of 2352 bp in length 226309 226408; gap of 100 bp 1226409 228849; contig of 2476 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99134 39133; contig of 39133 bp in length
39234 gap of 100 bp
39234 84228; contig of 44995 bp in length
84229 84328; gap of 100 bp
84329 106119; contig of 21791 bp in length
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/db_xref="taxon:10090"
/chromosome="X"
                                                 organism="Mus musculus"
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                                                                                                            ocation,
                                                                                     .239667
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218182: contig of 87650 bp in length
                                                                                                                                    239667: contig of 2848
                                                                                                                                                                                                                                                      231639:
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221609: contig of 3327 bp in length
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Best Local Similarity
                                             JOURNAL
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Direct
                Tsai,
                                                         Genome Sequencing of the Hepatocellular Carcinoma
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                 AP002022
                                         Unpublished
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                                                                                                                                                                 Homo sapiens DNA, clone:2198J12
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                            (bases 1 to 173933)
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Submission
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226409: .228884
/note="assembly_fragment:08648"
228985: .231639
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130533. ..218182
/note="assembly_fragment:09523
fragment_chain:1"
218283. ..221609
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231740. .236718
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119370. .130432
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fragment_chain:1"
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ragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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1. .39133
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ragment_chain:1"
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76.5%;
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Pred. No. 1.8e-22
                                                                                                                                                                                                                                                            173933 bp
                                                      Chromosome 4q Region Implicated Pathogenesis 1
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                                                                                                                                                                                                                                              NA linear PRI 01-JU
4q22-q24, clone:2198J12,
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Matches 58
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Sequencing vector: M13; 40%
Sequencing vector: plasmid; 60%
Sequencing vector: plasmid; 60%
Sequencing vector: plasmid; 60%
Chemistry: Dye-terminator Big Dye; 100% of read
Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 181880 bases at least Q40
Consensus quality: 184864 bases at least Q30
Consensus quality: 186595 bases at least Q20
Insert size: 187000; agarose-fp
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On Oct 28,
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (28-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 4 clone RP11-18319, WORKING DRAFT SEQUENCE, AC098674 AC013536
AC098674.1 GI:16506917
AC098674.1 GI:16506917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAY-2000) Shih-Feng Tsai, National Yang-Ming University, Institute of Genetics; 155 Li-Rong St. Section 2, Peitou, Taipei, Taiwan 11221, Republic of China (E-mail:ympetsai@ym.edu.tw, URL:http://genome.ym.edu.tw/, Tel:886-2-28267043, Fax:886-2-28264930) Tel:886-2-28267043, Fax:886-2-28264930) Ouality: the expected Phrag Calculated error rate (per 10kb) is 0.01; Estimated total number of errors is 0.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 188818)
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone
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/clone="2198J12"
34703 c 32692 g
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, 2001 this sequence version replaced gi:10047701
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59.8%;
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Quality coverage: 10.12 in Q20 bases; agarose-fp
Quality coverage: 10.23 in Q20 bases; sum-of-contigs
                                              59010
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                                                                   clone_end:SP6
                                                                                                   vector_side:left"
78155. .188818
                                                                                                                                  clone_end:T7
                                                                             /note="assembly_name:Contig59
                                                                                                                                                                  46014.
                                                                                                                                                                       /note="assembly_name:Contig57"
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25834. .45913
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1. .188818
                                                                                                                                        note="assembly_name:Contig58
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12457. .25733
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                                                                                                                                                                                                                                                                                              'note="assembly_name:Contig52"
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/db_xref="taxon:9606"
/chromosome="4"
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1631: gap of
2914: contig
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6: contig of 1047 bp in length
6: gap of unknown length
3: contig of 13277 bp in length
3: contig of 20080 bp in length
3: contig of 20080 bp in length
4: contig of 32041 bp in length
4: gap of unknown length
4: gap of unknown length
8: contig of 110664 bp in length
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unknown length
of 1283 bp in length
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                                      1104 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
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Score 34.6;

DB

<u>ب</u>

Length 188818;

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

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                                                                                             Submitted (16-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 29, 2002 this sequence version replaced gi:19571169.
                                                                                                                                                                                                           Direct Submission
Submitted (29-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (21-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                     Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                     Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                               MO 63108, USA
4 (bases 1 to 114594)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 114594)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-FEB-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                      MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114594 bp
Homo sapiens BAC clone RP13-588120
AC110999
AC110999.4 GI:19807878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H.
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Abbott, S. and Cotton, M.
The sequence of Homo sapiens
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                       (bases 1
             Center: Washington University Genome Sequencing Center Center code: WUCSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu
Center project name: H_FH0588120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-13 Human Female BAC Library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Baohui Zhao in our laboratory. Construction was funded by a grant from the National Human Genome Research Institute (NHGRI, NIH) (#1R01RG01165-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mapping information for this chone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-621120, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP13-588120;
actual end is at base position 43117 of RP11-621120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Data from AC108928 was used to finish this clone, AC110999. Location/Qualifiers
                                                      /rpt_family="CR1"
9235. .9405
                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich" 449. .. 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MIR" 353._.386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
                    /rpt_family="CR1"
9791. .9837
                                                                                                                                                                          /rpt_family="(TTG)n"
6295. .6599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP13-588I20"
/clone_lib="RPCI-13"
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                                                                                                                                                                                                                                                                                                                              note="similar to Homo sapiens EST AI147140 (NID:g3674822)
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rpt_family="L2"
                                                                                                           rpt_family="MIR"
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                                                                                                                                                                                                                                                                     _family="Alu"
                                                                                                                                                          .ly="Alu"
                            Query Match 19.5%; Score 33.6; Distribution Best Local Similarity 59.4%; Pred. No. 2.7; Matches 57; Conservative 0; Mismatches
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11090. .11117
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/note="similar to Mus musculus EST BB646518

(NID:g16480847)"
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27799. .27958
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33906. .34198
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(NID:g16488847)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match to EST AA354508 (NID:g2007063)
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;1525; .41747
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                                                                                                                                                                                                                                                                                                                                                                                                                   ly="AT_rich"
                                                                      DB 9;
                                    39,
                                                                      Length 114594;
                                    Indels
                                    0;
                                      Gaps
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of Molecular and Human Baylor Plaza, Houston, 5 (bases 1 to 158785) Direct Submission
Submitted (01-MAY-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Worley, K.C. Direct Submission Submitted (07-MAR-2002) Direct Submission) Human Genome Sequencing Genetics, Baylor College TX 77030, USA Center, Depar of Medicine, Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. Submitted (25-JUL-2002) Human Genome Sequencing Center, Depaid Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On May 1, 2001 this sequence version replaced gi:13877202. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email r of

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome
of a local database that includes entries
local mapping efforts. Res. 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (aspect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALSTAT-REPORT------

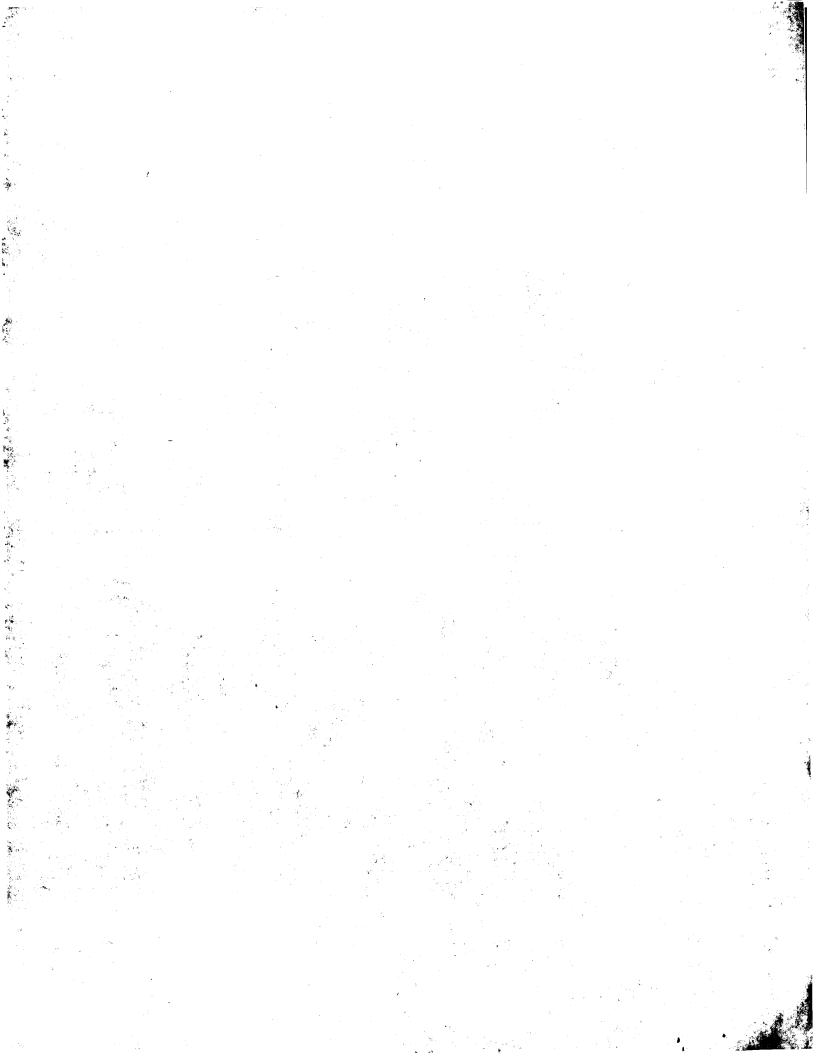
Position 10464 Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus: Contig length:
Phrap values in estimate: ttotonttnt (n) totototot ctccccttot (n) tootttotot cettetente (n) thetetete Original+Context Consensus Summary Statistics changing edite Edited+Context
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Search completed: April 15, 2003, 20:53:11 Job time : 618.696 secs

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57; Conservative
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AUTHORS
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                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 501)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., M., Hillider, L., Dibuyue, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore Schellenberg, M., Soares, M., Prange, C., Rifkin, L., Rohlfing, T., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                   EST 31-JAN-1997
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This Clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                 501 bp mRNA linear EST 31-.
ZISSB01.rl Stratagene muscle 937209 Homo sapiens cDNA clone
NAZ11591202.
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UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens CDNA clone
BM697644
                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
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Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 57; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:455347"
/db_xref="taxon:9606"
/clone="IMAGB:562057"
/clone_lib="Stratagene muscle 937209"
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.
                                                                                                                                                           Homo sapiens
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                                                                                                                                         human
RESULT 7
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BM697544
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-pac (Pharmacia) with a
modified polylinker; Site=1: EcoR I; Site=2: not I;
UI=DXO is a cDNA library containing the following
UI=BXO is a cDNA library containing the following
according to Bonaldo. Lennon and Soares, Genome Research,
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adiptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
lirst-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGAATCAAAA. This library
sequence tag for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                 B 97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
741: 319 315 9250
Fax: 319 315 9250
Fax: 319 315 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Son may beneated
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602251278F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338594 5',
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:9666"
| clone="UI-E-DX0-agn-i-12-0-UI"
| clone="UI-E-DX0"
| tissue type="fetal eyes"
| dev_stage="fetal"
| lab_host="PH10B (Life Technologies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 57; DB 14;
100.0%; Pred. No. 4.2e-10;
.ive 0; Mismatches 0;
                                                                                           Genome Res. 6 (9), 791-806 (1996)
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
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Sequence 1, Appl
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Sequence 12, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
                                                                  April 15, 2003, 18:42:01; Search time 3.37265 Seconds (without alignments) 5183.040 Million cell updates/sec
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Sequence 10,
Sequence 4, A
Sequence 4, A
Sequence 3, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                             US-09-647-019-7
57
1 ggataagactgcatgaatat......ccaatgttagagccatccag
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   GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*

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US-08-224-394A-22

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US-08-724-394A-22

US-08-724-394A-22

US-08-74-394A-23

US-08-724-394A-22

US-08-724-394A-22

US-08-724-394A-22

US-08-724-394A-22

US-08-724-394A-22

US-08-724-394A-22

US-08-724-394A-22

US-08-773-77-79-12

US-08-977-97-12

US-08-977-97-18

US-08-977-97-18

US-08-97-079-18

US-08-994-079-20

US-08-994-079-20
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US-08-094-948A-4
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US-08-121-057-3
US-08-509-187D-3
US-09-121-396-3
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Maximum Match 100%
Listing first 45 summaries
                                              - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 GGATAAGACTGCATGAAAATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Abund, Jie
APPLICANT: Abund, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. 6426186 021656.2CB1
US-09-484-970B-111
                US-08-121-057-5

US-08-121-057-5

US-09-121-396-2

US-09-121-396-2

US-09-221-0178-497

US-08-670-354-3

US-08-670-354-3

US-08-681-375-1

US-08-983-275-1

US-08-131-10

US-08-328-111-349

US-08-328-111-349

US-08-348-131-10

US-08-348-131-10

US-08-448-131-10

US-08-448-131-10

US-08-141-354-10

US-08-141-354-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10

US-08-141-31-10
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Sequence 111, Application US/09484970B
Sequence 111, Application US/09484970B
Sequence 111, Application US/09484970B
Sequence 111, Application US/09484970B
SEQUENCE INVENTION: BONE REMODELING GENES
TITLE OF INVENTION: BONE REMODELING GENES
TITLE OF INVENTION: BONE REMODELING GENES
CURRENT APPLICATION UNMBER: US/09/484,970B
CURRENT APPLICATION UNMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEQ ID NO 111
LENGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-668-680-13/C
; Sequence 13, Application US/09668680
; Patent No. 6436703
; GRNERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
    4011
4079
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4079
4079
1521
1521
1521
1521
427
427
427
678
986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 56; Conserv

    CONTRACTOR CONTRACTOR
    CONTRACTOR CONTRACTOR
    CONTRACTOR CONTRACTOR
    CONTRACTOR CONTRACTOR
    CONTRACTOR CONTRACTOR
    CONTRACTOR CONTRACTOR
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392 ATTITGTATCAGCCAGTTTCCCTTGTTAGGGCC 360
                  19 ATGTCGAAACAGCCAGTTTCCAATGTTAGAGCC
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                                                                                                                                                                                                                                                                                                                                                   Score 23.2; DB 4; Length 1539;
Pred. No. 3.5;
0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ENTERRISES, LTD., QBI
APPLICANT: ENTERRISES, LTD., QBI
APPLICANT: Deiss, Louis P.
APPLICANT: Yehiely, Fruma
APPLICANT: Vasquez-laslop, No. 6057111a C.
APPLICANT: Binat, Paz
TITLE OF INVENTION: GENE IDENTIFICATION METHOD
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6057111thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
38.2%; Score 21.8; DB 3; Length 519;
Best Local.Similarity 78.8%; Pred. No. 9.6;
Matches 26; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,782.7
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 13
LENGTH: 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09284782 Patent No. 6057111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, 1lene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
TELEBHONE: (248) 539-5050
TELEPAX: (248) 539-5050
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (130)..(1539)
US-09-668-680-13
                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-284-782-22/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-284-782-22
                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                  FEATURE
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                                                                                    APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Evenmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Hommal, Winston
APPLICANT: Thomas, Winston
APPLICANT: Truchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: CA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: ELDAPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILES, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION FOR SEQ 1D NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 65491 GATGAGACTTCAGGAATATGTTGACAAAGGCAG 65459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 21.8; E 78.8%; Pred. No. 42; tive 0; Mismatches
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US-08-724-394A-21/c
US-08-724-394A-21/c
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 246240 base pairs
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Best Local Similarity
Matches 26; Conserv
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Sequence 23, Application US/08468036

Patent No. 5728806

Fatent No. 5728806

GENERAL INFORMATION:

APPLICANT: DeMagdio, Anthony J.

APPLICANT: Hockstra, Merl F.

TITLE OF INVENTION: Interact with Casein Kinease I

NUMBER OF SEQUENCE: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 111inds

COUNTRY: United States of America

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATER: PLANCE STATES

COMPUTER: IBM PC COMPATER

COMPATER
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                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/724,394A

FLING DATE: 0.4-CT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitch Rene A

REGISTRATION NUMBER: 017957-000100

TELEPHONIN: 415-576-0300

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHRACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

TYPE: CDNA
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SOFTWARE: PECADICS/NB-DOS
SOFTWARE: PECADION DATA:
APPLICATION NUMBER: US/08/468,036
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 5728806and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
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Best Local Similarity 78.8'
Matches 26, Conservative
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                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Ruddy, David A.
APPLICANT: Touchihash, Zenta
APPLICANT: Touchihash, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
NUMBER OF SEQUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

38.2%; Score 21.8; DB 2; Length 246240;
Best Local Similarity 78.8%; Pred. No. 42;
Matches 26; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: UJ-07T-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Megabase Transcript Map: No. 58'
Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08724394A
| Sequence 22, Application US/08724394A
| Patent No. 5872237
| GENERAL INFORMATION:
| APPLICANT: Feder, John N. APPLICANT: Lauer, Peter M. APPLICANT: Thomal, Gregory S. APPLICANT: Thomas, Winston APPLICANT: Thouse, Winston APPLICANT: Touchihashi, Zenta APPLICANT: Wolff, Roger K. | TITLE OF INVENTION: Megabase Transcript Map: | TITLE OF INVENTION: Sequences and Antibodies T. NUMBER OF SEQUENCES: 31
| CORRESPONDENCE ADDRESS: ADDRESSE: TownSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLP
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LOCATION: 1.246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GATAAGACTGCATGAATATGTCGAAACAGCCAG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-724-394A-22/c
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Gaps

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Length 246240,

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3902 AAAAAACTICAICAATAAAGGGGATAIAGCCAITGIAAAATAITGIAICA 3951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Demagajo, Anthony J.
APPLICANT: Demagajo, Marl F.
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: Astronomy of the Conference of SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall. O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Thingois
CONTRY: United States of America
ZIP: 6606-6402
COMPUTES: IBN FOC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.2%; Score 21.2; DB Best Local Similarity 64.0%; Pred. No. 29; Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5846764and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31784
TELECOMMONICATION INFORMATION:
TELEFRONS: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-376-843-23

Sequence 23, Application US/08376843

Patent No. 5846764

GENERAL INFORMATION:
                TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                312/474-6300
312/474-0448
                                                                                                                                                                                                                                                         LENGTH: 5093 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-376-843-23
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-468-036-23
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                TELEFAX:
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DB 2; Length 246240;
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                                                           GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Frommal, Gregory S.
APPLICANT: Trommal, Gregory S.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger X.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 222283 raagreerraggaarargeeragaggeraarricarargri 222324
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING BATE: 01-OCT-1996
CLESSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                               TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.2%; Score 21.2; Di
Best Local Similarity 69.0%; Pred. No. 72;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US_08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            017957-000100
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; Sequence 20, Application US/08724394A
;, Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 5.2.
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-020
TELEPHONE: 415-576-020
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Feder, John N.
APPLICANT: Kromal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: not relevant MOLECULE TYPE: CDNA PEATITIPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 246240 base
TYPE: nucleic acid
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3 ATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCA 52

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APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Towchinash, Zenta
APPLICANT: Towchinash, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.0%; Pred. No. 72;
Matches 29; Conservative 0; Mismatches 13; Indels 0;
APPLICANT: Teuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 222283 TAAGTCCTTAGGAATATGCCTAGAGAGCTAATTTCATATGTT 222324
                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834

ZORPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.30

GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-724-394A-22

// Sequence 22, Application US/08724394A

// Patent No. 5872237

// GENERAL INFORMATION:
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ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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COMPUTER: IN TYPE READABLE PROPOSITION
COMPUTER: IN PROPER PROPERTY RECOMPUTER: IN PROPERTY RECOMPUTER: IN PROPERTY RECOMPUTER PROPERTY
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Conservative
                                           16 AATATGTCGAAACAGCCAG
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STRANDEDNESS: sing
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Best Local Similarity
Matches 31; Conserv
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MOLECULE TYPE:
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  25;
  Matches
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                                                                                                                                                                                          DB 1; Length 1357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dean, Caroline
APPLICANT: MacKnight, Richard C
APPLICANT: Bancroft, Ian
APPLICANT: Bancroft, Ian
APPLICANT: Lister, Clare K
TITLE OF INVENTION: Genetic Control of Flowering
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon & Vanderhye P.C.
STREET: 1100 No. 6140085th Glebe Road, 8th Floor
CITY: Arington
STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATA:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01332
FILING DATE: 01-DEC-1997
CURRENT APPLICATION DATA:
APPLICATION NUMBER: GB 9511196.9,
FILING DATE: 02-UN-1996
PRIOR APPLICATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-29
FILING DATE: 070.1996
PRIOR APPLICATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-29
TELEPHONE: (703) 816-4100
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FUNNTY: F113 base nairs
                                                                                                                                                                                                                                                                                                                     543 GATGTGACAGTTTCAAAAAGGCGAAATATTCAGAATACAATGGTGTAG 496
                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                               2 GATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                            Query Match
36.5%; Score 20.8; DB
Best Local Similarity 64.6%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.8;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana STRAIN: Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08973273 Patent No. 6140085 GENERAL INFORMATION:
                                                                                       MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5113 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
        1357 base pairs
      LENGTH: 1357 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA UVBOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                       US-08-370-975B-8
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  Gaps
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 22926 GATGTGACAGTTTGAAAAAGGCGAAATATTCAGAATACAATGGTGTAG 22879
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION UNMER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 20894/80
TELEPHONE: (716)263-1600
TELEPHONE: (716)263-1600
TELEPHONE: (716)263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 62;
0; Mismatches
  0; Mismatches
                                                                                             4571 AGTIGGICAAATAGCCAGITICCIATGICAG 4602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.5%; Score 20.8; illarity 64.6%; Pred. No. 62 Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COOK, Anne L
APPLICANT: CRAIG, Stewart
APPLICANT: CLEMENTS, John M
APPLICANT: EDWARNS, Richard M
APPLICANT: BROWN, David
APPLICANT: BROWN, David
APPLICANT: BROWN, David
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08094079 Patent No. 5512545 GENERAL INFORMATION:
                                                                                                                                                                RESULT 14
US_08-370-975B-1/c
; Sequence 1, Application US/08370975B
; Patent No. 5622851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT: 4q35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 26764 base pairs
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppedia.

MEDIUM TYPE: Floppedia.

MEDIUM TYPE: Floppedia.

MEDIUM TYPE: Floppedia.

MEDIUM TYPE: TAMP Compatible

OMPRATIOR SYSTEM: DeCDOS/MS-DOS

OFFRATIOR SYSTEM: DECDOS/MS-DOS

OFFRATIOR SYSTEM: US/08/094,079

FLING DATE: 24-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PET/GB92/00141

FLING DATE: 24-JAN-1992

PRIOR APPLICATION NUMBER: GB 9101645.1

FLING DATE: 24-JAN-1991

ATTORNEY/AGENT INFORMATION:
NAME: MCDORNEIL, John J

REGISTRATION NUMBER: 93,640

FELERHOWS: 312-715-1034

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs

TELECOMMUNICATION TO NOTE: A DATA STATE STATE

TOPOLOGY: Lines: A DATA STATE

MOLECULE TYPE: CDNA

MANKE/KEY: misc feature

LOCATION: 1.361

OTHER INFORMATION: And for funcated at 3'

OTHER INFORMATION: and for funcon to alpha factor and truncated at 3'

OTHER INFORMATION: and to remove C-terminal coding residues"

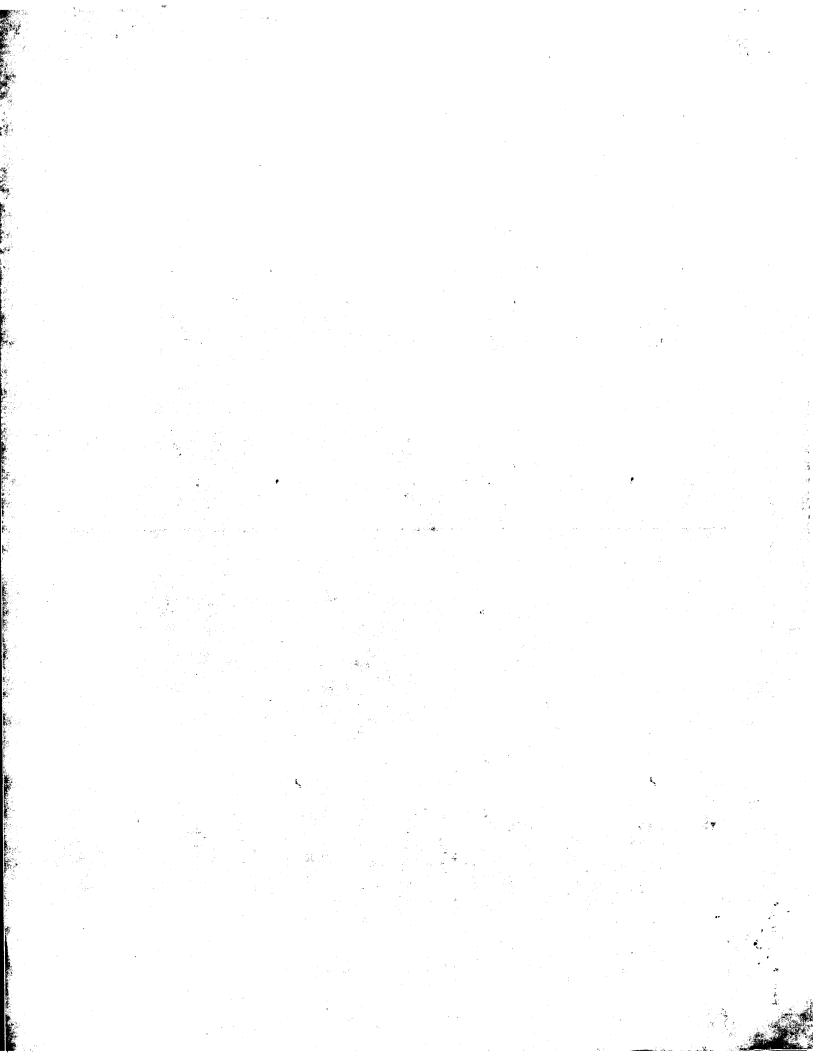
US-08-094-079-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 20,6; DB 1; Length 361; Best Local Similarity 67.4%; Pred. No. 26; Matches 29; Conservative 0; Mismatches 14; Indels
ADDRESSEE: Allegretti & Witcoff, Ltd. STREET: 10 S. Wacker Dr. CITY: Chicago STATE: Illinois COUNTRY: USA
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209 CCTGAGTAGGTCGACACTGAACGTTTCTGTTAGTAACGAACC 167 12 CATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATC 54 g ઠે

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0; Gaps

Search completed: April 15, 2003, 22:52:13 Job time : 328.373 secs



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	Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nuc	nucleic search, using sw model
Run on:	April 15, 2003, 19:13:41 ; Search time 5.69553 Seconds (Without alignments) 8778.558 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-647-019-7 57 1 ggataagactgcatgaatatccaatgttagagccatccag 57
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	593429 seqs, 438583890 residues
Total number of hits	hits satisfying chosen parameters: 1186858
Minimum DB seq 1 Maximum DB seq 1	length: 0 length: 2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : .	Published Applications NA:* 1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:* 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:* 3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* 4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* 5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* 6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 9: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 10: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 11: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 12: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 13: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	6. An	5. Ap	App	App	App	1. An	Appl	Appl	Appl	Appl	Appli	8 . A	1. An	74	Annli	1000	Ann	Appl
Description .	Sequence 4. Appl	Sequence 5216.	Sequence 3875	Sequence 715.	Sequence 102	Sequence 288	Segmence 1601	Sequence 14.	ance 24.	Sequence 14.	Semience 14	Semience 3. 2	Semience 1348	Segmence 3301	Semience 13274	Semience 1	Semience 3	Segmence 41	Sequence 31,
Descr	Seg	Seg	Seg	Segue	Seg	Seg	Seg	Segue	Secure	Seon	Eas	Segui	Seg	Seg	Seg	E ex	S G	T e	Seq
	US-09-880-192-4	US-09-960-352-5216	US-09-764-877-3875	US-09-764-872-715	.09-886-055-102	.09-070-927A-288	US-09-917-800A-1601	19-898-234-14	19-899-429A-24	US-09-792-356-14	US-09-899-422-14	JS-09-784-554B-3	US-09-833-381-1348	09-974-300-3301	09-864-761-13274	US-09-817-310-1	09-813-320-3	US-09-817-607-41	US-09-969-347-31
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DB	2	10	10	O	10	10	10	σ	0	6	10	σ	10	10	10	10	10	10	10
% Query Match Length DB	824	466	31314	533	957	7043	2130	2173	2173	2173	2173	4056	653	373	559	2556	397658	402	404
Query Match	100.0	84.2	42.1	40.7	40.7	40.0	39.6	39.6	39.6	39.6	39.6	38.6	38.2	37.9	37.9	37.9	37.9	37.5	36.8
Score	57	48	24	23.2	23.2	22.8	22.6	22.6	22.6	22.6	22.6	22	21.8	21.6	21.6	21.6	21.6	21.4	21
Result No.	-	8	m	n 4	υ ω	v	7	80	6	10	11	c 15	c 13	c 14	15	16	17	18	19

RESULT 2
US-09-960-352-5216
; Sequence 5216, Application US/09960352
; Patent No. US2002013/139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Norgbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

Sequence 4520, Sequence 4300,	Sequence 135 Sequence 135 Sequence 854 Sequence 1400 Sequence 1400 Sequence 1400 Sequence 244 Sequence 2, A Sequence 3, A Sequence 4, A	Sequence 3 Sequence 3 Sequence 3	H CARDIAC MUSCLE FUNCTION	Length 824; Indels 0; Gaps 0; TAGAGCCATCCAG 57 TAGAGCCATCCAG 262
US-09-960-352-4520 US-09-960-352-4300	US-09-960-352-14 US-09-960-352-81 US-09-960-352-40 US-09-960-352-40 US-09-960-352-40 US-09-864-761-11 US-09-938-842A-14 US-09-285-385-38 US-09-285-385-34 US-10-061-856-2 US-10-063-763-4	US-09-925-299-708 US-09-983-965-4805 US-09-983-965-4805 US-09-881-505-656 US-09-822-846-151 US-09-822-846-151 US-09-810-107-3683 US-09-810-107-349 US-09-854-133-320 US-09-738-973-320	CONMENTS ASSOCIATED WIT 10,192	Score 57, DB 10; Pred. No. 5.6e-13; O; Mismatches O; GAAACAGCCAGTTTCCAATGT
77	428 10 428 10 4431 10 4454 10 1395 10 4661 10 4661 10 55000 9 6479 9	, , , , , , , , , , , , , , , , , , ,	ALJ -192-4 e 4, Application US/09880192 No. US2002007470A1 NO. US2002007470A1 ANT: Walker, Michael G. ANT: Wolkmuth, Wayne ANT: Azimzal, Yalda OF INVENTION POLYNUCLEOTIDES HEFRENCE: PB-0009-1 CIP/09/88 TY TYLING DATE: 2001-06-12 OF SEQ ID NOS: 62 NO 4 H: 824 DNA IISM: Homo sapiens RE: RE: REY: misc feature INFORMATION: Incyte ID NO. US-192-4	100.0%; larity 100.0%; Conservative ACTGCATGAATATGTC
			ULT 1 19-880-192-4 equence 4, Application US/(equence 1, Application US/(ENERAL INFORMATION: APPLICANT: Walker, Michael APPLICANT: Volkmuth, Wayne APPLICANT: Azimzal, Yada APPLICANT: POLICANTON: POLYNUG FILE REFERENCE: PB-0009-1 CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- CURRENT FILING BATE: 2001- CORGANISM: Homo sapiens FRATURE: ORGANISM: Misc feature ORGANISW: misc feature OTHER INFORMATION: Incyte	Similarity 7; Conser TAAGACTGCA
	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	000000000000000000000000000000000000000	OZ AKKOMPE KZE HKK I	ಹ ೮
0.00		000 0 00	RESULT 1 US-09-880 Sequenc Sequenc Patent GENERAL TITLE TITLE TITLE TITLE TITLE TOUREN CURREN SOFTWAN SOFTWAN TYPET TYPE	Query M Best Lo Matches Oy 1

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CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-070-927A-288/c
                                                                                                                        RESULT 5
US-09-886-055-102/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 102
LENGTH: 957
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION CULE REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 SEQ ID NOS: 1516
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           91 GGATAAGACCGCGTCAGTATGTCGAAACAGCCAGTTTCCAATGTCAGAGCCATCCA 146
                                                                                                                                                                                                                                                                                                                                                                                                               1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCA 56
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Patent No. US20020147140A1

GENERAL INPORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TILE REPRENCE: PCOOS
CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application date removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 31314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 715, Application US/09764872
Publication No. US20030050231A1
GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVERFICON: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER: OF SEQ ID NOS: 957
                                                                                                                                                                                                                                                                                                                    Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1967 AAATCTGCAAAATTTGGTGAAAAGAGAGAGTCTGCAGTGTTTAAGCCA 2014
                                                                                                                                                                                                                                                                                                                  Query Match 84.2%; Score 48; DB 10; Length 46
Best Local Similarity 91.1%; Pred. No. 1.7e-09;
Matches 51; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.1%; Score 24; DB 10; Length 31 Best Local Similarity 68.8%; Pred. No. 23; Matches 33; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCA 52
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 23-BOVMS1-014-Q1-E1-F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.4%; Pred. No. 12;
Matcheg 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 715
LENGTH: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-764-872-715/c
                                                                                                                                                                                                                                                                   US-09-960-352-5216
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TRNGTH: 31314
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Sequence 288, Application US/09070927A

Sequence 288, Application US/09070927A

Patent No. US2020120116A1

GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch

Steven Barash

TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 982

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome. Sciences, Inc.

STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                               Sequence 102, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER; LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2000-06-22
; ANUMBER OF SEQ ID NOS: 522
; SOUTHARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  783 GGAGAAGGAGGAGGATGTAGAAACCAGGATGATGCCAATGTGGGAGCCA 732
532 AGAATATATGAAAAGGTGGTAACAGAACTTTCCAAAACTAAAAGGCATCCAG 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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APPLICATION NUMBER: US/09/070,927A
FILLING DATE: 04-MAY-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILLING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
APPLICATION NUMBER: 60/044,031
APPLICATION NUMBER: 60/046,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

40.7%; Score 23.2; D

Best Local Similarity 65.4%; Pred. No. 14;

Matches 34; Conservative 0; Mismatches
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REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-11-14 ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: PB369

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Gaps

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Indels

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Sequence 24, Application US/09899429A 
Patent No. US20020169118A1 
GENERAL INFORMATION:
                                                                 ; Sequence 14, Application US/09898234; Patent No. US20020155112A1; GENERAL INFORMATION: APPLICANT: Hauptmann, Rudolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-899-429A-24
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US-09-917-800A-1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                803 AGGAATGTATGAAGCTGTGCCTACCTCCAGTTGCAAATGTCACAAAACCCCCCAG 855
                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 7043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2081 GATAGCATGAATGTTTAACAACAGTACCTTTCTAAAATTAAAGTCATTCA 2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 GACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TOLUEL, WILLA
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE SPERENCE: 44921-5038-08
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR PLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-19
PRIOR PLILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
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66.0%; Pred. No. 41;
tive 0; Mismatches 17;
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64.2%; Pred. No. 32;
tive 0; Mismatches 19;
                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1601, Application US/09917800A Patent No. US20020119462A1 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION
                                                                          INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 7043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 66.01
Matches 33; Conservative
                           TELEFACNE: (301)
TELEFAX: (301) 3
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Best Local Similarity 64.21
Matches 34, Conservative
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APPLICANT: Magnerally, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
ITILE OF INVENTION: Them
ITILE OF INVENTION NUMBER: 08/98,234
CURRENT APPLICATION NUMBER: 08/25,998
PRIOR FILING DATE: 1992-02-01
PRIOR FILING DATE: 1993-02-01
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
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APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Rogy, Ingrid
APPLICANT: Maurer-Rogy, Ingrid
APPLICANT: Maurer-Rogy, Ingrid
APPLICANT: Maurer-Rogy, Ingrid
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFERENCE: 98-385-105-03
CURRENT APPLICATION NUMBER: 09/792,356
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 1955-06-07
PRIOR PELICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1955-02-01
PRIOR PELICATION NUMBER: 08/193,676
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1991-11-17
PRIOR APPLICATION NUMBER: 08/183,287
PRIOR FILING DATE: 1991-11-17
PRIOR FILING DATE: 1991-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1993-11-17
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; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: raINF-R8
US-09-898-234-14
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39.6%; Score 22.6; DB 9; Length 21
Best Local Similarity 64.2%; Pred. No. 33;
Matches 34; Conservative 0; Mismatches 19; Indels
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NUMBER OF SEQ ID NOS: 97
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39.6%; Score 22.6; Di
64.2%; Pred. No. 33;
tive 0; Mismatches
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APPLICANT: Schnorr, Rirk
APPLICANT: Jorgensen, Per Lina
APPLICANT: Schulein, Martin
TITLE OF INVENTION: PAMILY 4 XYLOGLUCANASES
TITLE REFERENCE: 10017.200-US
CURRENT APPLICATION NUMBER: US/09/784,554B
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/09784554B; Publication No. US20030032162A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Paenibacillus polymyxa
US-09-784-554B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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Best Local Similarity 63.0%;
Matches 34; Conservative
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Matches 34; Conservative
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LENGTH: 2173
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APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hauptmann, Rudolph
APPLICANT: Manuer-Fogy, Ingrid
APPLICANT: Manuer-Fogy, Ingrid
APPLICANT: Manuer-Fogy, Ingrid
APPLICANT: MANUER: Christian
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILL REFERENCE: 98,386.792,356
CURRENT APPLICATION NUMBER: 08/09/792,356
CURRENT PILING DATE: 1995-06-07
PRIOR PELING DATE: 1995-02-01
PRIOR PELING DATE: 1995-02-01
PRIOR PELING DATE: 1993-11-17
PRIOR FILING DATE: 1992-01-03
PRIOR FILING DATE: 1992-01-03
PRIOR FILING DATE: 1992-01-03
PRIOR PELING DATE: 1992-01-03
PRIOR PELING DATE: 1992-01-03
PRIOR PLING DATE: 1992-01-03
PRIOR PELING DATE: 1992-01-03
PRIOR PELING DATE: 1992-01-03
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR PELING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 14
FIENGTH: 2173
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COCATION: (245)..(1630)

CHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-792-356-14
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                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8; NAME/KEY: CDS; LOCATION: (255)..(1627)
US-09-899-429A-24
                                                                                                                                                                                                                                                                                                                                                                                             810 AGGAATGTATGAAGCTGTGCCTACCTCCAGTTGCAAATGTCACAAAACCCCCAG 862
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                                                                                                                                                                                                                                                     Length 2173;
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                                                                                                                                                                                                                                                   Score 22.6; DB Fred. No. 33; 0; Mismatches
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39.6%; Score 22.6; DB
Best Local Similarity 64.2%; Pred. No. 33;
Matches 34; Conservative 0; Mismatches
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Patent No. US20020090676A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Pogy, Ingrid
APPLICANT: Statowa, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09792356 Publication No. US20020183485A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64.2%;
Matches 34; Conservative (
                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
SEQ ID NO 24
LENGTH: 2173
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                                                                                                     FEATURE:
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TITLE OF INVENTION: Them

TITLE OF INVENTION: Them

FILE REPREBUCE: 98,385-H

CURRENT APPLICATION NUMBER: US/09/899,422

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 09/525,998

PRIOR APPLICATION NUMBER: 09/525,998

PRIOR PELIAGORE: 2000-03-15

PRIOR APPLICATION NUMBER: 08/383,676

PRIOR PELIAGORE: 1995-02-01

PRIOR PELIAGORE: 1995-02-01

PRIOR PELIAGORE: 1993-11-17

PRIOR PELIAGORE: 1993-11-17

PRIOR PELIAGORE: 1993-11-17

PRIOR PELIAGORE: 1993-11-17

PRIOR FILING DATE: 1993-01-02

PRIOR FILING DATE: 1990-04-20

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PATENTIN VET. 2.0
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; Patent No. US20020132090A1
; GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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LOCATION: (245)..(1630)
• OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
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Pred. No. 70;
0; Mismatches 20; Indels
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CTHER INFORMATION: MAP TO AL138498.2
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
US-09-864-761-13270
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13274
LENGTH: 559
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      PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-31

PRIOR PRIOR PLING DATE: 2000-09-31
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Job time : 11.6955 secs
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Best Local Similarity 68.2
Matches 30; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
PILE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILLING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Clausen, ib Groth
APPLICANT: Clausen, ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2001-10-36
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 AATGCAGGAATAGGATCACACAACGAAGTGCCAATGACATGGCCATCAA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCA 56
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68.2%; Pred. No. 45;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
38.2%; Score 21.8; DE
Best Local Similarity 65.3%; Pred. No. 45;
Matches 32; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-64-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 1348
LENGTH: 653
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PRIOR APPLICATION NUMBER: US 60/180,312
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-974-300-3301/c

Sequence 3301, Application US/09974300

; Patent. No. US20020146721A1

; GENERAL INFORMATION:

    LOCATION: (1)...(653)
    OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1348

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1 ORGANISM: Bacillus licheniformis
US-09-974-300-3301
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Best Local Similarity 68.24
Matches 30; Conservative
                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (1)...(653)
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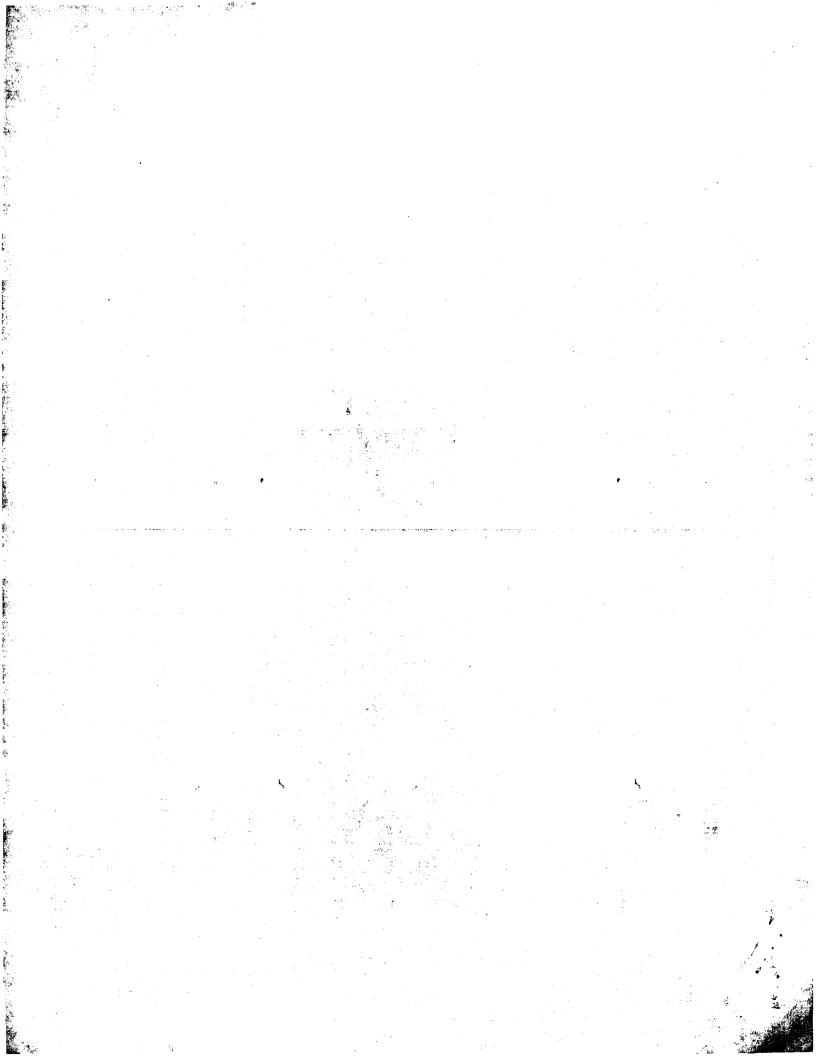
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Length 559;

DB 10;

Score 21.6; D Pred. No. 51; 0; Mismatches



Title: Perfect score: Sequence:

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Drosophila melanog Drosophila melanog Enterococcus faeca

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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                  Giordano J;
                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 1481
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                        AAH32330
AAS42259
ABK68605
                                                                                                           ABK37545
ABQ88355
ABQ88354
AAS59816
AAS59859
AAD19580
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AAS34734
ABN65201
                                     ABL07834
AAF22303
                                                  ABV18116
ABV47904
                                                                     ABL27258
AAS39818
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ABL29218
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                                                                                  AAK90174
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P-PSDB; AAG01477.
                                                  (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                  EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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CDNA encoding huma
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CDNA encoding muri
C albicans apoptos
Human biallelic po
Human biallelic po
Human prostate exp
Human prostate exp
                                        April 15, 2003, 16:26:41; Search time 15.2104 Seconds (without alignments) 8439.207 Million cell updates/sec
                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                              ggataagactgcatgaatat......ccaatgttagagccatccag
    GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                              2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                             - nucleic search, using sw model
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AAH29924
AAX12902'
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AAX90904
AAD27216
                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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Score

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The present sequence is the cDNA encoding the human chisel gene (Csl) that is mapped to the human chromosome Xq21.3-q22. It comprises 5 exons. It is a member of the EF-Hand protein super family and is involved in signalling pathways. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies skeletal myopathies such as buchemne muscular dystrophy and myocarditis, myofiber atrophy, heart failure, cardiac hypertrophy, myofiber atrophy, etc. The Csl gene sequence can also be used in gene therapy, for the production of transgenic animals and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, congestive heart failure, dilative cardiomyopathy; sudden death, hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; exterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids encoding chisel, used to develop products treating cardiomyopathy, cardiac hypertrophy, heart failure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
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residues 35384-35236 of
                                                                                           /label= Exon_5
/note= "Corresponds to residues 4101-3680 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 887;
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1. Similarity 100.0%; Pred. No. 2.8e-12;
57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenthal NA;
                                                                                                                                                                                                                                                                                                                                                                                               GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER & ELIZA.
         human cosmid clone U112E8"
                                                                                                                                    human cosmid clone U112E8'
'note= "Corresponds to
                                                                                                                                                                                                                                                                                                                                                                         CHAN-) CHANG CARDIAC RES INST VICTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harvey RP, Musaro A, Palmer SJ,
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Best Local Similarity
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                                                                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chisel gene; Csl; EF-Hand protein super family; muscle development; hear(Fakeletel muscle cell development; signalling pathway; regulation; Xq21.3-q22; adaptive process; muscle homeostasis; skeletal myopathy; detection; diagnosis; prophylaxis; treatment; cardiac hypertrophy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; differentiation; exon; gene therapy; transgenic animal; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
  diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 292
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/label= Exon_1
/note= "Corresponds to residues 19497-19327 of
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|label= Exon 3
|note= "Corresponds to residues 5220-5134 of
human cosmid clone U228B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 21; Length 428; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Corresponds to residues 15687-15631 human cosmid clone U228D4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 428 BP; 123 A; 111 C; 104 G; 90 T; 0 other;
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                                                Claim 1; SEQ ID 1481; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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173..229
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product= "Chisel
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/label= Exon 2
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/label= Exon_4
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100.0%;
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Best Local Similarity 100.
Matches 57; Conservative
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cDNA encoding murine chisel (Csl) gene.
       tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method for assessing the expression level of these genes. The method for a use for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat disease of the heart such as congestive heart failure, dilative cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary heart disease, valvular heart disease, congenical heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patent discloses novel target genes abnormally expressed in heart
congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone 66214; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases. The present DNA sequence is expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.2%; Score 55.4; DB 24; Length 886; 98.2%; Pred. No. 1.2e-11; 1.4e 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 886 BP; 278 A; 172 C; 191 G; 245 T; 0 other;
                                                                                                                                       /product= "Human 66214 protein"
298..588
/*tag= b
/note= "66214 cDNA fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Henkel T;
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2a; Fig 9b; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Beck J,
                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001WO-EP06165
                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-207400P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.24
Matches 56; Conservative
                                                                                                                            Ø
                                                                                                           184..450
                                                                                                                            /*tag=
                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-122073/16.
P-PSDB; AAE16632.
                                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDIGENE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                              Reuner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EST) 66214 clone.
                                                                                                                                                                                                                                                                 WO200192567-A2
                                                        Homo sapiens
                                                                                                                                                           misc_feature
                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                    06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bunk D,
                                                                                       Key
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that is mapped to the mouse X circomosome. It is a member of the EP-Hand protein super family and is involved in signalling pathways. It is protein super family and is involved in signalling pathways. It is proteinmantly expressed in heart and skeletal muscles and is activated after differentiation of cells. Cal functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle call development and functional activity is also used in the treatment of muscular and myotonic dystrophies, skeletal myopathies such as Duchenne muscular dystrophy and Becker's myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, myofiber atrophy, etc. The Cal gene sequence can also be used in gene therapy, for the production of transgenic animals and for drug screening.
Chisel gene; C81; EF-Hand protein super family; muscle development; heart(skelatel muscle cell development; signalling pathway; murine; X Chromosome; regulation; adaptive process; muscle homeostasis; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchanne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the cDNA encoding the murine chisel gene (Csl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids encoding chisel, used to develop products for treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Chisel (CSL) protein"
/note= "Expressed especially in heart muscles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 74.7%; Score 42.6; DB 20; Length 778; I Similarity 84.2%; Pred. No. 1e-06; 48; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 778 BP; 231 A; 166 C; 179 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harvey RP, Musaro A, Palmer SJ, Rosenthal NA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHAN-) CHANG CARDIAC RES INST VICTOR
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH29924 standard; DNA; 3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-AU00220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98AU-0002634
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                     199..456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-610852/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY28650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9950410-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH29924;
                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH29924
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GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 172 GGATAAGACTGCATGTATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG

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AAX90903 standard; cDNA; 778

AAX90903 RESULT

17-JAN-2000 (first entry)

AAX90903;

27-JUL-2001 (first entry)

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AAX10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers crepresented in AAX09121-X10268. The base occupying the polymorphic site indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual corn see in e.g. forenaiscs, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Bhlers-Danios syndrome, osteogenesis imperfecta, acute intermittent porphyria, hemorrhagic telangiectasia, familial oclonic polyposis, shreditary hemorrhagic telangiectasia, familial oclonic polyposis, shreaticary system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldmess, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                       New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                   determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.6%; Score 25.4; DB 19; Length 210; ilarity 74.4%; Pred. No. 3.4; Conservative 0; Mismatches 11; Todale o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human biallelic polymorphic DNA fragment EST398528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 210 BP; 56 A; 53 C; 50 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 ACAGCAGGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGC
                                                                       (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 301; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prophylaxis of such diseases
                         96US-0030455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0030455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX11743 standard; DNA; 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US20313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                          Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; marker; ss.
                                                                                                                                                                      WPI; 1998-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 32; Conserv
                         06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9820165-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1996;
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                                                                                                                        Hudson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX11743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                            Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.6%; Score 26; DB 22; Length 3098; 76.2%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luyten WHML, Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3098 BP; 1023 A; 528 C; 539 G; 1008 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2459 AGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGG 2500
                                           C albicans apoptosis associated coding sequence #68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human biallelic polymorphic DNA fragment EST398528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Claim 17; Fig 2; 218pp; English.

certain diseases

De Backer MD, Reekmans RJ;

Contreras RH, Nelissen BJM,

2001-367042/38.

P-PSDB; AAG70888

03-JUL-2000; 2000WO-BE00077.

Candida albicans

WO200102550-A2.

11-JAN-2001.

99EP-0870141

01-JUL-1999;

(JANC) JANSSEN PHARM NV.

AAX12902 standard; DNA; 210 BP.

AAX12902

g ð

Conservative

Local Similarity les 32; Conserv

Query Match Best Loca Matches (first entry)

30-MAR-1999

AAX12902;

treatment; marker; ss.

97WO-US20313

05-NOV-1997;

14-MAY-1998.

WO9820165-A2 Homo sapiens

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Gaps

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us-09-647-019-7.rng

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient, cancer in a patient,
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 7677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7677 BP; 2389 A; 1642 C; 1794 G; 1846 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1412 TGTATGTGGCAGTAGCCAGTTTCCGATGGCAGAGCCA 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 29033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25.4; DI
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                     Claim 1; Page 4173-4175; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9042/c
ABV29042 standard; cDNA; 7677 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 44.6%;
1 Similarity 74.4%;
32; Conservative
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16-MAR-2000; 2000US-189662P.
25-MAY-2000; 2000US-207454P.
09-UTN-2000; 2000US-211314P.
18-JUL-2000; 2000US-21191P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2000; 2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
     WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                 AAX10269-X12937 are human DNA fragments which contain biallelic
polymorphic markers which have been isolated using the primers
represented in AAX09121-X10268. The base occupying the polymorphic site
is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
c is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
c an be used in methods for determining polymorphic forms in an individual
c for use in e.g. forenaids, paternity/festing or for phenotypic typing for
diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Whan
c syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
c familial hyperrcholesterolemia, polycystic kidney disease, hereditary
c spharcome, osteogenesis imperfected, acute intermittent porphyria,
c stroatome, osteogenesis imperfected, acute intermittent porphyria,
c stroatome, osteogenesis inflammation, cancer, diseases of the nervous
c system, infection by pathogenic microorganisms, and characteristics such
c system, infection by pathogenic microorganisms, and characteristics such
c as longevity, appearance (e.g. baldness, obesity), strength, speed,
c endurance, ferrility, and susceptibility or receptivity to particular
c crugs or therapeutic treatments. The isolated polymorphic nucleic acid
c contains can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                             New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 ACAGCAGGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 210 BP; 56 A; 52 C; 50 G; 51 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 11 14.6%; Score 25.4; DB 19; Score 25.4; DB 19; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 23196,
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                                                                                                                                                                                           Claim 1; Page 189; 310pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis of such diseases
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16-WAR-2000; 2000US-189862P.
25-WAY-2000; 2000US-207454P.
09-UUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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Hudson T, Lander ES,
                                                WPI; 1998-286974/25.
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Matches 32; Conserv
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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ABV23205;

RESULT

Query Match

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Gaps

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are used in the methods for monitoring differential expression of genes
in a first filamentous fungal (FF) cell relative to expression of the
same genes in one or more second filamentous fungal cells. Monitoring
the global expression of genes from FP cells allows the production
challed expression of genes from FP cells allows the production
constitution of the microorganisms to be improved. New genes may be
discovered, possible functions of unknown open reading frames can be
classible functions of unknown open reading frames can be
dentified and gene copy number variation and stability can be
considered. The expression of genes can be used to study how FF cells
considered. The expression of genes can be used to study how FF cells
considered. The expression of genes can be used to study how FF cells
considered. The expression of genes conditions, environmental stress, spore
control of the continuous provides several advantages over genomic or
control of the gene or open reading frame, and organisation of the
control of the gene products to facilitate
control of the results. APRI1248 to AAFI1247 represents ESTS from Aspergillus
control of the control of the gene products of the formation of the control of the gene products of the formation of the control of the gene products of the formation of the gene formation of the gene products of the formation of the gene products of the formation of the gene formation of the gen
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 711 BP; 133 A; 224 C; 188 G; 153 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all specifically claimed in the present invention.
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2000US-0224518.
2000US-0224519.
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19-MAY-2000; 2000US-0205515.
07-JUN-2000; 2000US-0209467.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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2000US-0216647.
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17-MAR-2000; 2000US-0190076.
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Best Local Similarity
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14-AUG-2000;
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                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

cancer in a patient,

cancer in a patient,

(d) assessing the efficacy of a therapy for inhibiting prostate cancer

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcifiogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses General-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.9;
0; Mismatches
                Claim 1; Page 6152-6154; 11750pp; English
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les 32; Conservative
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2000US-0226681
2000US-0226681
2000US-0226868
2000US-0228924
2000US-0228924
2000US-0229343
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2000US-0241787.
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
30-AUG-2000;
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31-AUG-2000;
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05-SEP-2000;
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02-0CT-2000;
02-0CT-2000;
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13-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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29-SEP-2000;
29-SEP-2000;
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12-SEP-2000;
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2000US-0246532. 2000US-0246609. 2000US-0246610. 2000US-0249213. 2000US-0249214. 2000US-0249215. 2000US-0249216. 2000US-0249217. 2000US-0249218. 2000US-0249210. 2000US-0246611. 2000US-0246613. 2000US-0249207 2000US-0249208 2000US-0249244 2000US-0249264 2000US-0251856 2000US-0249209 2000US-0249212 2000US-0249245 2000US-0249297 2000US-0249300 2000US-0250160 2000US-0250391 2000US-0251030 2000US-0256719 2000US-0251479 2000US-0251868 08-DEC-2000; 2000US-0251869 05-JAN-2001; 2001US-0259678 2000US-0254097 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 11-DEC-2000; 17-NOV-2000; 17-NOV-2000;

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 33178; 3071pp + Sequence Listing, English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
colpuncleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic-derived cells. AKK4703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.

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01-SEP-2000; 2000US-0229343.
01-SEP-2000; 2000US-0229344.
01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229509.
06-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0230437.
06-SEP-2000; 2000US-0231242.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231413.
08-SEP-2000; 2000US-02312414.
08-SEP-2000; 2000US-02312414.
08-SEP-2000; 2000US-0231268.
08-SEP-2000; 2000US-0232081.
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14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232400.
14-SEP-2000; 2000US-0232401.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
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29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236370.
29-SEP-2000; 2000US-0236370.
02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237037.
03-OCT-2000; 2000US-023937.
03-OCT-2000; 2000US-023937.
03-OCT-2000; 2000US-024960.
03-OCT-2000; 2000US-0241785.
03-OCT-2000; 2000US-0241808.
03-OCT-2000; 2000US-0241808.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
03-OCT-2000; 2000US-0241809.
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08-NOV-2000; 2000US-0246523.

08-NOV-2000; 2000US-0246524.

08-NOV-2000; 2000US-0246525.

08-NOV-2000; 2000US-0246526.

08-NOV-2000; 2000US-0246527.

08-NOV-2000; 2000US-0246527.
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08-NOV-2000; 2000US-0246610

08-NOV-2000; 2000US-0246611

08-NOV-2000; 2000US-0246611

17-NOV-2000; 2000US-0246613

17-NOV-2000; 2000US-0249207
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21-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234998.
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27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235836.
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08-NOV-2000; 2000US-0246475
08-NOV-2000; 2000US-0246476
08-NOV-2000; 2000US-0246476
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                                                                                                                                                                                                                                              Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticoruvlaant; antibacteral; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                  Gaps
                                                                                                                                                                                                                          Human musculoskeletal system related polynucleotide SEQ ID NO 3875
                                                ö
                       / Match 42.1%; Score 24; DB 22; Length 20689; Local Similarity 68.8%; Pred. No. 35; Los 33; Conservative 0; Mismatches 15; Indels 0
 Sequence 20689 BP; 4818 A; 5626 C; 5868 G; 4377 T; 0 other;
                                                                                            5772 GAGAACTTAGCTTGAAGCTGTCGAAACCACCAACTTCCAGAGCTAGAG 5819
                                                                      GATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAG 49
                                                                                                                                                       ВР
                                                                                                                                                     AAL37510 standard; DNA; 31314
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2000US - 0199874.
2000US - 0199875.
2000US - 0205515.
2000US - 0214886.
2000US - 0214886.
2000US - 0214886.
2000US - 0217487.
2000US - 0217487.
2000US - 0217487.
2000US - 0227518.
2000US - 0225214.
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2000US-0229287
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                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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01-SEP-2000;
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                                                                                                                                                                           AAL37510;
                       Query Match
                                                                     N
                                              Matches
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BAC containing repeats from centromeres 1-4 #10.

(first entry)

20-MAR-2001

AAF22287;

AAF22287 standard; DNA; 103929 BP.

Centromere; michrosome; vector; ds

Arabidopsis thaliana

WO200055325-A2

21-SEP-2000

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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB3087-ABB04199) associated with the musculoskeletal system useful for preventing, treating or ameliocating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti-sgonists are useful in the disgnosis, treatment cancer of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune tract, liver, lung, or urogenital; (b) immune thyroidfils, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasitic infections.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.1%; Score 24; DB 22; Length 31314; Best Local Similarity 68.8%; Pred. No. 38; Matches 33; Conservative 0; Mismatches 15; Indels 0.
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                                                                 2000US-0249217.
2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249245.
2000US-0249265.
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2000US-0249300.
2000US-0250160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC,
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Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells

Keith K;

Copenhaver G,

Preuss D,

WPI; 2000-587529/55.

(UYCH-) UNIV CHICAGO

99US-0125219. 99US-0127409. 99US-0134770. 99US-0153584.

01-APR-1999; 18-MAY-1999; 13-SEP-1999; 17-SEP-1999;

18-MAR-1999

17-MAR-2000; 2000WO-US07392

Claim 102; Page 484-508; 1449pp; English

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The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                Db 99535 GGTATAAGTGCATGAGTATGTCAAAACGGACTATTACGGTTTTAAATGTTATCCAG 99480
                                                                                                                                                                                                                                                            5,
                                                                                                                                         Sequence 103929 BP; 32987 A; 19310 C; 18547 G; 33085 T; 0 other;
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                                                                                                                                                                            Score 24; DB 21; Length 103929;
Pred. No. 51;
                                                                                                                                                                                                                                                        2 GATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer; detection; non-A-B-C-D-E-F type hepatitis virus;
                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                Pred. No.
                                                                                                                                                                              42.1%;
                                                                                                                                                                                                                                                                                                                                                                                           AAV13779 standard; DNA; 219
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                                                                                                                                                                                            Best Local Similarity 64.3
Matches 36, Conservative
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                                                                                                                                                                              Query Match
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Search completed: April 15, 2003, 18:58:27 Job time : 36.2104 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                              New nucleic acid fragment, primers and probes - useful for detection of non-A-B-C-D-E type hepatitis virus
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                   A primer for the detection of non-A-B-C-D-E-F type hepatitis virus or hepatitis G virus (HGV), comprises a HGV nucleic acid fragment, e.g. the present sequence. The primers may be used for the detection of HGV via PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                         Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 25.
                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                               41 GGCGATGACTGCTTGATCATATGCGAACGGCCAGTTTGCGATCCTAGTGAC 91
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                                                                                                                                                                                                                                                                                                                                                             1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 25; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                        Sequence 219 BP; 44 A; 57 C; 61 G; 57 T; 0 other;
                                                                                                                                                                                                                                                                                                    Query Match
41.8%; Score 23.8; DE
Best Local Similarity 66.7%; Pred. No. 14;
Matches 34; Conservative 0; Mismatches
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                                                                                                                                                                        Claim 1; Page 58; 67pp; Japanese.
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                            96JP-0122288
96JP-0110411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 96JP-0184103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                    WPI; 1998-113595/11.
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                                                                       (SRLS-) SRL KK.
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                            19-APR-1996;
06-APR-1996;
25-JUN-1996;
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ID ABL161
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                            DB 23; Length 8661;
                                                                                                                                                                                                                                                                                           1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATC
                                                                                                                     Sequence 8661 BP; 2505 A; 1916 C; 1846 G; 2394 T; 0 other;
                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                         ; Score 23.6; DB
; Pred. No. 40;
0; Mismatches
                                                                                                                                                                      Query Match
Best Local Similarity 64.8%;
Matches 35; Conservative
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us-09-647-019-7.rge

Run on:

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April 15, 2003, 16:47:06; Search time 129.143 Seconds (without alignments) 12845.099 Million cell updates/sec
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                      2054640 segs, 14551402878 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_pat: *
em_pl: *
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em_un: *
em_un: *
em_vi: *
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em_htgo hum:*
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57
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Pred. No. is the number of results predicted by chance to have a

Homo sapiens, small muscle protein, X-linked, clone MGC:14584 INAGE:4246501, mRNA, complete cds. X-linked, clone MGC:14584 BC005948 BC005948.1 GI:13543590 MGC. BC005948 Homo sapi AJ550584 Homo sapi AF12505 Homo sapi AF1272370 Homo sapi AK322774 Sequence AX324774 Sequence AX324774 Sequence AX32477 Mus muscu AZ364071 Rattus no AZ364071 Rattus no AZ369691 Human DNA AZ157505 Homo sapi BAD1235 Home sapi AB029421 Martes zibe AB029421 Martes zibe AB012359 Martes zibe AB012359 Martes zibe AB012359 Martes zi AB01236 Martes zi AB01236 Martes zi AB01236 Martes zi AR048241 Martes zi AR048241 Martes zi AF44824 Martes zi AF AC119274 Mus muscu AC004259 Human Chr AC004600 Homo sapi AP321234 Mus muscu AC100774 Homo sapi AF321233 Mus muscu AC122258 Mus muscu G44373 WIAF-4237-8 Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo. Homo gapi Homo gapi U90942 Human myosi Y07759 H.sapiens m X68793 H.sapiens g score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. ALIGNMENTS SUMMARIES BC005948 HSA250584 AF129505 U73509 AL772370 AX322774 AY026524 AR364070 AF321235 AC119274 AC004259 AC004600 AF321234 AC10074 AC084009 AF321233 AC122258 AF364071 AC124177 AL589691 AL357505 D26519 L77957 AB029420 AB029421 AB029423 AB012356 AB012359 AB012359 AB012361 AF448241 AF448243 AP448244 AC004152 AF343894 AX489570 AX073292 AC060834 Homo saplens Eukaryota, Metazoa, C Mammalla, Eutheria; P 1 (bases 1 to 835) Srrausberg, R. Direct Submission 8 1140 11140 11140 11140 11140 11140 113686 34498 66142 118684 133863 155781 2598 3098 184595 190749 195974 6401 14206 44942 Length 230579 Homo sapiens. RESULT 1 BC005948 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE Result No.

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AF129505 886 bp mRNA linear PRI 22-DEC-1999
Homo sapiens small muscular protein (SMPX) mRNA, complete cds.
AF129505
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MNMSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEB
GVPPTSDEEKKPIPGAKKLPGPAVNLSBIQNIKSELKYVPKAEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (18-JAN-1999) Molecular Human Genetics, Institut for
Human Genetics, Fleischmannstr. 42/44, D-17487 Greifswald, Germany
Location/Qualiflers
Direct Submission
Submitted (102-NOV-1999) Kemp T.J., Molecular pathology, Imperial
College of Science Technology and Medicine, SAF Bldg, Level 2,
Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM
Related sequences: AJJ45772, U73508 to U73509.
Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 886)

Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.

Identification, mapping, and genomic structure of a novel

K-chromosomal human gene (SMPX) encoding a small muscular protein

20065879
                                                                                                                                                                                                                                                                                          /gene="Srmx"
184. .450
1940--85rmx"
/codon_start=1
/product="stretch responsive muscle (X-chromosome)"
/protef="GI:10178977"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 228
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1. Similarity 100.0%; Pred. No. 4.6e-11;
57; Conservative 0; Mismatches 0;
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Lissue_type="skeletal muscle"
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/db_xref="taxon:9606"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Srmx"
857. .862
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/gene="SMPX"
184. .450
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Patzak, D.
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                                                                                 WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Bmail: cgapba-rømail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6625646.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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111 g 227 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kemp,T.J., Sadusky,T.J., Simon,M., Brown,R., Eastwood,M.,
Sassoon,D.A. and Coulton,G.R.
Identification of a novel stretch-responsive skeletal muscle gene
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 bp mRNA linear PRI 12-APR
Homo sapiens mRNA for stretch responsive muscle (X-chromosome)
protein (Srmx gene).
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/clone lib="NIH MGC_81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pDNR-LIB"
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AJ250584.1 GI:10178976
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2 (bases 1 to 885)
Kemp, T.J.
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Matches 57; Conserv
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/product= semal Ala Hagas 13.1"
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190
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Homo sapiens cosmid clone U228D4 from Xp22.1-22.2, complete
sequence.
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 47440)
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Unbmitted (27-APR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY: WUGSC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              /gene="SMPX"
/note="alternate position for initiation methionine"
451. .9886
451. .88877. .862
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The sequence of Homo sapiens cosmid clone U228D4 Unpublished (1999)
3 (bases 1 to 47440)
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Pred. No. 4.6e-11;
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http://genome.wustl.edu/gsc
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Direct Submission
Submitted (04-OCT-1996)
4 (bases I to 47440)
Waterston, R.
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Sulston, J.E. and Water
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172 c
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Best Local Similarity 100.
Matches 57; Conservative
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between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. V., and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomics MAPPING INFORMATION:

SOURCE INFORMATION: (1997). 44:227-231

This clone is from a chromosome X-specific cosmid library LLOXNCC01 'U'. The source of the chromosomes was a human/hamster hybrid, GM07297-F, from Robert Nusabbaum at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livermore National Laboratory at http://www-bio.llnl.gov/genome to obtain the clone. VECTOR: Lawrist16

Location/Qualifiers

1. .47440 | Organism="Homo sapiens" | db_xref="texon:9606" | chromosome="x" | map="Xp22.1-22.2" clone="U228D4"

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(NID:g1281479) za96c10.r1" misc_feature misc_feature

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RESULT 5
AL772370/c
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complement(19314. .19413)
/note="match to EST AA092554 (NID:g1637327)"<sup>-</sup>
21260. .21572
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46645. .47185
/rpt family="MER21_g"
9644 c 9310 g 13336 t
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8945. 29005
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25276. 45339

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46393. 46517
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37345. 3745="Trpt_family="(TA)n"
37504. 37858
                                                                                                                                                                                  20867. .27210
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                                                                                            /rpt_taus_24236
24236. .24556
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8102. .38146
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AL772370 150319 bp DNA linear HTG 17-AUG-2002
Homo sapiens chromosome X clone RP11-184B10, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                        Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Callo 15A, UK. B-mail enquirites: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204612.
                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator ET-amersham; 0% of reads
Consensus quality: 14973 bases at least Q40
Consensus quality: 149914 bases at least Q20
Insert size: 150219; sum-of-contigs
Insert size: 15229; 2.5% error; agarse-fp
Coulity coverage: 17.18x in Q20 bases; sum-of-contigs Quality
coverage: 17.58x in Q20 bases; sum-of-contigs Quality
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                                                                                                               AL772370.5 GI:22416024
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                          Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
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4960. .150319
/note="assembly_fragment:05270
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ragment_chain:1"
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vector_side:right"
47436 a 29741 c 29722 g 43320 t
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Contact: humquery@sanger.ac.uk
Center project name: bA184B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
/chromosome="X"
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1. .4859
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Mammalia; Butheria; Primates;
1 (bases 1 to 150319)
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Db 15687 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 15631

1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG

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/protein id="AAK50388.1"
/db_xref="GI:13940508"
/translation="MSKQPISNVRAIQANINIPMGAPRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
                                                                                                                                                                                                                                                                                                                                                       ROD 04-MAY-2001
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Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel X-chromosomal human gene (SMPX) encoding a small muscular protein 20065879
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Patzak, D.
Patzak, D.
Patzak, D.
Submission
Submitted (26-MR-2001) E.M.-Arndt-Uni, Inst. f. Humang.,
Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
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                                                                                                                                                                            ch 74.7%; Score 42.6; DB 10; Length 787; I Similarity 84.2%; Pred. No. 1.5e-05; 48; Conservative 0; Mismatches 9; Indels 0.
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Mus musculus SMPX protein (Smpx) mRNA, complete cds.
AF364070
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Pred. No. 1.5e-05;
0; Mismatchee 9;
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/product="SMPX protein"
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                                                                                                                                                                              Query Match
Best Local Similarity
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Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryote, Metazoa, Chordata, Sciurognathi, Muridae, Murinae,
Mus.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
Mus.
Mus.
Mus.
Pahmer, S., Groves, M., Schindeler, A., Yeoh, T., Biben, C., Wang, C.-C.,
Sparrow, D. B., Barnett, L., Jenkins, N.A., Copeland, N.G., Koentgen, F.,
Mohun, T. and Harvey, R.P.
The small muscle-specific protein Csl modifies cell shape and
promotes myocyte fusion in an insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-FEB-2001) Developmental Biology, Victor Chang Cardiac Research Institute, 384 Victoria St, Darlinghurst, Sydney; New South Wales 2010, Australia
                                                                                                  PAT 07-JAN-2002
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Sparrow, D. Growes, N., Schindeler, A., Yeoh, T., Biben, C., Wang, C.-C.,
Sparrow, D. Barnett, J., Jenkins, N.A., Copeland, N.G., Koentgen, F.,
Mohun, T. and Harvey, R.P.
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Mus musculus muscle-specific protein CSL (Csl) mRNA, complete cds.
28459 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 28403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 886;
                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 18 06-DBC-2001;
Medigene AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.4; DB 6;
Pred. No. 1.9e-10;
0; Mismatches 1;
                                                                                                DNA
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J. Cell Biol. 153 (5), 985-998 (2001)
21275706
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                                                                                            Sequence 18 from Patent W00192567. AX322774
                                                                                                                                                                                                                                                                                                                            organism="unidentified"
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/organism="Mus musculus"
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172 c 191 g
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/db_xref="taxon:10090"
/chromosome="X"
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AY026524.1 GI:14575061
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Best Local Similarity 98.2%;
Matches 56; Conservative (
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206. .463
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unclassified.
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AX322774
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AY026524
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Mus musculus chromosome UNK clone RP23-193Cl0, WORKING DRAFT SEQUENCE, 6 unordered pieces.
AC124177.1 GI:21392586
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| db_xxef="di:13940510"
|/translation="WKKQPTSNVRSIQANINIPMGAFRFGAGQPPRRKESTPGTAEGA
|PATPEEKKPVPGMKKFPGPVVNLSEIQNVKSELKYVPKGEQ"
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Rattus norvegicus SMPX protein (Smpx) mRNA, complete cds.
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1 (bases 1 to 892)
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
Identification human gene (SMPX) encoding a small muscular protein
Hum. Genet. 105 (5), 506-512 (1999)
                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                 197 GGCTAAGACCTTGTGAATATGTCGAAGCAGCCAATTTCCAACGTCAGAGCCATCCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 892)
Patzak,D.
Direct Submission
Submitted (26-MAR-2001) B.M.-Arndt-Uni, Inst. f. Humang., Fleischmannstr. 42-44, D-17487 Greifswald, Germany Location/Qualifiers
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                                              ;
                                                                             1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
       Score 42.6; DB 10; Length 943; Pred. No. 1.5e-05; 0; Mismatches 9; Indels 0.
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llarity 80.7%; Pred. No. 0.00026;
Conservative 0; Mismatches 11;
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/db_xref="taxon:10116"
<1._.892
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/gene="Smpx"
/note="alternate"
/evidence=experimental
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/codon_start=1
/product="SMPX protein"
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862. .867
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190. .447
              74.7%;
84.2%;
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Query Match
Best Local Similarity 84.2%
Best Local Similarity
Loca 48; Conservative
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Matches 46; Conserv
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/codon_start=1
/product="stretch responsive muscle (X-chromosome)"
/protein_id="cAc08493.1"
/db_xref="fg1:10178963"
/translation="MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
                                MMU245772 943 bp mRNA linear ROD 12-APR-2001
Mus musculus mRNA for stretch responsive muscle (X-chromosome)
                                                                                                                                                        Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musi
1 (bases 1 to 943)
Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Eastwood, M.,
Sassoon, D.A. and Coulton, G.R.
                                                                                                                                                                                                                                                             Identification of a novel stretch-responsive skeletal muscle gene
                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial
College School Of Medicine, SAF Building, Exhibition Road, South
Kensington, London SW7 2AZ, UNITED KINGDOM
Location/Qualifiers
                                                                                                  AJ245772.1 GI:10178962
Srmx gene; stretch responsive muscle (X-chromosome)
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923. .928
/gene="Srmx"
943
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/gene="Srmx"
/function="mRNA destabilising motif"
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gene="Srmx"
function="mRNA destabilising motif"
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40. .744
gene="Srmx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/10"
/db_xref="taxon:10090"
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1. 943
/gene="Srmx"
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/organism="Mus musculus"
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gene="Srmx"
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gene="Srmx"
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192 c
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gene="Srmx"
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'qene="Srmx"
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/qene="Srmx"
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'gene="Srmx"
                                                                      protein (Srmx gene).
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Kemp, T.J.
                                                                                                                                          house mouse.
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Gape

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Unitect Submassion

Unitect Submassion

Unitect Submassion

Unitect Submassion

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On May 11, 2001 this sequence version replaced gi:1374045.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by resolve all sequencing and the assembly was confirmed by resolve all sequencing mumbers given in the feature table with their source databases: Em; EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/kProjects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Purwer of information can be found at http://www.sanger.ac.uk/HGP/Chr6

RPII-80A23 is from the library RPCI-11:1 constructed by the group of Pieter de Jong. For further details see
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NECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone

RP11-80A23 It may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.

The true left end of clone RP11-295F4 is at 44843 in this sequence.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44942 bp DNA linear PRI 09-MAY-2001 sequence from clone RP11-80A23 on chromosome 6, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           DD 61167 GGATAATAATGCTTCTACATGTGGACAAAGGAAGTTTATAAATTTTTGAGCCGTCTAG 61223
                                                                                                                                                                                                                                            52.3%; Score 29.8; DB 2; Length 230579; 70.2%; Pred. No. 0.91; ive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
                                                                                                                                                                    503 others
40553. .79281

/note=assembly_name:Contig5"

79382. .137890.

/note="assembly_name:Contig6"

/note="assembly_name:Contig6"

/note="assembly_name:Contig7"

a 46384 c 47285 g 69857 t
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/db_xref="taxon:9606"
/chromosome="6"
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McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (12-UNN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 230579) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
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Insert size: 230079; sum-of-contigs
Quality coverage: 13.39 in Q20 bases; agarose-fp
Quality coverage: 11.47 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20048: Gontig of 10862 bp in length 20148: gap of unknown length 40522: gap of unknown length 40522: gap of unknown length 79281: contig of 38729 bp in length 79381: gap of unknown length 137890: contig of 58509 bp in length 137890: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 0% Sequencing vector: plasmid; 10% Sequencing vector: plasmid; 100% Chemietry: Dye-primer ET; 0% of reads Chemietry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 22840 bases at least Q40 Consensus quality: 228615 bases at least Q20 Consensus quality: 228615 bases at least Q20
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230579: contig of 92589 bp in length
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/note="assembly_name:Contig2"
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/note="assembly_name:Contig3"
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                                                                                                                                                                               The sequence of Mus musculus clone Unpublished
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/organism="Mus musculus"
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McPherson, J.D. and Waterston, R.H.
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/chromosome="UNK"
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/note="19 copies 2 mer aa 84%

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note="L1PA7 repeat: matches 6071. .6143 of consensus"
465. .10107
note="HERVL repeat: matches 2230. .2900 of consensus"
0436. .10536
note="HERVL repeat: matches 3322. .3433 of consensus"
1333. .11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .309 of consensus" 7975. .18298 note="LiM4 repeat: matches 3414. .3733 of consensus" 8029. .18654 note="LiM8 repeat: matches 5805. .6162 of consensus" 8655. .19567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="LiME3 repeat: "matches 5464. .6057 of consensus" 9822. .30120 "note="Liz repeat: matches 570. .963 of consensus" notes="Liz repeat: matches 570. .963 of consensus" 20248. .30476
                                                                                                                                                                                                                                                                              matches 7060. .7665 of consensus"
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                                                                                                                                                                                                         note="AluJb repeat: matches 1. .306 of consensus" 134. .6390 note="AluSg repeat: matches 40. .296 of consensus"
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                                                                                      .733. .1770
note="19 copies 2 mer gt 81% conserved"
1884. .4190
note="AluSx repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluSx repeat: matches 1. .307 of consensus" 2524. .23039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 36. .135 of consensus" 4343. .24707 note="THEIB repeat: matches 1. .364 of consensus"
                                     .262 of consensus"
                                                                      note="AluSx repeat: matches 1. .297 of consensus"
                                                                                                                                                       1297. .4610
/note="MER2 repeat: matches 2. .344 of consensus"
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                                  note="MIR repeat: matches 156.
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7923. .28474
/clone lib="RPCI-11.1"
44. .153
                                                                                                                                                                                                                                                                              note="L1MC4 repeat:
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Homo sapiens chromosome 6 clone RP11-435E4, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces.
                                                                                                                                36748. .36771

/note="12 copies 2 mer aa 100% conserved"

3678. .35592

/note="LiM1 repeat: matches 4673. .5403 of consensus"

37630. .38305

/note="LiDB3 repeat: matches 5476. .6150 of consensus"

38048. .38931

/note="LiDB3 repeat: matches 5796. .6173 of consensus"

38488. .38931

/note="LiDB3 repeat: matches 1617. .1701 of consensus"

39518. .39819

/note="Aludb repeat: matches 1. .307 of consensus"

39894. .40040
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Mammalia; Eutheria; Primates; Catarrhini; Hóminidae; Homo.
1 (bases 1 to 168235)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /noce="Alusc repeat: matches 1. .283 of consensus"
40463. .40552
/noce="45 copies 2 mer aa 66% conserved"
41063. .41387
/note="LiMA5 repeat: matches 5969. .6294 of consensus"
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Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 6, 2000 this sequence version replaced gi:9930948.
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                                                                                                                .2690 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 114. .262 of consensus" 0186. .40461
13626. 333920
'note="Alux repeat: matches 1. 297 of consensus"
15070. 35171
                                                                 /note="MADE1 repeat: matches 1. .78 of consensus"
5597. .35745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER3 repeat: matches 2. .165 of consensus"
42050. .42175
/note="L2 repeat: matches 2622. .2750 of consensus
42248. .42419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 21043 TTAGGATGAATATTGCTAAAAGACCCAGCTTGTAATGTTCCAGCCATCTAG 20990
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                                                                                                              'note="L2 repeat: matches 2551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2323.
2590. .42625
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8968 c 8053 g 13179 t
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Center code: SC
Web site: http://www.sanger.ac.uk
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AL357505.7 GI:9988391
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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AL357505
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157864 163565: contig of 5702 bp in length
163566 163665: gap of 100 bp
163666 168235: contig of 4570 bp in length.
Location/Qualifiers
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21482. .29095
/note="assembly fragment:00150
fragment chain: 2"
29196. .37170
/note="assembly_fragment:00938
fragment_chain: 2"
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fragment_chain:
37271. .43364
/note="assembly_fragment:00292
fragment_chain:3"
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fragment chain:
43465. .4822
/note="assembly_fragment:00664
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fragment chain:
4833. .5326
/note="assembly_fragment:00712
****acment_chain:4"
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/note="assembly_fragment:00773

fragment chain:1"

9487. .13859

/note="assembly fragment:00477

fragment_chain:1"
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13960. .21381
/note="assembly_fragment:01334
~~cment_chain:1"
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154923. 157763
/note="assembly_fragment:01169"
157864. 163565
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/note="assembly_fragment:00170"
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note="assembly_fragment:00240"
.11799. .114237
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note="assembly_fragment:00376"
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note="assembly_fragment:00812"
28872. .132807
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/note="assembly_fragment:00039"
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32908. .145229
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45330. .148554
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148655. .154822
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/note="assembly_fragment:00203
Fragment_chain:5"
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fragment_chain:1"
2937. .9386
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                                                                                                                         1. .168235
/organism="Homo sapiens"
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/clone_lib="RPCI-11.2"
1. .2836
                                                                                                                                                                                db_xref="taxon:9606"
chromosome="6"
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                                                                                            FEATURES
                                                                                Assembly program: XGRA4; version 4.5
Assembly program: XGRA4; version 4.5
Assembly program: XGRA4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 155210 bases at least Q30
Consensus quality: 160764 bases at least Q30
Insert size: 165635; sum-of-contigs
Insert size: 183829; 3.1% error; agarose-fp
Quality coverage: 2.46x in Q20 bases; sum-of-contigs Quality
coverage: 2.33x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94153 94222: GORLIGO 1 7025 bp in length 11699 111798: gap of 100 bp 11798: gap of 11438 11437: concig of 2439 bp in length 119218 11921: concig of 4774 bp in length 119112 11921: gap of 100 bp 119212 119211: concig of 6783 bp in length 119212 125994: concig of 6783 bp in length 119212 125994: concig of 6783 bp in length 125995 126094: gap of 100 bp 126095 128771: concig of 6783 bp in length 128872 128871: gap of 100 bp 132908 145229: concig of 1325 bp in length 132908 145229: concig of 100 bp 14555 148654: gap of 100 bp 14655 148654: gap of 100 bp 14855 14854: gap of 100 bp 14855 14854: gap of 100 bp 154823 157423: concig of 6168 bp in length 154823 157763: concig of 2841 bp in length 157764 157863: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126: gap of 100 bp
64045: contig of 10619 bp in length
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53326: contig of 4994 bp in length
53426: gap of 100 bp
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9487 13859; contig of 4373 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bA435E4
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21482 29095: conf
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Search completed: April 15, 2003, 20:55:10 Job time: 248.143 secs
                                                                           cytochrome b.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pissipedia, Mustelidae, Mustellinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masuda, R.
Direct Submission
Submitted (17-JAN-1994) Ryuichi Masuda, Hokkaido University,
Chromosone Research Unit, Faculty of Science; North 10, West 8,
Kita-ku, Sapporo, Hokkaido 060-0810, Japan
(E-mail:masudary@ees.hokudai.ac.jp, Tel:81-11-706-3541,
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 375)
Masuda, R. and Yoshida, M.C.
A molecular phylogeny of the family Mustelidae (Mammalia,
Carnivora), based on comparison of mitochondrial cytochrome b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                           2636 others
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Pred. No. 22;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                     cytochrome b.
Mustela zibellina muscle mitochondrion DNA.
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47.0%; Score 26.8; DB
Best Local Similarity 68.5%; Pred. No. 13;
Matches 37; Conservative 0; Mismatches
                                                                        a 29954 c 31524 g 53321 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequences
Zool. Sci. 11 (4), 605-612 (1994)
95038277
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ilarity 71.4%;
Conservative 0
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Matches 35; Conserv
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AUTHORS
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RESULT 15 L77957/c

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L77957 401 bp DNA linear MAM 04-JAN-2000 Martes zibellina cytochrome b (cytb) gene, partial cds; mitochondrial product.
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ILTGLFLAMHYTSDTATAFSSVTHICRDVNYGWIIRYMHANGASMFFICLFLHVGRGL
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Are there two species of pine marten in North America? Genetic and Are there two species of pine marten in North America? Genetic and evolutionary relationships within Martes
(in) Proulx, G., Goddard, R. and Bryant, H. (Eds.);
PARTES: TAXONOWY, ECOLOGY, TECHNIQUES, AND MANAGEMENT: 15-28;
Provincial Museum of Alberta, Edmonton (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-APR-1997) Department of Biology, Memorial University
of Newfoundland, St. John's, Newfoundland AlB 3X9, Canada
                                                                                                                                             Martes zibellina.
Mitochondrion Martes zibellina
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Pissipedia, Mustelidae, Mustelinae,
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    .401
    /organism="Marteg zibellina"

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Pred. No. 22;
0; Mismatches
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1. .>401
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/gene="cytb"
/note="putative"
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Best Local Similarity 71.4%;
Matches 35; Conservative
                                                                                                   L77957.1 GI:6670761
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nucleic

Run on:

Seguence:

Searched:

Database

Regult No.

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W13738 mb32a12.r1
W18758 mb65b11.r1
W18392 mb88e01.r1
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F9260 Fetal heart Homo saplens cDNA clone F9260 5' end, mRNA
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AA060214 mj65h06.r
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 216)

Hwang, D.M., Pung, Y.W., Wang, R.X., Laurenssen, C.M., Ng, S.H., Lam, W.Y., Tsui, K.W., Pung, K.P., Waye, M., Lee, C.Y. and Liew, C.C.

Analysis of expressed sequence tags from a fetal human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library
Genomics 30 (2), 293-298 (1995)
96163883
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6177328915
Email: cliewerics bwh.harvard.edu
Seq primer: GGTGGGGACGACTCCTGGAGCC.
S
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                    BF126275
BF72902
BF790636
BF693124
BF575112
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BF790243
AU083330
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W13738
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W18392
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R58129
R58129.1 GI:828187
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R58129
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 R58129 F9260 Fetal
AA092554 115591.8e
AA249531 jj5022.8e
N56276 JJ5022F Hum
AA094015 C11599.8e
A1355905 3055-10R-
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7808.593 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                                                  - nucleic search, using sw model
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/loce="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."
63 a 49 c 57 g 56 t
                                                                 15022.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
CDNA 5', mRNA sequence.
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Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 225)
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JJ5022F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA
clone JJ5022 5', mRNA sequence.
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BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' CCAAATTAACCCTCACTAAAGGG 3'
Location/Qualifiers
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75 Francis St. Boston, MA 02115, USA
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CDNAs from human fetal heart (1997)
Unpublished (1997)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
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Unpublished (1995)
Contact: Liew CC
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Mammalia; Eutheria;
1 (bases 1 to 225)
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N56276
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              /db xare="none bagiess" / db xare="responsible bagiess" / db xare="responsible bagiess" / dcone="responsible bagiess" / dcone=
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/ Organism="Homo sapiens"
/ do ramism="Homo sapiens"
/ do xref="taxon:9606"
/ clone lib="Human fetal heart, Lambda ZAP Express"
/ lab_host="E. coli XL1-Blue"
/ lab_host="E. coli XL1-Blue"
/ note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dr adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214)
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BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
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1 Similarity 100.0%; Pred. No. 3.1e-10;
57; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 3.2e-10;
Conservative 0; Mismatches 0;
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Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Fat: 6177328915
Fax: 6179750995
organism="Homo sapiens"
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Unpublished (1996)
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Gaps

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EST 20-FEB-1996

FEATURES

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/Lissue_type="heart muscle"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="E. coli"
/note="Organ: heart; Vector: Lambda ZAP II, pKSII-;
Site_1: Not1; Site_2: Not1; Human heart cDNA library was
constructed in Lambda ZAP II vectors using Not1 linkers.
Clones from the primary cDNA library were deposited into
95 well trays for storage and retrieval. The 'Isolation of
chromosome-specific genes by reciprocal probing of arraed
cDNA and cosmid libraries' (Human Molecular Genetics, 1995
, Vol. 4, No 8; ppl373-1380) provided cDNA-Clones as
plasmids (vector pKSII-, E. coli)."
                                                                                                                                                                                                                                           EST 31-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: patzak@rz.uni-greifswald.de ( mwehnert@rz.uni-greifswald.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single path sequence (manual checked and edited) with a vector primer of clone xh8Hll. Sequence starts with base 1 following the determined vector sequence (ACGCGGTGGGGGCGCT, small letters: NotIsite). ESTS 305-10R-8Hll-2, 3055-10U-8Hll-2 (with vector primers) and 8Hll-Rl-C8-0Z, 8Hll-U1-C7-0Z (with gene specific primers) provide a contig of the whole insert of clone xh8Hll. Finest Length: 850 Std Error: 10.00 Plate: 8 row: H column: 11 Seq primer: 3055-10R (like Ml3 reverse)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      AI355905
3055-10R-8H11-2 Human heart cDNA (CCLee) Homo sapiens cDNA clone xABH11 3', mRNA sequence.
AI355905.1 GI:6649247
                  Gaps
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
2 Lobaces 1 to 360)
3 Zhuchenko, O., Patzak, D. and Wehnert, M.
ESTS of clone xh8H11 (human heart, M.
ESTS of clone xh8H11 (human heart, M.
Unpublished (1999)
Other ESTS: 8H11-R1-C7-OZ, 3055-10U-8H11-2
Contact: Patzak D., submitter; (Wehnert M.; supervisor)
Department of Molecular Human Genetics
Institut for Human Genetics
Fleischmannstr. 42/44, D-17487 Greifswald, Germany
Tel: 449 3834 8653-78(-74)
                                                                                          152 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 57
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                                                              1 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG
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               0; Indels
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="xh8H11"
/clone=1lb="Human heart cDNA (CCLee)"
/sex="male"
               0; Mismatches
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Best Local Similarity 100.0
Matches 57; Conservative
               57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         human.
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                                                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 bp mRNA linear EST 25-OCT-1996 cli599.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens AA094015
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone lib="Human fetal heart, Lambda ZAP Express"
/lab host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI, Site 2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dr adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into
                                                                                                                                                                                                                      /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site 1: EcoRi; Site 2:
Xhoi; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a Xhoi-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with Xhoi, for directional cloning into
predigested lambda ZAP Express."

8 49 c 57 g 56 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 284)
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FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
Location/Qualifiers
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74 c 70 q 61 t
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Harvard Medical School
Francis St. Boston, MA 02115, USA
Tel: 6177228915
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Tel: 6177328915
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seg primer: TCCAAAGAATTCGGCACGAG.
                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="JJ5022"
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Email: cliew@rics.bwh.harvard.edu
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Unpublished (1996)
Contact: Liew CC
                                                                                                    Location/Qualifiers
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Best Local Similarity
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AUTHORS
TITLE
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ACCESSION

PEATURES

RESULT 5

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DEFINITION

RESULT 7 AA211521 ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE

COMMENT

FEATURES

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University of Iowa
University of Iowa
451 Ecketein Medical Research Building Iowa City, IA 52242, USA
451 Ecketein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DHIOB (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: 19773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I, Site_2: Not I; U.E-DXO is a coNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF791178 12-JAN-2001 156 bp mRNA linear EST 12-JAN-2001 602251278F1 NIH MGC_81 Homo sapiens cDNA clone IMAGE:4338594 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI)."

142 c 163 g 186 t 2 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 756)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 184
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/dev_stage="fetal"
/lab_host="DH10B (Life Technologies)
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0
                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 57; DB 14;
Similarity 100.0%; Pred. No. 4.2e-10;
57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="UI-E-DXO-agn-i-12-0-UI"
/clone_lib="UI-E-DXO"
                                                                                   Genome Res. 6 (9), 791-806 (1996)
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[ (base) Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (base) Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (base) Butheria; Primates; Catarrhini; Hominidae; Homo.

Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Wohldman, P., Wateretch, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM697544 1719 bp mRNA linear EST 28-FEB-2002 UI-E-DX0-agn-i-12-0-UI.rl UI-E-DX0 Homo sapiens cDNA clone UI-E-DX0-agn-i-12-0-UI 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -26ml3 rev1 ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
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                                      AA211521
ZNSSD01.rl Stratagene muscle 937209 Homo sapiens cDNA clone
NAMCE:562057 5', mRNA sequence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 57; DB 9; Length 501; 100.0%; Pred. No. 3.8e-10;
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/dev_stage="adult"
/lab_host="SOLR (kanamycin_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Stratagene muscle 937209"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:4595347"
/db_xref="taxon:9606"/
/clone="IMAGE:562057"
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                                                                                                                                                                       AA211521.1 GI:1810175
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Fax: 314 286 1810
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Matches

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nRNA sequence.
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BF126275
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                                                                                                                                                                                                         /do_ranism="Homo sapiens"
/do_rate="Homo sapiens"
/do_rate="taxon:9606"
/clone="lib="NIH_MGC_81"
/lab_bbst="blibe" (Ti phage-resistant)"
/lab_bbst="blibe" (Ti phage-resistant)"
/note="Organ: muscle (skeleta); Vector: pDNR-LIB
/note="Organ: muscle (skeleta); Vector: pDNR-LIB
(clontech); Site_1: Sfil (ggccgccccggcc); Site_2: Sfil
(ggccattateggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence:
5'-ATTCTAGAGGCCCCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF671987 193 bp mRNA linear EST 21-DEC-2000 602152408F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293721 5',
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Umpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCMI141 row: o column: 02

High quality sequence stop: 665.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1214 row: 1 column: 19
High quality sequence stop: 619.
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100.0%; Score 57; DB 12; Length 756;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 57; Conservative 0; Mismatches 0; Indels (
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/db xref="taxon:9606"
/clone="INAGE:4293721"
/clone llb="NIH MGC 81"
/lab_host="DH10B (TI phage-resistant)"
Tissue Procurement: CLONETECH Laboratories, Inc
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158 c
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AUTHORS
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/clone_lib="NIH MGC_76"
/lab_host=="NIH MGC_76"
/lab_host=="NIH MGC_76"
/lab_host=="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgctcggcc); Site_2: Sfil (ggcattatggcc); S' and
3' adaptors were used in cloning as follows: S' adaptor
sequence: S'-CACGGCATATGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGAGGCGACATGATGGT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enamialia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 826)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CLONE distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 651.
(Clontech); Site 1: Sfil (ggcgctctggcc); Site 2: Sfil (ggccattatggcc); S' and 3' adaptors were used In cloning as follows: 5' adaptor sequence: 5' CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5' ATTCTAGAGGCCGAGGCGCGCATG-dT (30) BN-3' (where B = A, 5' or G and N = A, C' G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 57; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 57; Conservative 0; Mismatches 0;
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/clone="IMAGE:3934333"
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

FEATURES

DEFINITION

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RESULT 12

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1. .867
/organism="Homo sapiens"
/do_xref="taxon:9606"
/clone=Tib="NIH MGC_81"
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B. (Dases 1 to 871)

S. (Dases 1 to 871)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLCM1056 row: f column: 13
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 867)
III (bases 1 to 867)
III (Mag.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1212 row: 1 column: 14
High quality sequence stop: 514.
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                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/clone="Indage:429308"
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as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.04.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                              BF672902 855 bp mRNA linear EST 21-DEC-2000 602152759F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293878 5',
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BF790636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1142 row: e column: 15
High quality sequence stop: 682.
Location/Qualifiers
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1 (bases 1 to 855)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                     82 GGATAAGACTGCATGAATATGTCGAAACAGCCAGTTTCCAATGTTAGAGCCATCCAG 138
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KEYWORDS SOURCE ORGANISM

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RESULT 13

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BF790636

BASE COUNT ORIGIN

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Gaps

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Search completed: April 15, 2003, 22:02:31 Job time : 119.221 secs
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                                                                                                       /db xref="texon:9606"
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/Clontech); Site 1: Sfil (ggccgcctcggcc); Site 2: Sfil
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and 3' adaptor sequence: 5' -CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5' -CATGGCCATTATGGCC-3'
c, or G and N = A, C, G, or T).
Average insert size
1.55 kb (range 1:0-4:0 kb): 15/15 colonise contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
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Rom sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 879)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

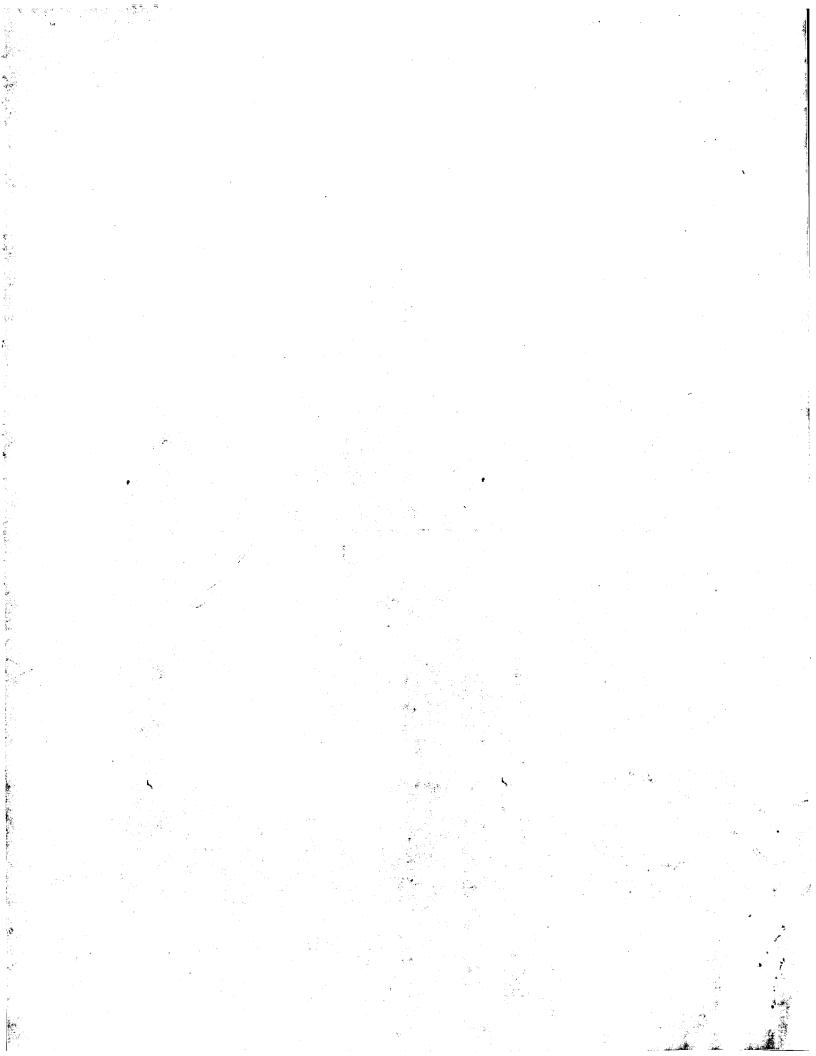
Flagh quality sequence stops: S95.

High quality sequence stops: 595.

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4289735"
/clone="IMAGE:4289735"
/clone="IDH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/noce="Organismuscle-/cskeletal); Vector: pDNR-LIB
(Clontech): Site_1: SiI (specucctoggec); Site_2: SfiI
(speccattatggec): 5. and 3. adaptors were used In cloning
as follows: 5. adaptor sequence: 5.-CACGGCCATTATGGCC-3.
and 3. adaptor sequence: 5.-CACGGCCATTATGGCC-3.
5.-ATTCTAGAGGCCGAGCGCGCCACATG-dT(30)BN-3. (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
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602134792P1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289735 5',
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                                                             1. .871
/organism="Homo sapiens"
High quality sequence stop: 575.
Location/Qualifiers
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inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)." 239 g 208 t 1 others
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100.0%; Pred. No. 4.40-10;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 57; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Email: est6watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -28m.3 rev1 ET from Amersham
High quality sequence stop: 191.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      209 GCANATATCAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 268
, Vol. 4, No 8; pp1373-1380) provided cDNA-Clones as plasmids (vector pKSII-, E. coli)."
109 a 92 c 88 g 71 t
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AA214155

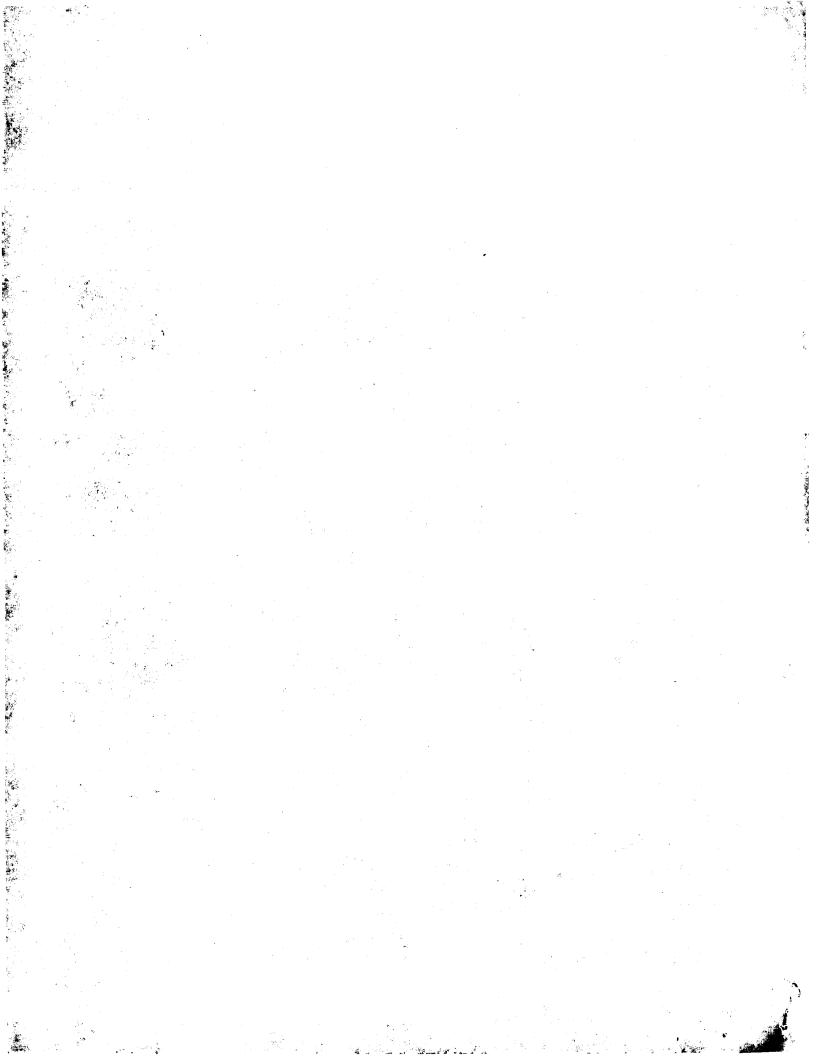
AA214155

AA214155.1 GI:1812792

AA214155.1 GI:1812792
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                                                                                                                                                            / Match 100.0%; Score 87; DB 9; I Local Similarity 100.0%; Pred. No. 6.3e-17; les 87; Conservative 0; Mismatches 0;
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/db_xref="GDB:4595701"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AAAGAATGTACTCCTGAAGTGGAGGAG 295
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Gaps

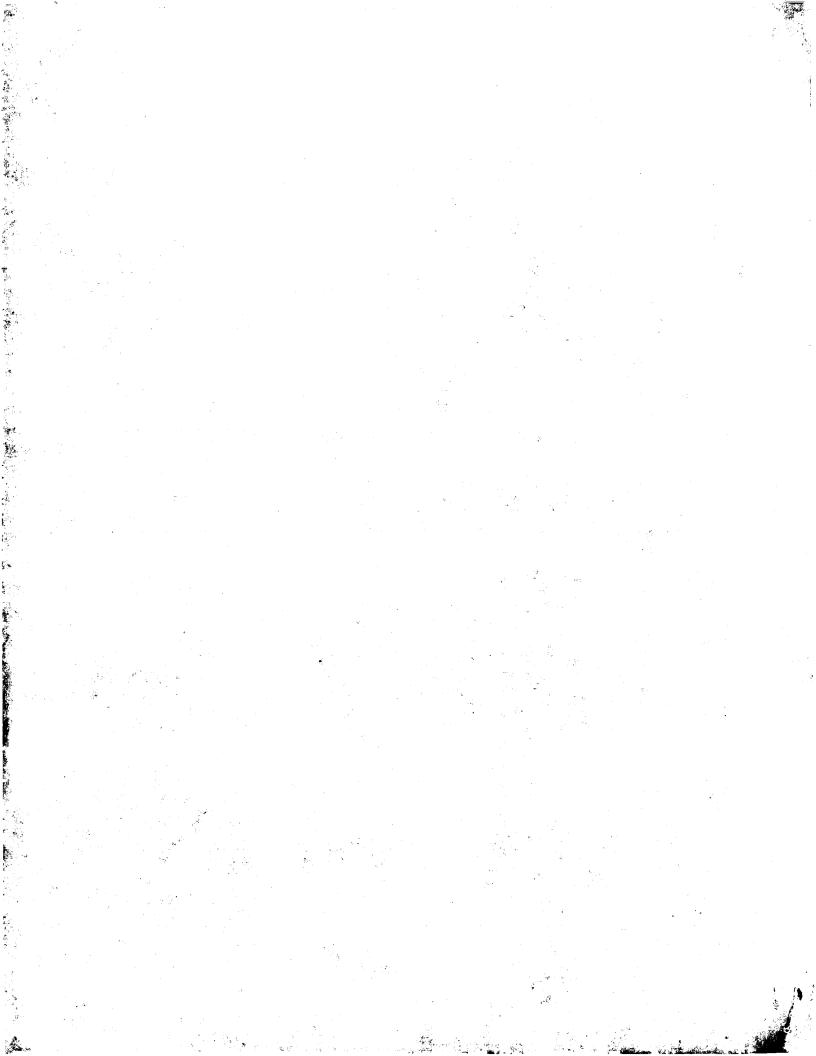
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/dev stage="fetal" |
// Lab_host="Petal" |
// Lab_host="DH10B (Life Technologies) (T1 phage resistant) |
// Lab_host="DH10B (Life Technologies) (T1 phage resistant) |
// Note="Organ: eye; Vector: pT713-Fac (Pharmacia) with a modified polylinker; Site=1: EccR I; Site=2: Not I;
UI-E-DXO is a CDNA library containing the following tisque(s): fetal eyes: The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EccR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tall. The sequence tag for this library is AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). "
                                                                                                                                                                                                                                                                                                                                                 EST 28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapieng Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordate; Catarrhini; Hominidae; Homo. 1 (bases 1 to 719)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                       BM697544 T19 bp mRNA UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo BUI-E-DXO-agn-i-12-0-UI 5', mRNA sequence.
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/db xref="taxon:9666"
/clone="Ul-E-DX0-agn-i-12-0-Ul"
/clone_lb="UT-E-DX0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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RESULT 6



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Sequence:

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Scoring table:

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BF126275 601650456
BF672902 602152759
BF67212 602152759
BF67212 602152580
BF790243 602249777
AU08330 AU08330
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BG358790 BOWNS1-01
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BF693124 602080151
W97451 M697451
A1098485 UC06C10.r
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BQ554133 H4026C08-
BG794218 UTSW_SMIG
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W13738 mb32a12.r1
W18646 mb98a05.r1
W18392 mb88e01.r1
A29828 mc07b11.r1
A434782 ve23c01.r
A1035961 ub50b12.r
A1033164 mi37c11.r
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1 (Dases 1 to 206)

Hwang, D.M., Fung, Y.W., Wang, R.X., Laurenssen, C.M., Ng, S.H., Lam, W.Y., Tsui, K.W., Fung, Y.W., Waye, M., Lee, C.Y. and Liew, C.C. Analysis of expressed sequence tags from a fetal human heart cDNA library
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F9260 Fetal heart Homo sapiens cDNA clone F9260 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tal: 6177328915
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GGTGGCGACGACCGACCTCCTGGAGCC.
1. 206
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                       BF672902
BF672112
BF672112
BF790243
AU083330
BF790243
BF7902305
BF7902365
BF721521
BF721521
BF721521
BF7212365
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BQ554133
BG794218
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 R58129
R58129.1 GI:828187
EST.
 Contact: Liew CC
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W07478 za96c10.r1
A1355905 3055-10R-
AA214155 zn58f10.r
BM697544 UI-E-DX0-
BF791178 602251278
                                                                         April 15, 2003, 16:52:31 ; Search time 180.443 Seconds (without alignments) 7808.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                    1 gcaaatatcaatattccaat......gtactcctgaagtggaggag
                                                                                                                                                                                                                                               32308132
   GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
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/organism="Homo sapiens"
/db_xref="F9560"
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/clone=lib="Fetal heart"
/lab_host="E. coli Y1,00"
/note="Vector: Lambda gt22; Site 1: NotI; Site 2: SalI;
mRNA was purified from human fetal hearts (10-12 weeks).
cDNA was constructed using a NotI-Oligo dT adaptors-primer.
SalI adaptors were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22.
Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333) "
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/dev_stage="19 weeks"

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/dev_s
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za96cilo.rl Soares fetal lung NbHill9W Homo sapiens cDNA clone
IMAGE:300402 5', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 320)
M., Hillier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
The Washh-Merok EST Project
Uppublished (1995)
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High quality sequence stop: 279.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 5.3e-17;
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ilarity 100.0%;
Conservative 0;
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/usb. heart muscle"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="E. coli"
/note="Corgan: heart, Vector: Lambda ZAP II, pKSII-;
Site i: NotI, Site 2: NotI; Human heart cDNA library was constructed in Lambda ZAP II vectors using NotI linkers.
Clones from the primary CDNA library were deposited into 96-well trays for storage and retrieval. The 'Isolation of chromosome-specific genes by reciprocal probing of arraed cDNA and cosmid libraries' (Human Molecular Genetics, 1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3655-10R-8H11-2 Human heart cDNA (CCLee) Homo sapiens cDNA clone xh8H11 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: patzak@rz.uni-greifswald.de ( mwehnert@rz.uni-greifswald.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single path sequence (manual checked and edited) with a vector primer of clone xh8H11. Sequence starts with base 1 following the determined vector sequence (ACGCGGTGGCGGCT, small letters: NotI-site). ESTS 3055-10R-8H11-2. 3055-10W-8H11-2. (with vector primers) and 8H11-R1-C8-0Z, 8H11-U1-C7-0Z (with gene specific primers) provide a contig of the whole insert of clone xh8H11. Insert Length: 850 Std Brror: 10.00 late: 8 row: H column: 11 Seq primer: 3055-10R (like M13 reverse) High quality sequence stop: 360.
          normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                    212 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 271
                                                                                                                                                                                                                                                                                                    1 GCAAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory O., Parzak, D. and Wehnert, M.

ESTS of clone xh8H11 (human heart)
Unpublished (1999)
Other ESTS: 8H11-R1-C8-OZ, 8H11-F1-C7-OZ, 3055-10U-8H11-2
Contact: Parzak D., submitter; (Wehnert M.; supervisor)
Department of Molecular Human Genetics
Institut for Human Genetics
Fleischmannstr. 42,44, D-17487 Greifswald, Germany
Tel: +49 3834 8653-78 (-74)
                                                                                                                                                                                                                                                      ó,
(Pharmacia). Library went through one round of
                                                                                                                                                                                                 Length 320;
                                                                                                                                                                                                                                                      Indels
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/sex="male"
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                      Score 87; DB 14;
Pred. No. 6.1e-17;
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                                                                                                                                                                                                                                                      0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="xh8H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 AAAGAATGTACTCCTGAAGTGGAGGAG 298
                                                                                                                                                                                                                                                                                                                                                                                                               61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
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                                                                                                                              83 C
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Best Local Similarity 100.0
Matches 87; Conservative
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AI355905
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1 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGA
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KEYWORDS
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BM697544
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1 (bases 1 to 480)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,Schellenberg,K., Soares,M.B., Tan,G.C., Rifkin,L., Rohlfing,T., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                EST 01-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 852 Std Brror: 0.00
                                                                                                                                                                      209 GCAAATATCAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 268
                                                                                                                                                1 GCAAATATCAATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
, Vol. 4, No 8; ppl373-1380) provided cDNA-Clones as plasmids (vector pKSII-, E. coli)."

92 c 88 g 71 t
                                                                                                                       0; Саря
                                                                                                                                                                                                                                                                                                                                        AA214155
zn58f10.rl Stratagene muscle 937209 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                    Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 87; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 87; Conservative 0; Mismatches 0; Indels
                                                                                                                     Indels
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                                                                                    ; Score 87; DB 9; 1; Pred. No. 6.3e-17; 0; Mismatches 0;
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                                                                                                                                                                                                                                        269 AAAGAATGTACTCCTGAAGTGGAGGAG 295
                                                                                                                                                                                                                    61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 87; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                            AA214155.1 GI:1812792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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Gaps

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/uradians"Homo sapiens"

/db_xref='taxon:9606"

/clone='Ul-B-DX0-agn-i-12-0-UI"

/clone='Ul-B-DX0-agn-i-12-0-UI"

/clone='Ul-B-DX0"

/tissue_types"fetal eyes"

/dev_tages"fetal"

/lab_host="DH108 (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polyllinker; Site 1: EcoR i; Site 2: Not I;

UI-B-DX0 is a cDNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double strandc cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI): "
                                                                                                                                                                                                                                                                                                                                                                     BM697544 119-0-UI.rl UI-E-DXO Homo sapiens CDNA clone UI-E-DXO-agn-i-12-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIELE CRETERING MEDICAL RESEARCH Building Iowa City, IA 52242, USA Tel: 319 335 8250

Fax: 319 335 9565

Fax: 319 335 9565

Email: mosares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencial by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencial by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencial by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgan.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 719)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                  216 AAAGAATGTACTCCTGAAGTGGAGGAG 242
                                                                                                                              61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .719
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BF126275 826 bp mRNA linear EST 24-OCT-2000 601650456F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:3934333 5',
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                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM141 row: o column: 02
High quality sequence stop: 665.
High quality sequence stop: 665.
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/clone="IMAGE:4297721"
/clone=line=NIH MGC &11"
/clone=line=NIH MGC &11"
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/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/clontech); Site 1: Sfil (ggcgcctcggcc); Site 2: Sfil
/ggcacattatggcc); S, and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC'3
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC'3
and 3'-CACGGCCACATGGCGCCACATGGCC'3
and 3'-CACGGCCCATTATGGCC'3
and 3'-CACGGCCCACATGGCCCACATGGCC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (base 1 to 826)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
602152408F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 87; DB 12;
100.0%; Pred. No. 8.2e-17;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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                                  mRNA sequence.
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TITLE
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                                                                                                                                                                                                                                                                                                              BF791178 12-JAN-2001 756 bp mRNA linear EST 12-JAN-2001 602251278F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338594 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
WIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                        185 GCAAATATCAATATTCCAATGGGGGCCTTTCGGCCAGGAGCAGGTCAACCCCCCCAGAAGA 244
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                                                                                                                    61 AAAGAATGTACTCCTGAAGTGGAGGAG
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BF791178
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Length 793; 0; Indels

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/clone lib=NNIH MGC 81"
/lab host="DHIOB (TI phage-resistant)"
/lab host="DHIOB (TI phage-resistant)"
/note="Organ muscle (skeletal); Vector: pDNR-LIB
/note=ongan muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: $fil (ggcgcgctcggcc); Site 2: Sfil
(ggccattatggcc); 5: and 3' adaptors were used In cloning
as follows: $' adaptor sequence: $'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: $'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: $'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: $'-CACGGCCATTATGGCC-3'
c, or G and N = A, C, G, or T). Average insert B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 879)

S NIH-MGC http://mgc.nci.nlh.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CLORA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://mage.llnl.gov

Plate: LLCWILLS I row: h column: 24
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/clone=lib="NHMAGE:4289735"

/clone=lib="NHH MAGC 81"

/lab_host==DH10B (TI phage-resistant)"

/note="Organ: mused-e (skeletal); Vector: pDNR-LIB

/note="Organ: mused-e (skeletal); Vector: pDNR-LIB

(Clontech); Site_1: SfiI (ggccgcccggcc); Site_2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used In cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGAGGCCGAGGCGCCGACATG-dI(30)BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GCAAATATCAATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 217
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                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4293878"
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Location/Qualifiers
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Matches 87; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1142 row: e column: 15
High quality sequence stop: 687.
Location/Qualifiers
               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM774 row: p column: 14
High quality sequence stop: 651.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Unpublished (1999)
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="INAGE:4328154"
/clone="INAGE:4328154"
/clone="INAGE:4328154"
/clone="INAGE:4328154"
/clone="INAH MGC 81"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(clontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used In cloning
as follows: S' adaptor sequence:
S' -ATTCTAGAGGCCGAGGCGCGACATG-dT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA).

Alto, CA).
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El (Dases 1 to 909)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: capabs-romail.ih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CLONETECH LABORATORIES (SIGNATION LIMICAL)

CLOR distribution: MGC clone distribution information can be the pi//image.llnl.gov

Plate: LLCM1187 row: i column: 19

High quality sequence stop: 626.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    BF790243 909 bp mRNA linear EST 12-JAN-2001
602249777F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4328154 5',
                                         100.0%; Pred. nc.
                                                                                                                                               219 AAAGAATGTACTCCTGAAGTGGAGGAG 245
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                                                                                                                        61 AAAGAATGTACTCCTGAAGTGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BF790243
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/db xref="taxon:9606"
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/clone="INAGE:4293763"
/clone="INAGE:4293763"
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/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(clontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 4' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 5' ATTCTAGAGGCCGAGGACATG-dT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF672126 906 bp mRNA linear EST 21-DEC-2000 602152580F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293763 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbe_r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1141 row: p column: 20
High quality sequence stop: 621.
Location/Qualifiers ...
1. 906
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I (Dases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                              190 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 249
                                                                                                                                                                                                                                                                                                                                  1 GCAAATATCAATATTCCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
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0
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100.0%; Score 87; DB 12; Length 906;

Best Local Similarity 100.0%; Pred. No. 8.5e-17;

Matches 87; Conservative 0; Mismatches 0; Indels (
                                                                                                                                            1 others
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Pred. No. 8.5e-17;
                                                                                                                                            208 t
                                                                                                                                                                                                                                                                                   0; Mismátches
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ilarity 100.0%;
Conservative 0
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(P)
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                                                                                                                  Alto,
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Best Local Similarity
Matches 87; Conserv
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VERSION

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                                                                                    228 GCAAATAICAATATICCAATGGGAGCCTITCGGCCAGGAGCCAGGACCCCCCAGAAGA 287
                                      Gaps
                                                                 1 GCAAATATCAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
                                    ó,
100.0%; Score 87; DB 12; Length 909; 100.0%; Pred. No. 8.6e-17;
                                                                                                                                                                                                                                                   linear
                                  0; Indels
                                                                                                                                                                                                                                                     mRNA
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AU083330
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Homo sapiens
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B I (bases 1 to 867)
S II (bases 1 to 867)
S NHH-MGC http://mgc.nci.nih.gov/.
I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
CLONE LIBRARIA: Tow: 1 column: 14
High quality sequence stop: 514.
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0
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                                                                                                                      Cavia porcellus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.

1 (bases 1 to 261)
Nakajima,T., Oshima,T., Wada,H., Ikeda,K. and Takasaka,T.
Characterization of novel and identified genes in guinea pig organ
of Corti cDNA library
AU083330 Guinea pig organ of Corti pKF3 library Cavia porcellus CDNA clone CLN11003, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCTGGGCAACCCCCCAGAAGA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gtrain="Hartley"
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/clone=lib="Guinea pig organ of Corti pKF3 library"
/tissue_type="organ of Corti"
/dev_stage="organ of Corti"
/dev_stage="organ of Corti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.8%; Score 79; DB 9; Length 261; Best Local Similarity 94.3%; Pred. No. 1.8e-14; Matches 82; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                  Tohoku University
Aoba-yama 01, Sendai, Miyagi 980-8579, Japan
TTE1: 81-22-217-4048
Fax: 81-22-217-6939
                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Takaya Nakajima
Micromachine laboratory, Dept. of Mech. Eng.
                                                                                                                                                                                                                                                                                                                                                                                                                 Smail: nakajima@wadalab.mech.tohoku.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Cavia porcellus"
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                                           AU083330.1 GI:9988038
                                                                                                       domestic guinea pig.
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BF790636
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/clone="IMAGE:4137821"
/clone="Ib="NIH_MGC 81"
/clone="Ib="NIH_MGC 81"
/clone="Organ: muscle (akeletal); Vector: pDNR-LIB
/note="Organ: muscle (akeletal); Vector: pDNR-LIB
/note="Organ: muscle (akeletal); Vector: pDNR-LIB
(clontech); Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil
(ggccattagggcc); S' and 3' adaptors were used In cloning
as follows: S' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5' CACGGCCATTATGGCC-3'
c, or g and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
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/db_xref="taxon:9606".
/lab_host="bar Fetal heart, Lambda ZAP Express"
/lab_host="bar Coli"
/note="Vector: Lambda ZAP, Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP, Site_1: C.C. Lidew, Unitvorsity of
Toronto, Ontario, Canada. mRNA was purified from human
fetal hearts (8-10 wks). cDNA was synthesized using at
form digestion with XhoI; for dispects were ligated,
followed by digestion with XhoI. for directional cloning
into predigested lambda ZAP Express.
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Manago,D.,, Fung.Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Llew,C.C.
Analysis of expressed sequence tags from a fetal human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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Pred. No. 2.3e-13;
0; Mismatches 0; Indels
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Shatin, New Territories, Hong Kong
Fax: 26035123
Email: ldskok@spider.net.hk
Seq primer: Forward Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .394
/organism="Homo sapiens"
                                                                    organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AAAGAATGTACT-CCTGAAGTGGAGGAG 87
                                                                                                      db xref="taxon:9606"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 g
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Department of Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA389647
AA389647.1 GI:2042633
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98.9%;
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Matches 87; Conservative
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93 c

126 a

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1; Gaps
                                  Query Match 86.2%; Score 75; DB 9; Length 394; Best Local Similarity 98.9%; Pred. No. 3.7e-13; Matches 86; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   227 AAAGAATGTACTCCTGAAGTGGAGGAG 253
                                                                                                                                     61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
94 g
 BASE COUNT
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Search completed: April 15, 2003, 22:02:32 Job time : 181.443 secs

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FEATURE
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Sequence 10, Appl
Sequence 102, App
                                                                           April 15, 2003, 18:42:01; Search time 5.14773 Seconds (without alignments) 5183.040 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 191, A
Sequence 11, Al
Sequence 7, Apl
Sequence 94, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101,
Sequence 2, A
Sequence 2, A
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Sequence 7
Sequence 3
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-484-970B-111

US-08-742-185-102

US-08-742-185-102

US-08-015-973-2

US-08-448-164-2

US-09-816-703A-1

US-09-544-193-3

US-09-54-193-3

US-09-54-193-3

US-09-55-107-107-107-108-191

US-09-103-875-11

US-08-86-340-7

US-09-103-875-11

US-08-103-875-11

US-08-103-875-11

US-08-103-875-11

US-08-316-346-1

US-08-316-345-1

US-08-847-655-1

US-08-847-655-1
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                                                                                                                                                                                                                                  441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      sw model
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Gapop 10.0 , Gapext 1.0
                                                      - nucleic search, using
                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                US-09-647-019-8
87
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Perfect score:
                                                                                                                                                                                        Scoring table:
                                                    nucleic
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                                                                                Run on:
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RESULT 2
US-09-780-173A-10
Sequence 10, Application US/09780173A
Sequence 10, Application US/09780173A
Sequence 10, Application US/09780173A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
FILE REFERENCE: RTS-0165
CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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339, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
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Sequence 9, 7
Sequence 339,
Sequence 8, 7
Sequence 8, 7
Sequence 17,
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100.0%; Score 87; DB 4; Length 909;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 87; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 021656.2CB1
US-09-484-970B-111
US-09-124-541-2

US-09-117-860-36

US-08-111-757-33

PCT-US95-05980-33

US-08-852-091-9

US-08-852-091-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-956-652-9

US-08-988-416-339

US-08-988-416-339

US-08-988-416-339

US-08-988-416-339

US-08-318-448-17

US-08-318-448-17

US-08-382-696-6

US-08-382-696-6

US-08-382-696-6

US-08-882-696-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 111, Application US/09484970B
Fatent No. 6426186 *
GENERAL INFORMATION:
APPLICANT: Volkmuth, Wayne
APPLICANT: Volkmuth, Wayne
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AAAGAATGTACTCCTGAAGTGGAGGAG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-484-970B-111
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34866 AACTCTGGAAGTTTCAAAGCGAGTCTTTTGTCTACCACCAGGTGAGAACTCAAGTTTAAA 34807
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                                                                                                                                                                                                                                         APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trecha
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AAATATCAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 43795;
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                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.3%; Score 24.6; DB 59.2%; Pred. No. 27; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATIOKNEI/ANDER AND PATTICIA
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-07A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                 RESULT 4
US-08-742-185-101/c
; Sequence 101, Application US/08742185
; Patent No. 602476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-015-973-2
: Sequence 2, Application US/08015973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 59.23
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                           Db 34806 AAAATATTTTC 34796
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Page, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Page, David C.
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
WUWBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                  DB 4; Length 1877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 40328;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429,7
FILING DATE: 22-SEP-1994
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   1022 ATATTCCGAAAGGAGCCATTCTTCCACGGCCAGGACAAC 1060
                                                                                                                                                                                                                  11 ATAITCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAAC 49
                                                                                                                                              Score 24.6; DB
Pred. No. 10;
0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.3%; Score 24.6; DB Best<sub>r</sub>Local Similarity 59.2%; Pred. No. 26; Matchès 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
TELECOMUNICATION INFORMATION:
TELEPAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 40328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102, Application US/08742185 Patent No. 6020476
                                                                                                                                              28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two Militia Drive
                                                                                                                                        Query Match
Best Local Similarity 76.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abusar
STREET: Two ...
CITY: Lexington
TTM: Massachusetts
                                                                    ; NAME/KEY: CDS
; LOCATION: (344)...(1396)
US-09-780-173A-10
                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                               Patent No. 6020476
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             US-08-742-185-102/c
LENGTH: 1877
                                                       FEATURE:
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Gaps

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Query Match
27.8%;
Best Local Similarity 62.3%;
Matches 38; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (148)..(7092)
US-09-816-703A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..6924
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; LOCATION:
US-08-448-164-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3935 T 3935
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US-09-816-703A-1
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APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: PHOSPHATASE-BETA
TITLE OF INVENTION: PHOSPHATASE-BETA
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDWONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: New York
STRATE: New York
STRATE: New York
STRATE: How York
STRATE: PHOSPHATA:
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: BAPPLICATION HORSE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1:25
CURRENT APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
TELEPAX: (212) 869-864/9741
TELEPAX: (212) 869-864/9741
TELEPAX: G6141 PENNIE
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6924 base pairs
TYPENDENCE: CDNA
PORTION: UNKNOWN
POLOCY: UN
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 62.3%;
Matches 38; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
1..6924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , NAME/KEY:
, LOCATION:
US-08-015-973-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3935 T 3935
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Sequence 1, Application US/09816703A;
Sequence 1, Application US/09816703A;
Patent No. 6455026
GENERAL INFORMATION:
APPLICANT: Meller, Thorsten
APPLICANT: Meller, Sabine
APPLICANT: Meller, Sabine
APPLICANT: Chin,Daniel
TITLE OF INVENTION: Treatment and Visualization of Brain Tumors
TITLE OF INVENTION: Treatment and Visualization of Brain Tumors
TITLE OF INVENTION UNMBER: US/09/816,703A
CURRENT APPLICATION NUMBER: US/09/816,703A
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 7941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.2; DB 2; Length 6924; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: US/08/448,164
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: US 08/015,973
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/015,973
ATTORNEY/AGENT INFORMATION:
NAMME: Misrock, S. Leelle
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
TELECOMMUNICATION INFORMATION:
TELEFPAICN (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.8%; Score 24.2; DE Best Local Similarity 62.3%; Pred. No. 22; Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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988 AAAAATCAATCCTGTTATAAGAGCGGTTGAACCTGCAGCATGTCCTTCATTAACAAAGG 1047
        3 AAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAA 62
                                                                                                                                                                                                            18-09-221-017B-191/C

Sequence 191, Application US/09221017B
FRATENT OF 6444799
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 4112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINTER READALLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastENG for Windows
SOFTWARE: FastENG for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.4%; Score 23.8; D 59.7%; Pred. No. 25; iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
FILING DATE: 09-APR-1998
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY, AGENT INFORMATION:
NAME: MONICOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 755 PAGE MILL ROAD CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1112 base pairs
nucleic acid
EDNESS: double
                                                                                                                                1048 GGTATATACTTATGA 1062
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                         63 AGAATGTACTCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 40; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
US-09-221-017B-191
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                                                                                                                                                                                                                                               APPLICANT: Lerman, Michael I.
APPLICANT: Lerman, Michael I.
APPLICANT: Minna, John D.
APPLICANT: Latif, Farida
APPLICANT: Wei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Duh, Fuh-Mei
TITLE OF INVENTION: Clacium Channel Compositions and Methods of Use Thereof
FILE REFERENCE: NIH-05043
CURRENT APPLICATION: CMMSER: US/09/470,443
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 AGGCCTTAAGCCTGTTGAAGGTCGAGCCCCCAAAAGGGTCACATATGCTCCTGCCTTGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09594193
Sequence 3, Application US/09594193
Patent No. 6441274
GENERAL INPORMATION:
APPLICANT: CAHOON, REBECCA E.
APPLICANT: CAHOON, S. CARL
APPLICANT: LOHMAN, KARIN
TITLE OF INVENTION: NOVEL PLANT TRYPTOPHAN SYNTHASE BETA SUBUNIT
FILE REFERENCE: BB1374 US NA
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: G0/139,568 "
PRIOR PELING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Microsoft Office 97
LENGTH: 1817
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Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1809)..(1810)..(1811)..(1812)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 60/114,359
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                  Sequence 7, Application US/09470443
Patent No. 6441156
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.73
Matches 37; Conservative
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Best Local Similarity 57.3
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-470-443-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: unsure
; LOCATION: (1814)
US-09-594-193-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1070
                                                                                4082 T 4082
                                                                                                                                                                  US-09-470-443-7
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US-09-594-193-3
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CITY: Madison
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Best Local Similarity
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US-09-453-702B-94
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Sequence 11, Application US/09103875A

GENERAL INFORMATION:
APPLICANT: Baye, Pascal
APPLICANT: Baye, Pascal
APPLICANT: Bamchandani, Shyam
TITLE OF INVENTION: OLICONUCLEOTIDES
TITLE OF INVENTION: OLICONUCLEOTIDES
FILE REFERENCE: 106101.194
CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT PILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: 06/069,865
EARLIER PILING DATE: 1997-12-17
EARLIER PILING DATE: 1997-12-17
EARLIER PILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                1473 AATCGGAGTTTTGCACCCGGGATATGGTGGAGCTCGTAGATGAAAGGCATTTCGTGTGTGGA 1414
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| Patent No. 6020318
| GENERAL INFORMATION
| APPLICANT: Sayf, Moshe
| APPLICANT: Bigey, Pascal
| APPLICANT: Ramchandani, Shyam
| TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
| TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
| TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
| TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
| NUMBER OF SEQUENCES: 64
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: HALE AND DORR LLP
| STREET: 60 State Street
| CITY: Boston
| STATE: MA
| COUNTRY: United States of America
90 cccrraddadcrerredccccccdcadecccccccccadcreaccadccrer 143
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Pred. No. 12;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
APPLICATION NUMBER: US/08/866,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.8%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-875-11
                                                                                                                                         1413 AGGGCG 1407
                                                                                               78 AGTGGAG 84
                                                                                                                                                                                                             RESULT 11
US-09-103-875-11
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LENGTH: 254
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Gaps
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NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                       90 cccrradgadcrefragccccccdargcaccccccccccaagcraacca
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                                                                                                                                                                                                                                                                                                 27.1%; Score 23.6; DB 3; Length 289; 64.8%; Pred. No. 13; tive 0; Mismatches 19; Indel8
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,7028
FILING DATE: 03-Dec-1999
CLASSIPICATION: <u >u</a>, <u >u</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.1%; Score 23.6; 1 58.6%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (seq ID NO: 94: US-09-453-702B-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION UNDER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Blattner, Frederick R. Burland, Valerie Perna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 94, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 94
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plunkett, Guy
Welch, Rod
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.81
Matches 35; Conservative
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ADDRESSEE:
                                                                               COUNTRY:
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                                         CITY:
STATE:
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APPLICANT: Carmen Vela Olmo
APPLICANT: Carmen Vela Olmo
APPLICANT: Jos Ignacio Casal Alvarez
TYTLE OF INVENTION: "PROCESS FOR PRODUCING A
TITLE OF INVENTION: RELATED VIRUSES"
TOWNER OF SINCENTION: RELATED VIRUSES"
CORRESPONDENCE ADDRESS:
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                                                                         2116 ccarridgeracharricggecaccaccaccccaccardarrahargaargrafta 2175
     0; Gaps
                                     10 GGAGCAGTTCAACCAGACGGTGGTCAACCTGCTGTCAGAAATGAAAGGCTACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%; Score 23.4; DB 4; Length 1752; llarity 63.2%; Pred. No. 27; Conservative 0; Mismatches 21; Indels 0
 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                         APPLICANT: Tarpey, Ian
APPLICANT: Greenwood, Neil
TITLE OF INVENTION: Canine parvovirus DNA vaccination
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6187759el Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30(EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,949
FILING DATE: 11-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                           STREET: Akzo No. 6187759el Patent Dept. STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville CITY: Maryland CONTE: Maryland STOWNEY: US
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                 Sequence 1, Application US/09022949
Patent No. 6187759
GENERAL INFORMATION:
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Patent No. 5882652
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REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
TELEFAX: 301-948-750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-09-022-949-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 301-948-9751
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                     2176 ATATCTGAGG 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                 76 GAAGTGGAGG 85
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 41;
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette 5.25 inch., 1.2 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 266-276
DATE: JAN, 1988
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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FRACMENT TYPE: Complete VP2 sequence of CPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1755 base pairs (585 amino acids)
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
26.9%; Score 23.4; DB
Best Local Similarity 63.2%; Pred. No. 27;
Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS (version 3.30)
SOFTWARE: Wordberfect5.1 (WP5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,785
3: HARRISON & EGBERT
1018 Preston Street, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/983,577
FILING DATE: 26-JAN-1993
APPLICATION NUMBER: PCT/ES92/00031
FILING DATE: 26-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: John S. Bgbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 15, 2003, 22:52:34
Job time : 26.1477 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: John S. Egbert
REGISTRATION NUMBER: 3627
REFRENCE/DOCKET NUMBER: 115:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 223-4034
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: Complete VP2 se
ORIGINAL SOURCE:
ORGANISM: Canine Parvovirus
STRAIN: CPV-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF CANINE PARVOVIRUS"

Journal of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Jones, E.V. : Miller, T.J. "NUCLEOTIDE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: Genomic PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: CPV-N
IMMEDIATE SOURCE:
                                                                                   Houston
                                                                                                                                                                                                                 77002
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AUTHORS:
AUTHORS:
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April 15, 2003, 19:13:41 ; Search time 8.69318 Seconds (without alignments) 8778.558 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT7_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593429 segs, 438583890 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                       US-09-647-019-8
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length DB	88	ΙD	Description
	1 87	100.0	824	100	US-09-880-192-4	Sequence 4, Appli
. 4	2 74.2	85.3	466	10	US-09-960-352-5216	Sequence 5216, Ap
(*)	3 29.4	33.8	507	10	US-09-783-590-8009	Sequence 8009, Ap
υ	28	32.2	1497	10	US-09-779-144A-6	Sequence 6, Appli
41	5 26.4	30.3	211	10	US-09-974-300-1137	Sequence 1137, Ap
~	5 25.8	29.7	473	07	US-09-864-761-14995	Sequence 14995, A
Ü	7 25.6	29.4	199	σ	US-09-989-920-147	Sequence 147, App
Ü	3 25.6	29.4	1897	σ	US-09-989-920-148	Sequence 148, App
-1	3 25.6	29.4	2350	10	US-09-880-192-36	Sequence 36, Appl
o T	25.2	29.0	4	10	US-09-816-685-3	٠,
0	1 25	28.7		10	US-09-864-761-14346	Sequence 14346, A
1	24.6	28.3		10	US-09-923-876-4026	Sequence 4026, Ap
0	3 24.4	28.0		12	US-10-002-600-3	Sequence 3, Appli
Ä	24.2	27.8	3 278	10	US-09-878-574-8855	Sequence 8855, Ap
;; 0	5 24.2	27.8	373	σ	US-09-796-692-4296	Sequence 4296, Ap
0 0	5 24.2	27.8	1 407	70	US-09-917-800A-269	Sequence 269, App
H	7 24.2	27.8	4883	0	US-10-118-513A-5	ad
ភ	8 24.2	27.8		0	US-10-118-513A-13	Sequence 13, Appl
ä	9 24.2	27.8	7215	σ	US-10-118-513A-15	Sequence 15, Appl

Sequence 1812, Ap Sequence 6014, Ap Sequence 19708, A Sequence 2927, Ap Sequence 7, Appli Sequence 2558, Ap Sequence 1218, Ap Sequence 1218, Ap		Sequence 190, App Sequence 190, App Sequence 944, App Sequence 944, App Sequence 37, Appl Sequence 37, Appl	Sequence 1, Appli Sequence 369, App Sequence 369, App Sequence 364, App
US-09-954-456-1812 US-09-781-590-6014 US-09-864-761-19708 US-09-864-761-2927 US-10-116-949-7 US-09-796-692-2558 US-10-015-219-1218 US-09-777-564-1218 US-09-777-564-1218	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	5 5	US-10-079-035-1 US-10-079-854-369 US-09-764-878-369 US-10-079-854-364
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                                     Sequence 4, Application US/09880192
| Sequence 4, Application US/09880192
| Patent No. US20020077470a1
| GENERAL INFORMATION:
| APPLICANT: Walker, Mingler, Tod M. APPLICANT: Wilngler, Tod M. APPLICANT: Azimzai, Yalda
| TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION FILE REFERENCE: PB-0009-1 CIP
| CURRENT APLICATION NUMBER: US/09/880,192
| CURRENT PILING DATE: 2001-06-12
| NUMBER OF SEQ ID NOS: 62
| SOFTWARE: PERL PROGRAM
| SEQ ID NO 4
| LENGTH: 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCAAATATCAATATCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCCAGAAGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1
US-09-880-192-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 87; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 AAAGAATGTACTCCTGAAGTGGAGGAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-960-352-5216
Sequence 5216, Application US/09960352
Petent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
RESULT 1
US-09-880-192-4
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                LOCATION: (233)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                          LOCATION: (254)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
I.O.CATION: (258)
                                                                                                                                                                                                                                                LOCATION: (258)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                               LOCATION: (261)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
CCACTION: (275)
CTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (292)

TTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (293)

THER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION: (296)
THER INFORMATION: n equals a,t,g,
MANE/KEY: misc feature
CCATION: (301)
THER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (367)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (368)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R INFORMATION: n equals a,t,g,
/KEY: misc feature
IION: (383)
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THER INFORMATION: n equals a,t,g,
TAME/KEY: misc feature
CCATION: (329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (345)
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATION: (370)

OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: (302)

NTHER INFORMATION: n equals a,t,g,

NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                   OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc feature
OCATION: (350)
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R INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                      OCATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND FAI DEPOSITION
TITLE OF INVENTION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5.216
LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Haedeline, William A.
APPLICANT: Li, Haddong
APPLICANT: Li, Haddong
APPLICANT: Ruben, Craig A.
TILLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2CI
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT APPLICATION NUMBER: 08/420,856
PRIOR PELING DATE: 1995-04-12
PRIOR PELING DATE: 1995-04-12
PRIOR PELING DATE: 1995-11-21
NUMBER OF SEQ ID NOS: 12465
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GCAAATATCAATATCCCAATGGGAGCCTTTCGGCCAGGAGCTGGGCAACCCCCTAGAAGA 207
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 466;
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                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 23-BOVMS1-014-Q1-E1-F3
US-09-960-352-5216
                                                                                                                                                                                                                                                                                                                                                                                                    Score 74.2; DB 10;
Pred. No. 2e-18;
0; Mismatches 8;
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (51)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (124)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (150)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.8%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
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US-09-783-590-8009
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LENGTH: 507
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Sequence 14995, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1329 TATGCCACTGAGAGGTTTATGGCGAAAAGGATTCCAACCCCCACCTAGAAACGAATAACC 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Length 1497;
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US-09-974-300-1137
| Sequence 1137, Application US/09974300
| Patent No. US20020146721A1
| GENERAL INFORMATION:
| APPLICANT: Berka, Randy M.
| APPLICANT: Clausen, Ib Groth
| TITLE OF INVENTION: Expression
| FILE REFERENCE: 10085.50-008
| CURRENT PRILING DATE: 2001-10-05
| PRIOR APPLICATION NUMBER: US/09/974,300
| CURRENT PILING DATE: 2000-10-05
| PRIOR APPLICATION NUMBER: 09/680,598
| PRIOR PILING DATE: 2000-10-06
| PRIOR FILING DATE: 2000-10-06
| PRIOR FILING DATE: 2001-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
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                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 10
Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 1.
CURRENT APPLICATION NUMBER: US/09/779,144A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US 09/106,926
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 GAAGGTGATTTTGCCGATGAAGGG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bacillus licheniformis
US-09-974-300-1137
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                                                                                                                                                                                                                                                                                                                                                              ch 32.2%;
1 Similarity 63.2%;
43; Conservative
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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US-09-864-761-14995
                                                                                                                                                                             SEQ ID NO 6
LENGTH: 1497
                                                                                                                                                                                                                                                                                                      US-09-779-144A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1137
LENGTH: 211
                                                                                                                                                                                                                                               TYPE: DNA
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US-09-779-144A-6/c
Sequence 6, Application US/09779144A
Sequence 6, Application US/0977914A
Sequence 6, Application US/0
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ilarity 60.0%; Pred. Ng. 0.16;
Conservative 0; Mismatches 32;
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OTHER INFORMATION: n equals a,t,g, or c
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US-09-783-590-8009
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (434)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                           OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                        LOCATION: (424)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (425)
OTHER INFORMATION: n equals a,t,g,
                                                                                LOCATION: (419)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (457)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
CACATION: (458)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KBY: misc feature
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                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (424)
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LOCATION: (504)
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Best Local Similarity
Matches 48; Conserva
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us-09-647-019-8.rnpb

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RESULT 8
US-09-989-920-148/c
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; ORGANISM: HOMC
US-09-989-920-147
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LENGTH: 1897
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 661
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FILE KEEKENLEY APONICAS ACTION OF THE APONICAS ACTION OF THE APONICAS ACTION OF A CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-05-06

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,3366

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR PRIOR NUMBER: PCT/US01/00669

PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR PRIOR PRIOR DATE: 2001-01-30

PRIOR PRI
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Patent No. US20020172957A1
GENERAL INFORMATION:
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Best Local Similarity 58.4%;
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Procurent PILICE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT APPLICATION NUMBER: 60/252,500
PRIOR PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 147
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Patent No. US20020172957A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mecipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REPERENCE: DEX-0291
CURRENT FILIAG DATE: 2001-11-21
PRIOR PILING DATE: 2000-11-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 661;
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29.4%; Score 25.6; Di
Best Local Similarity 57.5%; Pred. No. 6.2;
Matches 46; Conservative 0; Mismatches
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Best Local Similarity 57.5%; Pred. No. 4.6;
Matches 46; Conservative 0; Mismatches
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US-09-880-192-36
US-09-880-192-36
, Sequence 36, Application US/09880192
; Patent No. US20020077470A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin versio
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapien
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US-09-989-920-148
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Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
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Best Local Similarity
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                      APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Azimzal, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
CURRENT APPLICATION NUMBER: US/09/880,192
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ 1D NOS: 62
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09816685
Sequence 3, Application US/09816685
Patent No. US20020053091A1
GENERAL INFORMATION
GENERAL INFORMATION: LEGATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERENCE: CL000856
CURRENT PELLING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 2350;
                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte ID No. US20020077470A1 3434460CT1
US-09-880-192-36
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Best Local Similarity 57.5%; Pred. No. 6.6;
Matches 46; Conservative 0; Mismatches 34;
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(41104)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      938 raadaarcraaaccradadr 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AAAGAATGTACTCCTGAAGT 80
APPLICANT: Walker, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.0
Best Local Similarity 60.0
Matches 42; Conservative
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 20695 GAATAAAGTA 20686
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US-09-864-761-14346/c
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LENGTH: 41104
TYPE: DNA
                                                                                                                                                                                                               SEQ ID NO 36
LENGTH: 2350
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0; Mismatches
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Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANIZM: Glycine max
; OTHER INFORMATION: Clone ID: 701101759H1
US-09-878-574-8855
                     2599 AAAAGGTAACACATTACATGAA 2578
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71.1%;
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Best Local Similarity
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Sequence 4026, Application US/09923876

Sequence 4026, Application US/09923876

Patent No. US20020013958A1

GENERAL INPORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYVUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT APPLICATION NUMBER: 09/298,329

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram

SEQ ID NO 4026

LENGTH: 276
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CTHER INFORMATION: Incyte ID No. US20020013958A1 700454286H1

NAME/KEY: unsure

CHARTIN: 1740 A1 CONTRACTION: 1 CONTRACTION: 1700 A1 CONTRACTION: 1700 A1
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APPLICANT: Hopkins, Christopher M.
APPLICANT: Peterson, David P.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS;
FILE REPERENCE: PA-0042 US
CURRENT APPLICATION NUMBER: US/10/002,600
CURRENT APPLICATION NUMBER: 60/243,521
PRIOR APPLICATION NUMBER: 60/243,521
PRIOR PILLING DATE: 2001-10-25
PRIOR FILLING DATE: PROFILE TOWNS: 116
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Pred. No. 8.4;
0; Mismatches 14;
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; OTHER INFORMATION: Template ID: 238104.1
US-10-002-600-3
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70.2%;
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56.1%;
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Matches 33; Conservative
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ORGANISM: Homo sapiens
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Matches § 46; Conserva
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ORGANISM: Zea mays
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LENGTH: 3829
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US-US-1956-622-4296/C
Sequence 4296, Application US/09796692
Publication No. US20020198362A1
GENERAL INCORPARIATION:
APPLICANT: Adjact. Paul A.
APPLICANT: Adjact. Paul A.
APPLICANT: Adjact. Paul A.
APPLICANT: Manion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: UNMER: 1200-03-01
CURRENT APPLICATION NUMBER: 60/186,126
PRIOR PLILNG DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/200,345
PRIOR PLILNG DATE: 2000-04-27
PRIOR PLILNG DATE: 2000-04-28
PRIOR PLILNG DATE: 2000-05-04
PRIOR PLILNG DATE: 2000-06-04
PRIOR PLING DATE: 2000-06-04
US-09-878-574-8855
; Sequence 8855, Application US/09878574
; Patent No. US20201010548A1
; Patent No. US20201010548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR PRILICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; *NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 8855
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Human breast cell Human foetal liver Probe #2167 used t Human genome-deriv Human gene express

Human secreted pro

Human cDNA clone (Polynucleotide seq Human immune/haema

Corn anthranilate

Cervical cancer pr Human overy specif Human normal bladd Human reproductive DNA encoding novel Human genomic DNA

Human bone marrow Probe #6228 used t Human genome-deriv Human immune/haema

Fragment HGJ1775 o Human prostate exp

Human G-protein co Human foetal liver

Arabidopsis thalia Arabidopsis thalia DNA encoding a Sta Drosophila melanog Human DAZ genomic Human DAZ genomic

Drosophila melanog CDNA of human 84 r Human CDNA clone (Pinus radiata cycl

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTe and for

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Result No.

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; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
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                                                                    AACS9785
AAS07822
ABN87872
AAZ42152
AAZ42152
AAS32838
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AAS32838
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AAI37542
ABS06420
AAK81626
AAV23082
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AAC33555
AAT84169
ABL10268
AAZ92584
AAZ92583
AAZ92583
AAK99629
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P-PSDB; AAG01477.
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                                                                                                                                                                                                                                                                                                                                                                   5' EST;
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                                                                                                                                                                                                                                                                                                                                                                          gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                  Human;
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Human 66214 EST cl
CDNA encoding huma
CDNA encoding muri
Maize C-24 Bterol
Corn SMT CDNA. Ze
Human cervical can
Human immune/haema
Bacillus lichenifo
                                                      (without alignments)
8439.207 Million cell updates/sec
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                                            April 15, 2003, 16:26:41 ; Search time 23.2159 Seconds
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     GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                          2185239 segs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                               nucleic search, using sw model
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AAD27216
AAX90904
AAX90903
AAX90903
AAY1474
AAK1118
AAK11474
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Gapop 10.0 , Gapext 1.0
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Match I
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100.0
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32.2
31.0
31.0
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Post-processing:

Database

0B 0B

Minimum Maximum

Title: Perfect score:

Sequence:

nucleic

δ

Run on:

Scoring table:

Searched:

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyAh RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypetrrophic cardiomyopathy; intythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvuiar heart disease; valvuiar heart disease; valvuiar heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone 66214; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 352
diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCAAATATCAATATTCCAATGGGGGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                           Sequence 428 BP; 123 A; 111 C; 104 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 87; DB 21; Best Local Similarity 100.0%; Pred. No. 4.4e-22, Matches 87; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Human 66214 protein"
298..588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "66214 cDNA fragment"
857..862
                                   Claim 1; SEQ ID 1481; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 AAAGAATGTACTCCTGAAGTGGAGGAG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAAGAATGTACTCCTGAAGTGGAGGAG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD27216 standard; DNA; 886 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2001; 2001WO-EP06165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000; 2000US-207400P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 66214 EST clone DNA
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tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders syncope and sudden death, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary heart disease, congenital heart disease, pericardial disease and endocardiis. Sequences of the invention are also used in gene therapy, are useful for the development for medicaments for the treatments of heart disease. The present DNA sequence is expressed sequence tag
                                                                                                           Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chisel gene; Csl; EF-Hand protein super family; muscle development; heart/Sekeletal muscle call development; signalling pathway; regulation; XQ21.3-q22, adaptive process; muscle homeostasis; skeletal myopathy; detection; diagnosis; prophylaxis; treatment; cardiac hypertrophy; muscular and myotonic dystrophy; buchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; differentiation; exon; gene therapy; transgenic animal; drug screening; ss.
                                                                                                                                                                                                                                              The patent discloses novel target genes abnormally expressed in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGGCAGGGGTCAACCCCCCAGAAGA 288
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human cosmid clone U228D4"
173..229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 886;
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100.0%; Pred. No. 5.7e-22;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human chisel (Csl) gene.
                 Henkel T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAAGAATGTACTCCTGAAGTGGAGGAG
                                                                                                                                                                                                           Claim 2a; Fig 9b; 154pp; English
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                 Beck J,
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                                                       WPI; 2002-122073/16.
                 Reuner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EST) 66214 clone.
                                                                         P-PSDB; AAE16632
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                 Bunk D,
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exon
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us-09-647-019-8.rng

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The present sequence is the cDNA encoding the human chisel gene (Cal) that is mapped to the human chromosome Xq21.3-q22. It comprises 5 exons. It is a member of the EF-Hand protein super family and is involved in signaling pathways. It is predominantly expressed in heart and skeletal muscles and is activated after the differentiation of calls. Cal functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases cut as those involving aberrant muscle call development and functional activity. It is also used in the treatment of muscular and myotonic dystrophy, heart failure, cardiac hypertrophy and myocarditis, myofiber atrophy, eart failure, cardiac hypertrophy, myocarditis, myofiber atrophy, etc. The Cal gene sequence can also be used in gene therapy, for the production of transgenic animals and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids encoding chisel, used to develop products for treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
                                                                /*tag= c
product= "Chisel (Csl) protein"
/note= "Expressed predominantly in heart muscles"
             /note= "Corresponds to residues 15687-15631 of numan cosmid clone U228D4"
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                                                                                                                                                                                                                                                                                               /*tag= f
/label= Exon_5
/note= "Corresponds to residues 4101-3680 of
human cosmid clone Uj12E8"
                                                                                                                                                                ð
                                                                                                                                                                                                                                                to residues 35384-35236
                                                                                                                                            /label= Exon_3
/note= "Corresponds to residues 5220-5134
human cosmid clone U228D4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 887 BP; 279 A; 172 C; 192 G; 244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harvey RP, Musaro A, Palmer SJ, Rosenthal NA;
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HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                              /*tag= e
/label= Exon_4
hote= "Corresponds to res:
human cosmid clone Ull2E8"
466..887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAN-) CHANG CARDIAC RES INST VICTOR.
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label= Exon_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-AU00220.
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                                                                                                               230..316
                                                .85..451
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P-PSDB; AAY28651.
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myofiber atrophy, etc. The Cal gene sequence can also be used in gene therapy, for the production of transgenic animals and for drug screening
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                                                                                                                                                                                                                                              Chisel gene; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; therapy; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids encoding chisel, used to develop products for treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
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/note= "Expressed especially in heart muscles"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 778 BP; 231 A; 166 C; 179 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Musaro A, Palmer SJ, Rosenthal NA;
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                                                                                                                                                                                                                cDNA encoding murine chisel (Csl) gene.
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Location/Qualifiers
199..456
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                                                                                                          BP.
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Best Local Similarity 85.1%;
Matches 74; Conservative
                                                                                                          AAX90903 standard; cDNA; 778
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/product= '
                                                                                                                                                                                 (first entry)
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(GEHO ) GEN HOSPITAL
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                                                                                                                                             AAX90903;
                        290
                                                                        RESULT 4
AAX90903
ID AAX9
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Gaps

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230 GCAAATATCCAATGGGAGCCTTTCGGCCAGGAGCTCAACCCCCCAGAAGA 289

61 AAAGAATGTACTCCTGAAGTGGAGGAG 87

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GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60

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This sequence represents CDNA encoding maize endosperm C-24 sterol
methyltransferase ESMT-1. The CDNA encoding ESMT-1 was selected from an
EST (expressed sequence tag) database on the basis of its sequence
identity with the N-terminal portion of the yeast ERG6 protein. The
predicted amino acid sequence of ESMT-1 shows 66% similarity and 46%
control predicted amino acid sequence of ESMT-1 shows 66% similarity and 46%
control predicted amino acid sequence of ESMT-1 shows 66% similarity and 46%
control methyltransferases, respectively. ESMT-1 catalyses the
alkylation of sterol intermediates at carbon 24. Nucleic acids encoding
ESMT-1 may be used in the generation of transgenic plants having altered
maintenance of membranes of most eukaryotic cells; however, insects,
nematodes and some species of fungi do not produce their own sterols,
contained and some species of fungi do not produce their own sterols,
contained and some species of fungi as their life cycles. DNA encoding
ESMT-1 is useful in altering sterol metabolism in plants and protects
contained and some species of fungi sterol metabolism in plants and some
confinging Plants produced using ESMT-1 DÑA are resistant to pest
infestation, without the need for chemical pesticides which may be toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a /*tag= A /*tag= //product= "Maize C-24" sterol methyltransferase ESMT-1"
                      238 GCGAATATCAATATTCCAATGGGAGCCTTTCGTCCGGGAGCTGGGCAGCCTCCCAGAAGG 297
1 GCAAATATCAATATCCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 60
                                                                                                                                                                                                                                                                                                                                                                 C-24 sterol methyltransferase; ESMT-1; maize; endosperm; alkylation; sterol metabolism; ERG6 homologue; EST; expressed sequence tag; transgenic plant; pest resistance; insect; nematode; fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment for altering sterol metabolism in plants to give protection against infestation by pests, encodes sterol methyltransferase
                                                                                                                                                                                                                                                                                                                               Maize C-24 sterol methyltransferase ESMT-1 cDNA.
                                                                                                 298 AAAGAGAGTACTCCTGAAACTGAGGAG 324
                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 22-25; 25pp; English.
                                                                            61 AAGAATGTACTCCTGAAGTGGAGGAG
                                                                                                                                                                                                              AAZ92614 standard; cDNA; 1383 BP
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                                                                                                                                                                                                                                                                                           (first entry)
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P-PSDB; AAY80992.
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Sequence 1383 BP; 377 A; 276 C; 370 G; 360 T; 0 other;

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This DNA molecule codes for the S-adenosyl-L-methionine-delta24(25)
sterol methyltransferase (SMT) enzyme (see AAM70838) of corn. SMT
catalyses the transfer of a methyl group from S-adenosyl-L-methionine
to the C-24 centre of the sterol side chain. Full-length corn SMT
cDNA was isolated from a commercial corn cDNA library by PCR
amplification. The invention relates to transgenic plants with
modified sterol biosynthetic pathways. Phytosterol compositions are
modified sterol biosynthetic pathways. Phytosterol compositions are
modulated in the transgenic plants to confer resistance to insects,
nematodes, pythiaceous fungi and/or other environmental stresses
such as drought or cold, and/or to improve nutritional value, e.g.
by increasing levels of cholesterol-lowering sterols. SMT DNA
molecules (including antisense molecules) can be transformed into
plant cells, and plants (especially tomato, corn or soybean) having
altered sterol compositions are then regenerated.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic plants with altered sterol levels - obtained using DNA comprising a coding sequence which encodes an enzyme which binds a first sterol and produces a second sterol
                                                             12 TATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTAC
                                    ö
                                                                                                                                                                                                                                                                                                                                                     S-adenosyl-L-methionine-delta24(25)-sterol methyl transferase; SMT; phytosterol; transgenic plant; disease resistance; insect resistance; pest resistance; stress tolerance; crop protection; corn; maize; ds.
    Length 1383;
                                  25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1497 BP; 413 A; 292 C; 394 G; 397 T; 1 other;
    DB 21;
   Score 28; DB;
Pred. No. 3.3;
                                  0; Mismatches
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66..1100
                                                                                                                                                                                                                                AAV70839 standard; DNA; 1497 BP.
32.2%;
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1470..1497
/*tag= b
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                 l Similarity 63.2
43; Conservative
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                                                                                                                                                        1281 TCAAGCAG 1274
                                                                                                                          72 TCCTGAAG 79
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                                                                                                                                                                                                                                                              AAV70839;
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   Query Match
Best Local 8
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                                  Matches
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AAH71474;

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us-09-647-019-8.rng

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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36130.
                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                 AAK81318 standard; DNA; 42519 BP.
                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000; 2000US-0186350
16-MAR-2000; 2000US-0189874
17-MAR-2000; 2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000; 2000US-0205515
07-JUN-2000; 2000US-0209467
28-JUN-2000; 2000US-0214886
                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01354
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                                                                                                                      (first entry)
504 AAAATTTCTTCTAA 518
                                                                                                                                                                                                                     Homo варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                            AAK81318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-mallgnant condition; to monitor the progression of cervical cancer or a premallgnant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                     Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer -
                                     Gaps
                                                       444 AAAAAAAAAGCCCAAATTTGGGCCTTTGGGCTAAAAGGGGCCCACCCTCTCTTAAAAA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AATAICAATAITICCAATGGGAGCCITITCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Score 28; DB 20; Length 1497;
Pred. No. 3.4;
0; Mismatches 25; Indole '
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                                                                                                                                                                                                                                                                                         Human cervical cancer marker nucleic acid 2748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.0%; Score 27; DB 2 60.0%; Pred. No. 5.9; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL+) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 564-565; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berger A,
                                                                                                                                                                                                            AAH71474 standard; cDNA; 612 BP
    Ouery Match
Best Local Similarity 63.2%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000; 2000US-018350; 12-MAR-2000; 2000US-0189315; 12-MAR-2000; 2000US-020391; 09-UUN-2000; 2000US-0220114.
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                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-375006/39.
                                                                                                                                         1269 ŤĊAAĠCÁG 1262
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Matches 45; Conserv
                                                                                                              72 TCCTGAAG 79
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Query Match

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2000US-0249299
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
10-0CT-2000;
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                                    14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-20
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
couplement diseases and polymucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
collinear and cancer metastrases of haematopoietic-related diseases, especially
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastrases of haematopoietic antigen genomic
conformation the present invention. AAK84942 to AAK87691 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6464 AAATACAAAAATTCGCTGGGCATGGTGGCAGGCAGCCTCAGGAGGCTGAGAAGAAT 6523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCCAGAAGAAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 36130; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.0%; Score 27; DB 22; Length 42519; 57.8%; Pred. No. 26; ive 0; Mismatches 35; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis genomic sequence tag (GST) #1137.
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                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK73846 standard; DNA; 211 BP
                                                                 20000S-0251988.
20000S-0256719.
20000S-0251479.
20000S-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                               2000US-0251990.
2000US-0254097.
                 2000US-0250160.
2000US-0250391.
                                                      2000US-0251030
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                                                                                                                                                                2000US-0251869
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
                                                  05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                    01-DEC-2000;
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate concaining array of Bacillus genomic sequenced tags (GST), examining the array, and determining calative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring opposible functions of unknown open reading frames and genes in one copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, and the manal stress or other physiological provocation. Extensive follow—up characterisation is unnecessary, when one spot on an array cequals one gene or one open reading frame, since sequence information is available. This sequence represents a genemic information is not not the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 1137; 200pp; English.
                                                                                                                                                                                                                                                   (NOVO ) NOVOZYMES BIOTECH INC (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                   06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                             05-OCT-2001; 2001WO-US31437.
                 Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                   Clausen IG;
                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequenced tag array
                                                         WO200229113-A2.
                                                                                                   11-APR-2002
                                                                                                                                                                                                                                                                                                                   Berka R,
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4 AATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAA 63 ö 30.3%; Score 26.4; DB 24; Length 211; 57.1%; Pred. No. 6.7; ive 0; Mismatches 36; Indels 0; Sequence 211 BP; 71 A; 33 C; 62 G; 45 T; 0 other; Query Match
Best Local Similarity 57.1;
Matches 48; Conservative ઠે

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64 GAATGTACTCCTGAAGTGGAGGAG 87
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166 GAÁGGIGATITIGCCGAIGAAGGG 189 셤

AAH06869 standard; cDNA; 891 26-JUN-2001 (first entry) AAH06869; AAH06869/ 232X2X

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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 1'-end sequence, where the

oligonucleotide which comprises a 1'-end sequence, where the

complementary strand of a polynucleotide out the combination of

the 5'-end sequence 13'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesiang polynucleotides,

constant full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

constant and seasily without any specialised methods. AAH03166 to AAH13628 and

AAH3633 to AAH13642 represent human cald sequences; and AAH13629 to AAH13632

represent oligonucleotides, all of which are used in the exemplification

of the present invention.
                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                    IBOgai T, Nishikawa T, Hayashi K, Saito K, Yí
, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 3704; 2537pp + CD ROM; English.
    Human cDNA clone (5'-primer) SEQ ID NO:3704.
                                                                                                                                                                                                                                                                         27-AUG-1999; 99-JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                      Homo sapiens
                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                                                         29-JUL-1999;
                                                                                                                                                                     07-FEB-2001.
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Ishii S,
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Gaps ô DB 22; Length 891; Score 26.4; DB 22; Length Pred. No. 11; 0; Mismatches 18; Indels Sequence 891 BP; 195 A; 206 C; 232 G; 254 T; 4 other; 30.3%; Matches 36; Conservative Best Local Similarity Query Match ò

of the present invention.

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26 CCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAAAATGTACTCCTGAAG AAX20536 standard; DNA; 11516 BP. AAX20536; RESULT 11 AAX20536/c

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05-MAY-1999 (first entry)

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06-SEP-2000; 2000US-0230438.

08-SEP-2000; 2000US-0231243.

08-SEP-2000; 2000US-0231244.

08-SEP-2000; 2000US-0231413.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0231414.

12-SEP-2000; 2000US-0231818.
                                                                                                                            2000US-0216647.
2000US-0216880.
2000US-0217487.
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14-SEP-2000; 2000US-0233998.
14-SEP-2000; 2000US-0232999.
14-SEP-2000; 2000US-0232400.
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22-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0227009
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01-SEP-2000; 2000US-0229287
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01-SEP-2000; 2000US-0229344
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05-SEP-2000; 2000US-0229509
05-SEP-2000; 2000US-0229513
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                                                                                                2000US-0214886.
2000US-0215135.
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2000US-0225268
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02-OCT-2000;
                                       17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
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14-AUG-2000;
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ö
                                                                                                                                                                                                                                                                                                                                                                                                              AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune, haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 TAITCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTAC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20288
                                                                                                                                                                                                                                                                                                                      New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                Treponema pallidum infection; syphiliß; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 11516;
             Polynucleotide sequence from the genome of Treponema pallidum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.2; DB 20; Length 1
Pred. No. 32;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 402-408; 1150pp; English
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Best Local Similarity 60.6%;
Matches 43; Conservative 0
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                                                                                        Treponema pallidum.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
cc activity, and can be used in gene therapy and vaccine production. (I)
c proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) axpression. For
cx mample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient 's genome
that affect the activity of (I) by expressing inactive proteins or to
constructedides may be used to produce the secreted (I), by inserting
cc supplement the patients own production of (I). Additionally, (I)
cc supplement the patients own production of (I). Additionally, (I)
cc supplement the patients own production of (I), by inserting
cc the nucleic acids into a host cell and culturing the cell to express the
cc the nucleic acids into a host cell and culturing the cell to express the
cc diagnose and treat immune/haematopoietic-related diseases, especially
cc ancers and cancer metastasses of haematopoietic antigen genomic
cancers and cancer metastasses of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87994 ceptesent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.1%; Score 26.2; DB 22; Length 27435; Best Local Similarity 60.6%; Pred. No. 43; Matches 43; Conservative 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn anthranilate synthase beta subunit nucleotide sequence.
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P-PSDB; AAY42121.
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2000US-0246526
2000US-0246527
2000US-0246619
2000US-0246610
2000US-0246611
2000US-024920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483426/52
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0C
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17-NOV-2000;
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08-NOV-2000;
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The present invention describes isolated anthranilate synthase alphasbubnit (ASAS), and thranilate synthase beta-subunit (ASAS), and thranilate synthase beta-subunit (ASAS), and thranilate synthase beta-subunit (ASAS), and thranilate synthase alpha-subunit (TSAS) mucleic acids, and protein encoded by them, obtained from corn, rice, soybean and wheat cDNA in the nucleic acid fragments may be used to create transgenic libraries. The nucleic acid fragments may be used to create transgenic contents in which the disclosed ASAS, ASAS or TSAS are present at higher or lower levels than normally found. This would have the effect of altering which they are not normally found. This would have the effect of altering to the level of tryptophan in those cells. Manipulation of the levels of pathogen attack. Because this pathway is not followed for the production content the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. Nucleic acid fragments can also be used a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. AAZ25109 to AAZ25127 represent specifically claimed nucleic acids from the present invention cand AAV42112 to AAV42112 represent the proteins encoded by them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         757 TCCAGGGTGTCCAATTCCACCCGGAGAGCATCATCACCCTGAAGGCAAGAAATCATCC 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 29.9%; Score 26; DB 20; Length 1133; Local Similarity 62.1%; Pred. No. 17; Onservative 0; Mismatches 25; Indels C
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; cancer; ss.
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21-SEP-2000;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for bound to each probe of the microarray of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tay microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the invention. Note: The sequences of the invention printed specification, but was obtained in electronic format directly from WIPO at ftp.WiPo.int/Pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                              Claim 1; SEQ ID NO 2210; 327pp + sequence listing; English.
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04-OCT-2000; 2000GB-0024263.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                           Claim 1; SEQ ID NO 2270; 639pp + sequence listing; English.
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Query Match . 29.7%; Score 25.8; DB 22; Length 473; Best Local Similarity 58.4%; Pred. No. 15; Matches 45; Conservative 0; Mismatches 32; Indels 0; Sequence 473 BP; 177 A; 95 C; 92 G; 109 T; 0 other;

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Title: US Perfect score: 87 Sequence: 1	US-09-647-019-8 87 1 gcaaatatcaatattccaatgtactcctgaagtggaggag 87
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Searched: 20	2054640 segs, 14551402878 residues
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IMAGE: 4246501, mRNA, complete cds.

BC005948.1 GI:13543590

MCC.

Homo sapiens.

Homo sapiens Eutheria; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg, R.

Direct Submission ACCESSION VERSION KEYWORDS SOURCE ADRGANISM

REFERENCE AUTHORS TITLE

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/trānslation="mmmskQpvsnvralqanınıpmdafrpgagQpprrkECTPEVEE
GVPPTSDEEKKPIPGAKKLPGPAVNLSBIQNIKSELKYVPKAEQ"
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                                                                            Direct Submission
Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial
Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial
College of Science Technology and Medicine, SAF Bldg, Level 2,
Exhibition Road, South Kenaington, London SW7 2AZ, UNITED KINGDOM
Related sequences:AJJ45772, U73508 to U73509.
Location/Qualifiers
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product="stretch responsive muscle (X-chromosome)"
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/db xref="taxon:9606"
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/organism="unidentified"
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/codon_start=1
/product="small muscle protein, X-linked"
/product="small muscle protein, X-linked"
/protein_id="AAH05940.1"
/db_xref="GI:13543591"
/translation="MNMSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEE
GVPPTSDEEKKPIPGAKKLPGPAVNLSEIQNIKSELKYVPKAEQ"
171 g 227 t
                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6625646.
Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 885)

Kemp. T. J., Sadusky, T. J., Simon, M., Brown, R., Eastwood, M., Sassoon, D.A. and Coulton, G.R.

Identification of a novel stretch-responsive skeletal muscle gene
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSA250584 885 bp mRNA linear PRI 12-APF
Homo sapiens mRNA for stretch responsive muscle (X-chromosome)
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Srmx gene; stretch responsive muscle (X-chromosome)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Skeletal Muscle"
/clone lib="NIH MGC_81"
/lab_host="DH10B"
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/evidence=not_experimental
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/product="small muscular protein"
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/db_xref="G1:662547"
/translation="MNMSKQPVSNVRAIQANINIPMGAFRPGAGQPPRRKECTPEVEE
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Submitted (18-JAN-1999) Molecular Human Genetics, Institut for
Human Genetics, Fleischmannstr. 42/44, D-17487 Greifswald, Germany
Location/Qualifiers
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 886)
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Edentification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein
229 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGGAGGTCAACCCCCCAGAAGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GCAAATATCAATATTCCAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGA 288
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note="alternate position for initiation methionine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                             289 AAAGAATGTACTCCTGAAGTGGAGGAG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AAAGAATGTACTCCTGAAGTGGAGGAG 315
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<1. .>886
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                                           61 AAAGAATGTACTCCTGAAGTGGAGGAG
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184. .450
/gene="SMPX"
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/gene="SMPX"
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Thes 87; Conservative
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Submitted (21-JUL-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 47440)
Waterston, R.
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St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
U73509 47440 bp DNA linear PRI 27-APR-1999
Homo sapiens cosmid clone U228D4 from Xp22.1-22.2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is from a chromosome X-specific cosmid library LLOXNCC01
'U'. The source of the chromosomes was a human/hamster hybrid,
GMOJ297-F, from Robert Nussbaum at the University of Pennsylvania
School of Medicine. Please contact the Lawrence Livermore National
Laboratory at http://www-bio.llnl.gov/genome to obtain the clone.
VECTOR: Lawristl6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
[1] (bases I to 47440)
Sulston, J. B. and Waterston, R.
Toward a complete human genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. V., and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomics 44:227-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens cosmid clone U228D4 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Waterston, R.
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Waterston, R.
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complement(19314. 19497)

/rote="match to EST AA248485 (NID:g1879506)"

complement(19314. 19478)

/note="match to EST W07478 (NID:g1281479) za96c10.rl"

complement(19314. 19478)

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/note="match to EST N87511 (NID:g1440713)"

complement(19314. 19423)

/note="match to EST N87511 (NID:g1440713)"

complement(19314. 19413)

/note="match to EST AA092554 (NID:g1637327)"
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2020__.2180
/rpt_family="Retroviral"
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/rpt_family="(CAAT)n"
complement(5131..5223)
/note="match to EST M87511 (NID:g1440713)"
complement(5133..5223)
/note="match to EST W07478 (NID:g1281479) za96c10.rl"
complement(5148..5222)
/note="match to EST AA092554 (NID:g1637327)"
complement(5169..5222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (15622, .15689)
fnote="match to EST AA248485 (NID:g1879506)"
complement (15622, .15689)
complement to EST W07478 (NID:g1281479) za96c10.rl"
6751, .16837
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21964. .22282

/rpt_family="Retrovirgl"

22399. .223673

/rpt_family="MIR"

2439. .23673

/rpt_family="MIR"

24236. .2456

/rpt_family="L1"

2479. .2469

/rpt_family="L1"

2479. .26860

/rpt_family="L1"

25920. .26860

/rpt_family="L1"

26867. .27210
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rpt_family="Retroviral"
8945, .29005
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rpt family="Retroviral"
9715. .30007
                                                              clone lib="LL0XNCC01-U"
                                                                                                                                                                                                                                                                                                                                                                               rpt_family="U2"
1721. .11940
rpt_family="MER1_type"
2770. .12961
db xref="taxon:9606'
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/rpt_family="Alu"
30773. .31151
/rpt_family="Malk"
                chromosome="X"
"map="Xp22.1-22.2"
'clone="U228D4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13059...13107

'Typt family="L2"

13897 amily="Alu"

| Typt family="Alu"

14233...14397

/ Typt family="MIR"

complement(15622...
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7213. .27810
                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MIR"
3039. .13107
                                                                                                                                                                                                                                                                                                                                            rpt_family="MIR"
781. .8842
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8727...28815
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AL772370 150319 bp DNA linear HTG 17-AUG-2002
Homo sapiens chromosome X clone RP11-184B10, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150319)
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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46645. .47185
/rpt_family="MER21_g"
9644 c 9310 g 13336 t
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/rpt_family="rlu"
39241. .39431
/rpt_family="Retroviral"
39469. .39659
/rpt_family="Retroviral"
39877. .39946
                                                                                                                                                               88794. .38914
'rpt_family="Retroviral"
8939. .39240
                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MaLR"
45063. .45245
/rpt_family="MIR"
45276. .45399
/rpt_family="MER1_type"
46393. .46517
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3876, .44349
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           /rpt_family="L1"
33587..37330
/rpt_family="L1"
37345..3745..37345..3745..37858
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                                                                                                /rpt_family="L1"
38102. 38146
/rpt_family="MIR"
38578. 38706
38794. 38914
                                                                                                                                                                                                                                                                                                                                              rpt family="Alu"
2307. .42488
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0027. .40328
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AL772370/c
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305 AAAGAGAGTACTCCTGAAACTGAGGAG 331
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Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 787)
Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,C.-C., Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentgen,F.,
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                                                                     Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator ET-amersham; 0% of reads
Quality: 199793 bases at least Q40
Consensus quality: 149914 bases at least Q20
Insert size: 150219; sum-of-contigs
Insert size: 152259; 2.5% error; agarose-fp
Coverage: 17.18x in Q20 bases; sum-of-contigs Quality
coverage: 17.58x in Q20 bases, sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150319;
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4860 4959; gap of 100 bp
4960 150319; contig of 145360 bp in length.
Location/Qualifiers
1. 150319
/organism="Homo sapiens"
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100.0%; Score 87; DB 2; Length 15
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 87; Conservative 0; Mismatches 0; Indels
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/clone=1b="RPCI-11.1"
1. .4859
/note="assembly fragment:05115
fragment chain:1"
/note="assembly fragment:05210
/note="assembly fragment:05270
fragment chain:1
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           Contact: humquery@sanger.ac.uk
Web site: http://www.sanger.ac.uk
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                                                     Center project name: bA184B10
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Palmer, S., Groves, N., Schindeler, A., Yeoh, T., Biben, C., Wang, C.-C., Sparrow, D.B., Barnett, L., Jenkins, N.A., Copeland, N.G., Koentgen, P., Direct Submission
Submitted (O1-RB2-201) Developmental Biology, Victor Chang Cardiac Research Institute, 38 4 Victoria St, Darlinghurst, Sydney, New Location/Qualifiers

Location/Qualifiers
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/product="muscle-specific protein CSL"
/protein id="AAK07682.1"
/db_xref="G1:14575062"
/translation="WSKQPISWVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGAFTRSEEKKPIPGMKKPPGPVVNLSEINVKSELKFVPKGEQ"

PTTSEEKKPIPGMKKPPGPVVNLSEINVKSELKFVPKGEQ"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (mases 1 to 936)
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein
Hum. Genet. 105 (5), 506-512 (1999)
Mohun, T. and Harvey, R.P. The small modifies cell shape and promotes myocyte fusion in an insulin-like growth factor labendant manner.
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Direct Submission
Submitted (26-MAR-2001) B.M.-Arndt-Uni, Inst. f. Humang., Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF364070 936 bp mRNA linear 1 Mus musculus SMPX protein (Smpx) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Cal"
206. .463
/gene="Cal"
/note="ortholog of Homo sapiens SMPX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

76.1%; Score 66.2; DB 10
Best Local Similarity 85.1%; Pred. No. 4.8e-13;
Matches 74; Conservative 0; Mismatches 13
                                                                                                       J. Cell Biol. 153 (5), 985-998 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .787
/organiam="Mus musculus"
/strain="C57BL/6"
/db xref="taxon:10090"
/chromosome="X"
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Rattus norvegicus SMPX protein (Smpx) mRNA, complete cds.
AF364071.1 GI:13940509
\translation="mskQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
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Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein
Hum. Genet. 105 (5), 506-512 (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (26-MAR-2001) B.M.-Arndt-Uni, Inst. f. Humang.,
Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
                                                                                                                                                                                                                                                              658. .662
/gene="Srmx"
/function="mRNA destabilising motif"
                                                                                                                                                                                                                                                                                                                                       06. .710
|gene="Srmx"
|function="mRNA destabilising motif"
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    . 892
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"

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/gene="Srmx"
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                                                                                                           535. .539
/gene="Srmx"
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gene="Srmx"
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/gene="Srmx"
                                                                                      gene="Srmx"
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/qene="Srmx"
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Patzak, D.
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Best Local Similarity
Matches 74; Conservat
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AF364071
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                                                                                                                                                                                                                 /protein_id="AaK50398.1"
| Da xref="901:13940508"
| translation="WSKQPTSNVRATQANINIPMGAFRPGAGQPPRRKESTPETEEGA
| PTTSEEKKPIPGMKKPPGPVVNLSEIQNVKSELKFVPKGEQ"
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Direct Submission
Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial
College School Of Medicine, SAF Building, Exhibition Road, South
Kensington, London SW7 2AZ, UNITED KINGDOM
Location/Qualifiers
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codon start=1
foodor_t="stretch responsive muscle (X-chromosome)"
protein id="CAC08493.1"
db_xref="GI:10178963"
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AJ245772.1 GI:10178962
Srmx gene; stretch responsive muscle (X-chromosome).
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/organism="Mus musculus"

/strain="C5/BL/10"

/db xref="taxon:10090"

/tissue type="skeletal muscle"

1. .943

/gene="Srmx"
               'organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                  /evidence=experimental
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                                                                                                                                                                     /codon_start=1/product="SMPX
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199. .456
/gene="Smpx"
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gene="Srmx"
                                                                                                                                                                                                                                                                                                                                               /gene="Smpx"
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TITLE
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Gaps

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7: contig of 1317 bp in length
7: gap of unknown length
6: contig of 1383 bp in length
7: gap of unknown length
7: contig of 1344 bp in length
7: gap of unknown length
7: contig of 1520 bp in length
7: gap of unknown length
7: contig of 1004 bp in length
7: gap of unknown length
7: contig of 1098 bp in length
7: gap of unknown length
7: gap of unknown length
7: contig of 1118 bp in length
7: contig of 1146 bp in length
7: gap of unknown length
               Moser, M., Neal, D., Newtson, J., Newtson, N.
                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 82586)
Worley, K.C.
Direct Submission
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8266:
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                                                                                   /godon_grart=1
/product="SMPX protein"
/protein_id="AAK50399.1"
/db_xref="G1:1340510"
/translation="MSKQPISNVRSIQANINIPMGAPRPGAGQPPRRKESTPGTAEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82586 bp DNA linear HTG 11-JUL-2002
Rattus norvegicus clone CH230-2911, *** SEQUENCING IN PROGRESS ***,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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80.5%; Pred. No. 1e-10;
tive 0; Mismatches 1
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/gene="Smpx"
/evidence=experimental
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/note="alternate"
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/gene="Smpx"
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Nguyen, N. Nickerson, E., Newheshwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Newheshwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, B., Pull. B., Peery, J., Perez, L., Rives, M., Ren, Y., Rayes, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Suderk, T., Sparks, A., Stanley, H., Stone, H., Sutcon, A., Svatek, T., Taylor, P., Tanerisa, A., Tamerisa, R., Tanerisa, A., Tamerisa, R., Tanerisa, R., Tang, H., Usman, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wand, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wailtans, G., Williams, G., Williams, G., Walliams, G., Wall
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NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the piaces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17943701.
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center ode: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Nguyen, N.,
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Barbaria, J. Banes, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adiabsos, S. H., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bubok, S. L., Amaratunge, H.C., Aret, J.R., Bytch, N.C., Carron, P., Baryan, P., Bretter, P., Brieva, M., Brown, R., Bryan, N.C., Charez, D., Cox, C., Burrell, K.L., Bytch, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Charez, D., Cox, C., Davila, M. L., Davis, C., Davy-Carroll, T., Dederich, D.A., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dind, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Balls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garra, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Haule, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Hullyk, S., Joudah, S., Karlsson, E., Kelly, S., Kharl, W., Landey, M., Marcinez, E., Mahhimey, E., Mathins, E., Makhimey, E., Mathins, E., Pickens, R., Pathus, E., Sone, H., Svatek, A., Fabor, P., Tameria, A., Svatek, A., Taneria, A., Taneria, K., Vugun, M., Nickerson, E., Nachola, M., Svatek, A., Robostari, N., Sisson, I., Sutton, A., Svatek, A., Robostari, N., Sutton, A., Svatek, A., Robostari, N., Wang, O., Warne, N., Villalon, S., Warlen, S., Warten, R., Sonalke, T., Packer, M., Svatek, A., Robostari, N., Wang, O., Wang, G., Warren, S., Warten, R., Warten, R., Warten, R., W
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Rattus norvegicus clone CH230-20D15, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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0
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Location/Qualifiers
1. .82586
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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a 17332 c 15913 g 21644 t 49
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Best Local Similarity 80.59
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Rattus norvegicus
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AUTHORS
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COMMENT

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                                                                                                  Worley, K.C.

1. Submitted (18-70L-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Daylor Plaza, Houston, TX 77030, USA

1. Submitted (18-70L-2002) Human Genetics, Baylor College of Medicine, One Center: Baylor College of Medicine

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Contact: higsc-help@bcm.tmc.edu

Center project name: CH230-20015

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Center project name: CH230-2015

Consensus quality: 142614 bases at least Q30

Consensus quality: 142614 bases at least Q30

Consensus quality: 154556 bases at least Q20
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Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D. Weinstock,G. and Gibbs,R. Direct Submission Unpublished
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Mammalia; Eucheria; Primates; Catarini; Homininde; Homo.
Marchia, D., Adama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.
Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T.,
Barbaria, J., Bowde, S., Briver, M., Brown, R., Brom, M., Brown, D.,
Bouck, J., Bowde, S., Briver, M., Brown, E., Brom, M., Brown, D.,
Carron, T. F., Carter M., Cavazos, S. R. Chacko, J. Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chiu, D., Dathorne, S. R., David, R.,
Delaney, K.R., Delgar, D., Edwards, C.C., Relefing, S.,
Barnhart, C., Edgar, D., Edwards, C.C., Relefing, S.,
Earnhart, C., Edgar, D., Edwards, C.C., Riag, M., Pord, J., Foster, P.,
Frantz, P., Gabisi, A., Gaevie, C.C., Riad, M., Pollh, H.H.,
Douthwaite, K.J., Daper, H. Dugan, Rocha, S., Dubbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Riad, M., Polle, Foster, P.,
Frantz, P., Gabisi, A., Gaevie, C., Riad, M., Polle, Foster, P.,
Frant, P., Gabisi, A., Gaevie, C., Rartie, M., Hart, M., Havis, P.,
Hamilton, K., Han, J., Harris, C., Hartie, K., Hart, M., Havis, P.,
Hamilton, K., Han, J., Harris, C., Hartie, K., Hart, M., Havis, P.,
Hamilton, K., Han, J., Harris, C., Hartie, K., Hart, M., Havis, P.,
Hune, J., Ioshikhes, I., C., Lawis, L., Li, J., Li, J., Lu, X.,
Johnson, R., Jolivet, R., Joudah, S., Karlsson, B., Kelly, S., Khan, U.,
King, L., Lee, E., Lewis, L.C., Lawis, L., Li, J., Li, T., Lindry, N.,
Incier, A., Lucier, R., Martindale, A., Martinez, B., Massey, E.,
Marchiney, B., Monigomery, K.T., Morgan, M., Molton, M., Molyen, N.,
Neal, D., Nelson, D., Newtson, J., Newtson, N., Muyen, N.,
Neal, D., Nelson, D., Newtson, J., Newtson, N., Muyen, N.,
Neal, D., Nelson, D., Newtson, J., Shim, C., Shooshtari, N., Taylor, C., Taylor, T., Telfcod, B., Thomas, N.,
Tansey, J., Taylor, C., Taylor, T., Telfcod, B., Thomas, N.,
Nauli, K., Wanguez, L., Wanguez, L., Shim, C., Wuyen, N., Wulliamson, M., Wulliamson, M., Walfer, M., Railas, M., Rolle, M., Wulliam
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                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          AC079455 50-JUN BAC RP11-147D16 (Roswell Park Cancer Institute
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of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                  Numan BAC Library) complete sequence.
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Direct Submission
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Direct Submission
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

1 (Dases I to 923)

Palmer, S., Groves, N., Schindeler, A., Yeoh, T., Biben, C., Wang, C.-C., Sparrow, D.B., Barnett, L., Jenkins, N.A., Copeland, N.G., Koentgen, F., Mohun, T.J. and Harvey, R.P.

The small muscle-specific protein Csl modifies cell shape and promotes myocyte fusion in an finsulin-like growth factor
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                                                                                                                                                                                                                                                                  DD 115912 GCCAATATTAATATTCCAATGGGAGCCTTTCGTCCGGGAGCTGGGCAGCCTCCCAGAAGG 115971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobases 1 to 923)
Sparrow, D.B., Mohun, T.J. and Harvey, R.P.
Direct Submission
Submitted (30-JAN-2001) Developmental Biology Unit, Victor Chang Cardiac Research Institute, 384 Victoria St, Darlinghurst, NSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 2.2e-10;
0; Mismatches 17.
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Xenopus laevis Chisel (Csl) mRNA, complete cds.
AF343894
          contig of 6796 bp in length
gap of unknown length
contig of 8467 bp in length
gap of unknown length
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Pred. No. 1.5e-09;
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1. .923

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435. .710

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21275706
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1 Similarity 78.2%;
68; Conservative
          156271:
156371:
164838:
164938:
                                                                                                                                       68.7%;
80.5%;
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Best Local Similarity 80.5'
Matches 70; Conservative
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name="RH80030"

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Direct Submission
Submitted (26-JUN-2002) Human Genome Sequencing Center, Department
Submitted (26-JUN-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 26, 2002 this sequence version replaced gi:21327310.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

(More Acids Res. 25:3389-3402) similarity are identified by BLAST EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot ation.html.

Location/Qualifiers

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FEATURES

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Gaps ö 41.8%; Score 36.4; DB 9; Length 50479; 70.0%; Pred. No. 0.057; 1ve 0; Mismatches 21; Indels 0; 49; Conservative Local Similarity Query Match Matches

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17 CAATGGGAGCCTTTCGGCCAGGAGCAGGTCAACCCCCCAGAAGAAAAGAATGTACTCCTG 76 ò 셤

77 AAGTGGAGGA 86

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14495 GAAGGGAGGA 14486

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Direct Submission
Submitseion
Submitted (129-MAY-1999) Genome Sequencing Center, Washington
Submitted (129-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
University School of Medicine, 4444 Forest Park Parkway,
University School of Medicine, Attachington
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Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 108969)

Waterston, R. H.
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41.8%; Score 36.4; DB 9; Length 108969;
Best Local Similarity 70.0%; Pred. No. 0.063;
Matches 49; Conservative 0; Mismatches 21; Indels 0;
                                                108969 bp DNA lin
Homo sapiens clone 277F10, complete sequence.
AC004813.2 GI:4926912
HTG.
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Search completed: April 15, 2003, 20:57:25 Job time: 332.114 seca

Db 95283 GAAGGGAGGA 95292 77 AAGTGGAGGA 86

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1CE 1 (bases 1 to 501)

PRS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore
, B., Morris, M., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,

Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

E Generation and analysis of 280,000 human expressed sequence tags
INE 9704478

TO Contact: Wilson RK

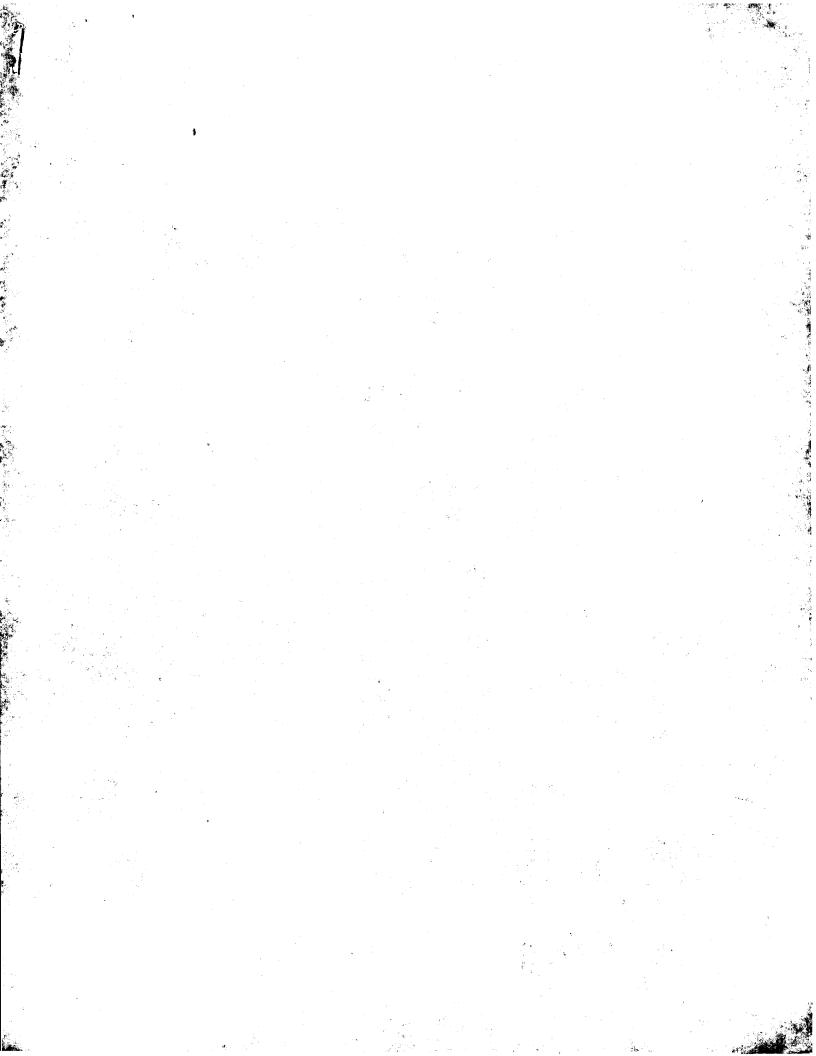
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA211521 501 bp mRNA linear EST 31-JAN-1997
EN55501.r1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:562057 5', mRNA sequence.
AA211521
AA211521 GI:1810175
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 683)
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683 bp mRNA linear EST 29-
7£70c03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA cl
IMAGE:3300004_3' similar to TR:Q9UHP9 Q9UHP9 SMALL MUSCULAR
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Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 443.
                                                                                                                                                                                                                     High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                                                                                                                                                                  Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/lab_host="Solrk (kanamycin resistant)"
/lab_host="Solrk (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
/note="Organ: skeletal muscle; Cloned unidirectionally.
Site_1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from patient with
malignant hyperthermia. Average from patient with
malignant hyperthermia. Average 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
/db xref="taxon:3566"
/db xref="taxon:3606"
/clone="TMAGE:3300004"
/clone="Soares NSF_F8_9M_OT_PA_P_S1"
/lab host="UPH10B"
/lab host="UPH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
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/db_xref="GDB:4595347"
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/tissue_type="muscle"
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/clone="IMAGE:562057"
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Pred. No. 4.7e-31;
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                                                                                                                                                                                                                           Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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UI-E-DXO-agn-i-12-0-UI.rl UI-E-DXO Homo sapiens cDNA clone
UI-E-DXO-agn-i-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                    Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHF pool 1:
309384-310919, 323208-325895 Soares NbHP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NbHF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-305311, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-74099 Subtraction by Bento Soares and M. Fatima Bonaldo."
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/clone="UI-E-DX0-agn-i-12-0-UI"
/clone lib="UI-E-DX0"
/rissue type="fetal eyes"
/dev_stage="fetal"
                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                              Location/Qualifiers
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Pred. No. 4.7e-31;
D; Mismatches 0;
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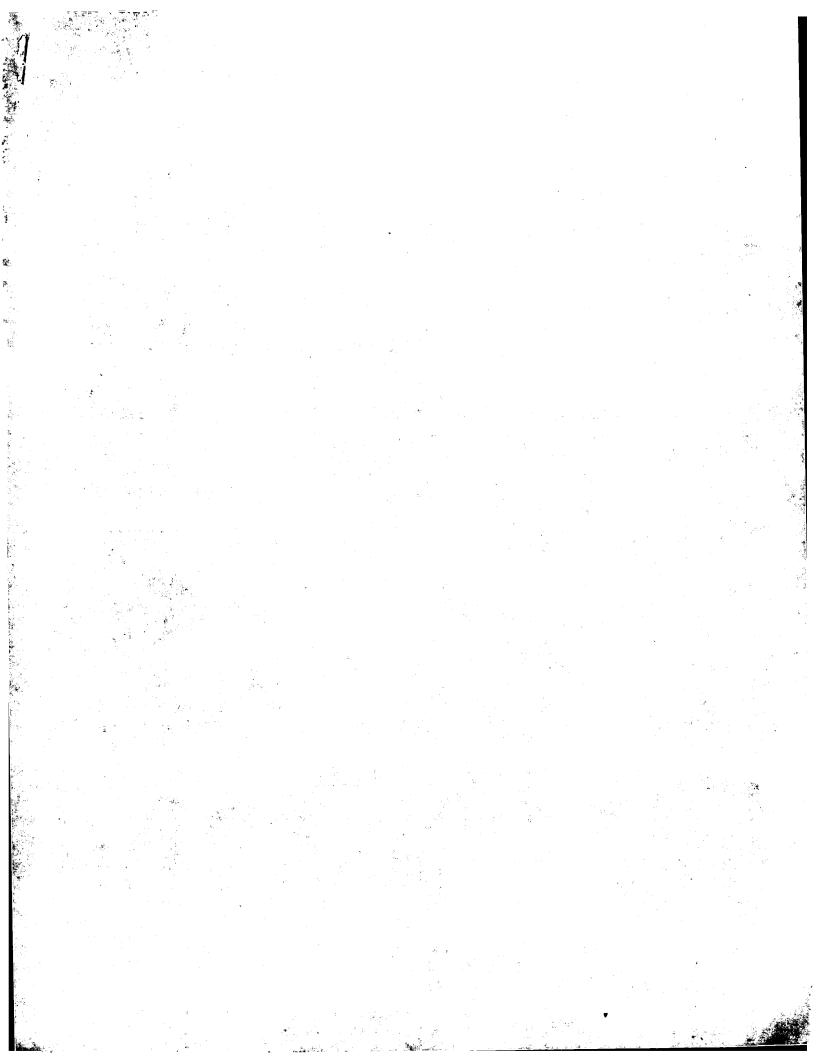
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BASE COUNT ORIGIN Ouery Match Best Local Similarity 100.0%; Score 149; DB 14; Length 719; Best Local Similarity 100.0%; Pred. No. 4.7e-31; Matches 149; Conservative 0; Mismatches 0; Indels 0. 392 AAAGCTGAACAGTAGTAGGAAGAAAAAAG 4,70 121 AAAGCTGAACAGTAGTAGGAAGAAAAAG 149 332 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCC 391 272 GGTGTTCCTCCCACCTCGGATGAGGAGGAGGAGCGAATTCCGAGGAGCGAAGAAACTTCCA 331 61 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120 1 GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60 226 a /lab_host="DH108 (Life Technologies) (T1 phage resistant) "
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DXO is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
with an oligo-dT primer containing a Not I site. Double
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucloctide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
sequence tag for this library is AGAATCAAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)." 0; Gaps 0

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BF126275 601650456
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DEFINITION REFERENCE AUTHORS Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohifing,T.,
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohifing,T.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

9704478 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu AA211521 501 bp m zn55001.rl Stratagene muscle 937209 IMAGE:562057 5', mRNA sequence. Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the Contact: Wilson RK human. AA211521.1 GI:1810175 mRNA Homo sapiens cDNA clone linear 8 63108 EST 31-JAN-1997

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RESULT 2
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Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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683 bp mRNA linear EST 29-
7£70003.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA cl
IMAGE:3300004 3' similar to TR:Q9UHF9 Q9UHP9 SMALL MUSCULAR
PROTEIN: , mRNA sequence.
BE856875
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/db_xref="GDB:4595347"
/db_xref="taxon:9606"
/clone="IMAGE:562057"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
/tev_stage="adult"
/lab_host="SOLR (kanamycin_resistant)"
                                                                   /clone="IMAGE:3300004"
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                                                                                                                                      organism="Homo sapiens"
db_xref="taxon:9606"
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100.0%; Pred. No. 4.7e-31;
tive 0; Mismatches 0;
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1 (bases 1 to 719)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM697544 719 bp mRNA linear EST 28 UI-E-DX0-agn-i-12-0-UI.rl UI-E-DX0 Homo sapiens cDNA clone UI-E-DX0-agn-i-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
                                                                                                                                                                                                              Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             discovery
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                                                                                                                                                                                                                                                                                                                                                                                Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                          primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries were mixed, and ss circles were made in vitro
/clone="UI-B-DX0-agn-i-12-0-UI"
/clone_lib="UI-B-DX0"
/tissue_type="fetal eyes"
/dev_stage="fetal"
                                                                                                                                                                 ocation/Qualifiers
                                                                                                 db_xref="taxon:9606"
                                                                                                                     organism="Homo sapiens"
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Best Local S
Matches 149
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                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 756)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                              High quality sequence stop: 619.
                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DX0 is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGAATCAAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
/clone="IMAGE:4338594"
/clone lib="NHH MGC Bl"
/lab_host="DH10B (TT phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: Sfil (ggccgcctcggcc); Site_2:
(ggccattatggcc); 5' and 3' adaptors were used In c
                                                                                                                                                             organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                                                                                                 ocation/Qualifiers
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Pred. No. 4.7e-31;
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ggcc); Site 2: SfiI were used In cloning
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RESULT 4 BF791178 LOCUS

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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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and 3' adaptor sequence:
5'-ANTCTAGAGGCGAGGCGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palc
                                                                                                             /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="InhAGE:4293721"
/clone=lib="NIH_MGC_81"
/lab host="PH10B (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: Sfi (ggccgctcggcc); Site_2: Sfi (ggccattatggcc); 5; and 3; adaptors were used In cloning as follows: 5; adaptor sequence: 5; -CACGGCCATTATCGCCC-3;
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5'-ATTCTAGAGGCCGAGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: CLONETECH Laboratories, Inc
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National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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Plate: LLCM1131 row: h column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone="IMAGE:4289735"
/clone="IMAGE:4289735"
/clone=lib="NNH MGC 81"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (TI phage-resistant); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/clontech); Site_1: Sfil (ggcogtctoggc); Site_2: Sfil
(ggcoattatggco); 5; and 3; adaptors were used In cloning
/ggcoattatggco); 5; and 3; adaptors were requested 5; CACGGCCATATGGCC-3;
and 3; adaptor sequence: 5; CACGGCCATATGGGCC-3;
and 3; adaptor sequence
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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a 147 c 239 g 208 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:11648824
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                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 149; DB 12; 100.0%; Pred. No. 4.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 879;
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RESULT 9
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AUTHORS
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SOURCE
ORGANISM
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BF672126
LOCUS
                            DEFINITION
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VERSION
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                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 149; DB 12; Best Local Similarity 100.0%; Pred. No. 4.7e-31; Matches 149; Conservative 0; Mismatches 0;
                                                                                                                                        366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
                                                                                                                                                                          121
                                                                                                                                                                                                                                                                        246 GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 305
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                                                                                                                                                                                                                                                                                                   1 GGTGTTCCCTCCCACCTCCGATGAGGAGGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60
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National Institutes of Health, Mammalian Gene Collection (MGC)

LUnpublished (1999)

Contect: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1141 row: p column: 20

High quality sequence stop: 621.

Location/Qualifiers
                                                                                                                                                                                                                      GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
                                                                                                                                                         AAAGCTGAACAGTAGTAGGAAGAAAAAAG 149
                                                                                                                                                                                                   GGACCTGCAGTCAATCTATCGGAAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCC
                                                                                                                                  AAAGCTGAACAGTAGTAGGAAGAAAAAAG 394
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         BF790243 909 bp mRNA line 602249777F1 NIH_MGC_81 Homo sapiens cDNA clone mRNA sequence.
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1 (bases 1 to 906)
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208 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="taxon:9606"
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/lab host="DH10B (TI phage-resistant)"
/lab host="branch (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: Sfil (ggccgctcggcc); Site 2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used In cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCCC-3'
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                     linear EST 12-JAN-2001
lone IMAGE:4328154 5',
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AUTHORS
TITLE
                                                                                                                                                             DEFINITION
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VERSION
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Query Match
Best Local Similarity
Matches 148; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                      AAAGCTGAACAGTAGTAGGAAGAACAAAG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 374
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
                                                                                                                                                                                                       mRNA sequence
BF672902
                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 909)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                            BF672902.1
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Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETE Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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BF790243.1
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Location/Qualifiers
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200 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:9666"
/db xref="taxon:9666"
/clone="IMAGE:4328154"
/clone="IMAGE:4328154"
/clone="IMAGE:4328154"
/clone="IMAGE:4328154"
/clone="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/clontech; Site 1: SfiI (ggccgcctggcc); Site 2: SfiI
/ggccattatggc;); 5' and 3' adaptors were used In cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
sold 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
S'-ATTCTAGAGGCCGAGGGGGGCGATG-dT(30)BN-3' (where B = A,

S'-ATTCTAGAGGCCGAGGGGGGGCGATG-dT(30)BN-3' (where B = A)
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Pred. No. 1.3e-30;
0; Mismatches 1
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JOURNAL COMMENT
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AUTHORS
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TITLE
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Best Local
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGCTGAACAGTAGTAGGAAGAACACA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGCTGAACAGTAGTAGGAAGAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC
                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 745)
1 (bases 1 to 745)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, PMTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                 AQ751265

AQ751265

AQ751265

BAC Library Homo HS 5574 B2 G02 SP6 RPCI-11 Human Male BAC Library Homo genomic clone Plate=1150 Col=4 Row=N, DNA sequence.

AQ751265
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High quality sequence stop: 687.
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                                                                                                                                                                                                                                                                                                                                                           AQ751265.1 GI:5538423
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     Contact: Mahairas GG,
                               99380589
                                                     Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                               scanning the human genome
                                                                                                    Sequence-tagged connectors: A sequence approach to mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4293878"
/clone=11b="NIH MGC 81"
/clone 11b="NIH MGC 81"
/clone 11b="NIH MGC 81"
/lab host="DH108 (T1 phage-resistant)"
/not="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: Sfil (ggcggctcgggc); Site 2: Sfil
(ggcgattatggc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
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/db_xref="taxon:9606"
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98.6%;
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Pred. No. 6.8e-30;
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       Wallace JC,
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TITLE
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Best Local Similarity
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1150 row: N column: 4
Seq primer: SP6
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Location/Qualifiers
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 330)
Zhuchenko, O., Patzak, D. and Wehnert, M.
ESTs of clone xh8H11 (human heart)
Unpublished (1999)
Other ESTs: 8H11-R1-C8-OZ, 3055-10R-8H11-2, 3055-10U-8H11-2
Contact: Patzak D., submitter; (Wehnert M.; supervisor)
Department of Molecular Human Genetics
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          8H11-F1-C7-OZ Human heart cDNA
                    Institut for Human Genetics
Pleischmannstr. 42/44, D-17487 Greifswald, Germany
Tel: +49 3834 8653-93
Fax: +49 3834 8653-93
                                                                                                                                                                                                                                                                                                                                                                              AI355903.1
                                                                                                                                                                                                                                                                                                                                                                                                                   xh8H11, mRNA sequence.
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Email: patzak@rz.uni-greifswald.de ( mwehnert@rz.uni-greifswald
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ilarity 99.3%;
Conservative
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132 c 139 g 228 t 1 others
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/db xref="taxon:9606"
/clone="Plate=1150 Col=4 Row=N"
/clone lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Pred. No. 5.1e-28;
0; Mismatches 0
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cDNA clone
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AI355904
LOCUS
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Best Local Similarity
Matches 137; Conserv
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                    Unpublished (1999)

Other ESTS: BH11-F1-C7-OZ, 3055-10R-8H11-2, 3055-10U-8H11-2

CONTACT: PALTAK D. Submitter; (Wehnert M.; Supervisor)

Department of Molecular Human Genetics

Institut for Human Genetics

Fleischmannstr. 42/44, D-17487 Greifswald, Germany

Tel: +49 3834 8653-78(-74)

Fax: +49 3834 8653-93
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 330)

Zhuchenko,O., Patzak,D. and Wehnert,M.

ESTs of clone xh8H11 (human heart)
                                                                                                                                                                                                                                                                                                                                                                          AI355904
AI355904.1 GI:6649246
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                                                                                                                                                                                                                                                                                                                                   human.
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//dev_stages"adult"

//lab_hosts"E. coli"

//notes"Organ: heart; Vector: Lambda ZAP II, pKSII-;

Site_1: NotI; Site_2: NotI; Human heart cDNA library was
constructed in Lambda ZAP II vectors using NotI linkers.

Clones from the primary cDNA library were deposited into
96-well trays for storage and retrieval. The 'Isolation of
chromosome-specific genes by reciprocal probing of arraed
cDNA and cosmid libraries' (Human Molecular Genetics, 1995

Vol. 4, No 8; pp1373-1380) provided cDNA-Clones as
plasmids (vector pKSII-, E. coli)."
      patzak@rz.uni-greifswald.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="xh8H11"
/clone_lib="Human heart cDNA (CCLee)"
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Pred. No. 9.7e-28;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              (CCLee) Homo sapiens
( mwehnert@rz.uni-greifswald.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 330;
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JOURNAL COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCCCAAAGCTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acctrogatgadgadgadgadccaattrocaggagcgaagaaaacttrocaggacctrocagtro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTCGGATGAGGAGAAGACCAATTCCAGGAGCGAAGAACTTCCAGGACCTGCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137;
    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -40UP from Gibco
High quality sequence stop: 470.
                                                                                                                                 Tumor Gene Index
Unpublished (1997)
                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anar
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 683)
                                                                                                                                                                                                                                                                                                                                                                                BF111459 683 bp mRNA linear EST 20-0
7134h12.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clu
IMAGE:3523462 3' Similar to TR:Q9UHP9 Q9UHP9 SMALL MUSCULAR
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                           PROTEIN. ;, mRNA sequence.
BF111459
                                                                                                                                                                                                                                                                                                                                      BF111459.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single path sequence (manual checked and edited) with a gene specific primer of clone xh8H11. ESTB 3055-10R-8H11-2, 3055-10R-8H11-2 (with vector primers) and 8H11-R1-C8-OZ, 8H11-U1-C7-OZ (with gene specific primers) provide a contig of the whole insert of clone xh8H11. Insert Length: 850 Std Error: 10.00 Plate: 8 row: H column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: C8 (gene specific)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="E. coli"
/lab_host="E. coli"
/note="rorgan: heart; Vector: Lambda ZAP II, pKSII-;
Site_1: NotI; Site 2: NotI; Human heart cDNA library was
constructed in Lambda ZAP II vectors using NotI linkers.
Clones from the primary cDNA library were deposited into
96-well trays for storage and retrieval. The 'Isolation of
chromosome-specific genes by reciprocal probing of arraed
cDNA and cosmid libraries '(Human Molecular Genetics, 1995
, Vol. 4, No 8; pp1373-1380) provided cDNA-Clones as
plasmids (vector pKSII-, E. coli)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 330.
Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human heart cDNA (CCLee)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="heart muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="xh8H11"
                                                                                                                                                                                                                                                                                                                                  GI:10941149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 137; DB 9; Pred. No. 9.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                            Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                          Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                           EST 20-OCT-2000
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BASE COUNT
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BG223652
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 TCCTTCCCACATCGCATGAGTAGAAAATGCCAATTCCAGGAGCGAAGAAACTTCCAGGAC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 CTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAAATATGTCCCCAAAG 487
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hes 138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAGTCAATCTATCGGAAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACAGTAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAACAGTAGTAGGAAGAAAAAA 462
Tel: 780 492 0169
Fax: 780 492 4265
Email: smoore@afins.ualberta.ca
The sequence best matches gb:HSA250584 (Homo sapiens mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene).
9/2000 ) in GenBank main database at E-value of le-115.
PCR PRimers
FCRMARD: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 bp mRNA linear EST 07-FEB-:
1M00010F05 Bovine Mixed Skeletal Muscle cDNA Library Bos taurus
cDNA 5', mRNA sequence.
B0223652
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 412)
Moore, S.S., Hansen, C., Li,C., Fu,A., Meng,Y., Li,G., Murdoch,G. Dixon,W. and Christopherson,B.
cDNA's from bovine mixed skeletal muscle
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG223652.1 GI:12709185
EST.
                                                                                                                                                                                                              Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410-Agri/For Centre, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                   Contact: Dr. Stephen S. Moore
                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodectyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in viro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was pCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NDHSP pool 1: 309384-310919, 323206-325895 Soares ND2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares ND2HPs pool 1: 752880-760583, 772104-774407 Soares NDHPA pool 1: 758280-760583, 772104-774407 Soares NDHPA pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                          Edmonton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 07-FEB-2001
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Search completed: April 15, 2003, 22:02:35
Job time : 312.035 secs
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Best Local Similarity
Matches 139; Conservat
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High quality sequence stop:
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/db_xref="taxon:9913"
/clone_lib="Bovine_Mixed Skeletal Muscle_cDNA_Library"
/sex="Two males and one female mixed"
/tissue_type="masseter, longissmusclorsi, biceps femoris,
semimembrances"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="muscle"
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/lab_host="XII-BlueMRF-strain"
/lab_host="XII-BlueMRF-strain"
/note="Organ: Skeletal muscle; Vector: Uni-2ZAPXR; Site_1:
/note="Organ: Skeletal muscle; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3%;
93.3%;
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Pred. No. 1.2e-26;
0; Mismatches 10;
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Perfect score:
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                                                                           IDENTITY_NUC Gapop 10.0 ,
                                                                                                                                                                                              April 15, 2003, 18:42:01; Search time 8.81622 Seconds (without alignments) 5183.040 Million cell updates/sec
                                       441362 seqs, 153338381 residues
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149
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                                                                             Gapext 1.0
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5836 5836 5836 5836	1796 3810 3810 4156 5835	2133 2653 2959 3171 3813 4281 51952 51952 2073 33000 98844	Length 909 2973
ביןטטבב	400444	44344444444	DB
-09-614 -08-380 -08-721 -08-891 -09-033	08-548- 08-475- -US95-(08-961- 09-033-	.US-09-164-034B-1 US-08-325-553-1 US-08-394-152A-1 US-09-710-092-1 US-09-710-092-1 US-09-710-092-17	ID US-09-484-970B-111 US-09-133-962A-15
Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli	9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	L INI 1, 1 1, 1 1, 1 1, 1 1, 1 1, 1 1, 1 1,	Description Sequence 11, App Sequence 15, Appl

28 27 18.1 5836 4 US-09-614-495-2 29 27 18.1 55827 4 US-09-813-133A-3 30 26.8 18.0 605 1 US-09-892-126-77 31 26.8 18.0 1929 4 US-09-178-252-24 32 26.8 18.0 1929 4 US-09-178-252-24 33 26.8 18.0 2118 4 US-09-1328-571A-12 33 26.8 18.0 2539 3 US-08-749-522-3 36 26.6 18.0 2539 3 US-08-749-522-2 36 26.6 17.9 1113 4 US-09-134-001C-1329 37 26.6 17.9 5115 3 US-09-134-001C-1329 38 26.6 17.9 5115 3 US-09-476-509B-3 39 26.6 17.9 5115 3 US-08-476-509B-3 39 26.6 17.9 18575 4 US-09-476-290-1 40 26.4 17.7 405 4 US-09-134-001C-23 41 26.4 17.7 828 4 US-09-134-001C-23 42 26.4 17.7 828 4 US-09-134-001C-23 43 26.4 17.7 828 4 US-09-693-147-1 44 26.4 17.7 828 4 US-08-858-207A-172 45 26.4 17.7 180 4 US-08-858-207A-172
27 18.1 5836 4 27 18.1 55827 4 .8 18.0 605 4 .8 18.0 1929 4 .8 18.0 2925 4 .8 18.0 2539 3 .8 18.0 2539 3 .8 17.9 1113 4 .6 17.9 5115 3 .6 17.9 5115 3 .6 17.9 18575 4 .4 17.7 735 2 .4 17.7 866 4 .4 17.7 866 4 .4 17.7 866 4 .4 17.7 866 4
5836 4 55827 4 605 1 1929 4 1929 4 2118 4 2118 3 3558 4 1113 3 5115 3 16875 4 4075 4 4087 4 1172 1
441444333333333333333333333333333333333
4 US-09-614-495-2 4 US-09-131-133A-3 1 US-08-592-126-77 4 US-09-178-252-24 4 US-09-134-001C-2519 3 US-08-178-252-2 4 US-09-134-001C-1329 4 US-09-134-001C-1329 3 US-08-1478-518C-3 3 US-08-1478-518C-3 3 US-08-1478-518C-3 3 US-08-1478-518C-3 4 US-09-134-001C-13 4 US-09-134-001C-23 4 US-09-134-001C-23 4 US-09-693-147-1 5 US-08-693-147-1 6 US-08-868-2078-172 1 US-07-945-288-9
US-09-614-495-2 US-09-613-133A-3 US-08-592-126-77 US-09-178-252-24 US-09-178-001C-2519 US-09-178-252-3 US-09-178-252-22 US-09-178-252-22 US-09-178-252-22 US-09-178-001C-1329 US-08-476-509B-3 US-08-476-509B-3 US-08-476-509B-3 US-08-476-509B-3 US-08-476-001C-23 US-08-476-001C-23 US-08-186-2078-172 US-08-693-147-1 US-08-693-147-1 US-08-683-2078-172 US-07-945-288-9

ALIGNMENTS

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APPLICANT: Jones, Karen A.

APPLICANT: Walker, Michael G.

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL Program

SEQ ID NO 111

LENGTH: 909

TYPE: DNA

ORGANISM: Homo mapiens

FEATURE:
NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6426186 021656.2CB1

US-09-484-970B-111
RESULT 2
US-09-133-962A-15/c
; Sequence 15, Application US/09133962A
; Patent No. 6372965
; GENERAL INFORMATION: DWARD LIGHTNER
; APPLICANT: JOHN JOSEPH OKULEY
; TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID
DELTA-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 149; DB 4; Length 909; Best Local Similarity 100.0%; Pred. No. 1e-38; Matches 149; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111, Application US/09484970B Patent No. 6426186 CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       474
                                                                                                                                                                                                                                                                                                                                                          121 AAAGCTGAACAGTAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAAACTTCCA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
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                                                                                                                                                                                                                                                                                                                               AAAGCTGAACAGTAGTAGGAAGAAAAAAG 502
                                                                                                                                                                                                                                                                                                                                                                                                                       GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATATGTCCCC 473
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Gaps

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET

CITY: WILMINGTON STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA

NUMBER OF SEQUENCES:

ADDRESSEE: William S. Ramsey,

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RESULT 3
US-09-164-034B-1
; GENERAL INFORMATION:
; APPLICANT: Mincheff, Milcho S.
APPLICANT: Mincheff, Milcho S.
Loukinov, I. Dmitri
Tombak, Serguei
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WANTE/KEY: intron; LOCATION: 521..1654; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-133-962A-15
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                             1259 AAAAGAAAACAGTTGAAGTGATGTATAAGCCACCAGAATTTGTCGACATCATATATCAGA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)992-5481
                                                                                                                                                                                                                                                                      86 ТССАGAATATTAAAAGTGAAСTAAAATATGTCCCCAAAGCTGAACAGT 133
                                                                                                                                                                                                                                                                                                                                                 26 AGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAA 85
                                  TITLE OF INVENTION: Immunotherapy of Cancer Through Expression of Truncated Tumor- or Tumor-Associated Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-Aug_1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          59;
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
SPONDENCE ADDRESS:
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433..520
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Pred. No. 2.3;
0; Mismatches
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US-08-325-553-1
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APPLICANT: Israeli
APPLICANT: Heston,
APPLICANT: Fair, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Applic
Patent No. 5538866
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN NUMBER OF SEQUENCES: 38
                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/164,034B
FILING DATE: 30-5ep-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ramsey, William S.
REGISTRATION NUMBER: 32,715
REFERENCE/DOCKET NUMBER: bril
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                                                                          CITY: New York STATE: New Yorl
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAACAGTAGTAGGAAGA 143
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TELEFAX: (410) 992-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramsey, Cook, Looper & Kurlander, STREET: 10420 Little Patuxent Parkway, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                          Heston, Warren D.W. Fair, William R.
                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Israeli, Ron S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21044
                                                                                                                                                                                                                Floppy disk
                                                                                                                    us/08/325,553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29.2;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 2.7;
Mismatches
                                                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
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REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:

28,678

1747/41426

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LOCATION:
US-08-325-553-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 644-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic seid
STERNITCHNESS: 4.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08394152A Patent No. 5935818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
        CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1074 TTACCCAGCAAATGAATA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014 TGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGG 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 TGAACAGTAGTAGGAAGA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 TGCTGACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGATGGTTGGAATCTTCCTGGAGG 1013
                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ТССАСТСЛАТСТАТСССАЛАЛІССАСЛАТАТТАЛАЛІСТАЛАЛІТАТСТССССАЛАЛСС 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 19.6%;
Local Similarity 50.7%;
les 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: Prostate-Specific Membrane Antigen
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                             United States of America
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262..2511
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  41426-B
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427 TATCGGAAATACAAAATTGACAAACAGATCAATAATTTAATAACTAAAGTTTATAGTAGG 486

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                                         Query Match
Best Local S
Matches 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Ale:
                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity 50.7%;
Matches 70; Conservative
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                                                                                                                                                                                                                                     APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6462186el Human ATPase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0085-USA
CURRENT FILING APPLICATION NUMBER: US/09/710,092
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/164,624
PRIOR FILING DATE: 1999-11-10
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TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                             LENGTH: 2919
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                         Local Similarity
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LOCATION: 262
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TYPE: nucleic acid
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TATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilbun,
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Friedrich, Glenn
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                                         Conservative
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                                                          19.3%;
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Pred. No. 2.9;
O; Mismatches
                                       Score 28.8; DB 4;
Pred. No. 4;
0; Mismatches 27;
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137 AGGAAGAAAAA 148

487 AAAGAGAAAAAA 498

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Donoho, Gregory

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Hilbun, Erin

APPLICANT: Helbun, Erin

APPLICANT: Priedrich, Glenn

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

TITLE OF INVENTION: No. 6462186el Human"ATPase Proteins and

TITLE OF INVENTION: NO. 646218
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US-09-710-092-9
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APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander
APPLICANT: Hibbun, Erin
APPLICANT: Nehls, Michael C. APPLICANT: Friedrich, Glenn
                                                                                                            SEQ ID NO 9
LENGTH: 3813
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Patent No. 6462186
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6462186el Human ATPase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0085-USA
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CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/164,624
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                            TYPE; DNA
ORGANISM: homo sapiens
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No. 6462186
WATIO
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Pred. No. 4.2;
0; Mismatches 27;
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Best Local Similarity
Thes 45; Conserve
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; ORGANISM: homo sapiens
US-09-710-092-13
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6462186el Human ATPase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0085-USA
CURRENT APPLICATION NUMBER: US/09/710,092
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/164,624
PRIOR PILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09710092 Patent No: 6462186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Priedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6462186el Human ATPase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0085-USA
CURRENT APPLICATION NUMBER: US/09/710,092
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/164,624
PRIOR PILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
                                                                                                                                                                                                                                                            APPLICANT: Donoho, Gregory APPLICANT: Turner, C. Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Ale
APPLICANT: Hilbun, Brin
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                                                                                                                                                                                                                                                                                                                                                                                                                                         487 AAAGAGAAAAA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 AGGAAGAAAAA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 19.3%;
Similarity 62.5%;
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turner, C. Alexander Jr. Hilbun, Erin Nehls, Michael C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28.8; DB Pred. No. 4.6; 0; Mismatches
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Pred. No. 4.4;
0; Mismatches
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                                             US-08-947-823-1
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; ORGANISM: homo sapiens
US-09-710-092-17
Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                              TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                      NAME: BABLIAN, KEVIN L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/I
PILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524 AAAGAGAAAAAA 535
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                                                                         TOPOLOGY:
                                                                                  STRANDEDNESS:
                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 ТАТССБВААТССАБААТАТТААЛАБТБВАСТАЛААТАТБТССССАЛАБСТБААСАБТАБТ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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p. 6114605
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                                                                                 nucleic acid
pedness: single
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Two Embarcadero Center, Eighth Floor
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Yaghoobi, Jafar
Bodeau, John
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Kaloshian, Isgouhi
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                                                                                                                                                                        (415)
                                                         DNA (genomic)
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 Score 28.4;
Pred. No. 14;
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Pred. No. 5.1;
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             DB 3;
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            Length 51952;
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                                                                                                                  Matches
                                                                                                                                             Query Match
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Patent No. 6232454
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                          1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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APPLICANT:
APPLICANT:
2035 AAGAAAAAGAGAAAAAGAAAAA 2058
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LIBRARY: PANCT
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES NUMBER OF SEQUENCES: 9
                           125 CTGAACAGTAGTAGGAAGAAAAA 148
                                                                           65 CTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAAATATGTCCCCAAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                    CAGTTCCTAGATGTCACAAACTAGCACAAACTCATGTCATTTCAGCACAAATCAAAATA 6060
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Corley, Neil C
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3174 Porter Drive
                                                                                                                                                                                                   PANCTUT01
                                                                                                                                                                                                                                                                                                                                  650-845-4166
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                                                                                                                Conservative
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                                                                                                                            18.8%;
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                                                                                                                              Score 28;
Pred. No.
                                                                                                               ed. No. 6.5;
Mismatches
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                                                                                                                                          DB 4;
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                                                                                                               35;
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                                                                                                                                          Length 2073;
                                                                                                               Indels
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US-09-215-694-18
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US-09-215-694-18
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APPLICANT: Wisconsin
APPLICANT: Hutchinse
APPLICANT: Kennedy,
APPLICANT: Park, Che
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SEQ ID NO 18
LENGTH: 33000
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10
LENGTH: 98844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.5%;
Best Local Similarity 63.6%;
Matches 42; Conservative
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CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                               NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30226 AAAGAA 30231
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NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
                                                                                    NAME/KEY: unsure LOCATION: 65471
                                                                                                                          NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                  OTHEत् INFORMATION: unknown
                                                                                                                                                                                                                                                                                               OCATION: 64383
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09215694B
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Park, Cheonseok n.m.i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wisconsin Alumni Research Foundation
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                                                                                                   Matches
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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LOCATION: 89049
OTHER INFORMATION: U
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93147 CTGTCACCCAGGCTGGAGTGCAGTGGCGCAATCCCGGCTCACTACAACTTCCACCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93207 GGTTCAAGCTATTCTCCTGCCTCAGTCTCCCAAGTAGCTGAAATTA 93252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: Herewith CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 1267 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 31, STREET
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                                                                                                                      Local
14 CCTCGGATGAGGAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 САСТСААТСТАТССБАЛАТССАБЛАТАТТАЛАЛСТБАЛСТАЛЛАТА 113
                                                                                                                                                                                                                                                   LIBRARY: BRSTN
CLONE: 1363873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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Pred. No. 3;
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1: //ggn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: //ggn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*

3: //ggn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*

4: //ggn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*

4: //ggn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*

6: //ggn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*

7: //ggn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

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Sequence 4, Appli
Sequence 468, App
Sequence 468, App
Sequence 3453, Ap
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 627, Appli
Sequence 302, Appli
Sequence 302, Appli
Sequence 278, Appli
Sequence 278, Appli
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10-176-991	10-176	10-176-985	10-176-750-	-10-176-747-	-10-176-492-	US-10-176-488-103 .	-10-175-743-	-10-175-740-	-10-175-739-	-10-174-588-	-10-174-582-	-10-174	-10-174-572-	-10-173	-10-180-557-	-10-180	-10-176-913-	-10-176-757-	-10-176-	-10-175-752-	-10-175-738-	-10-173-706-	US-10-175-737-103	-10-176-758-	US-10-174-590-103
Sequence 103, App	103	B 103	e 103	103	103	103	100	2 0	מי ב	102	103	103	103	B 103	e 103.	103	e 103	9 103	103	103	B 103	103	2 6	2 0	

ALIGNMENTS

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1
US-09-880-192-4
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US-09-880-192-4
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CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 824
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                     Query Match 100.0%; Score 149; DB 10; Best Local Similarity 100.0%; Pred. No. 4.3e-37; Matches 149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09880192
Patent No. US20020077470A1
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                                                                                         GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
                                                                                                                                           GTGTTCCTCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAACTTCCA 409
                                                                                                                                                                 GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA
                                                                 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC
AAAGCTGAACAGTAGTAGGAAGAAAAAAG
498
                                                                                                                                                                                                                                                         DB 10; Length 824;
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GRGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 23-BOVMS1-014-Q1-E1-F3
US-09-960-352-5216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-960-352-5216
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                                                                                                                                                                                                                                  FEATURE:
, NAME/KEY: misc feature
, OTHER INFORMATION: n=a,t,g or
US-09-962-436-468
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Best Local (
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APPLICANT: Warren, 1
APPLICANT: Tao, Ne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 135; Conserv
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 468 LENGTH: 587
                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturitle OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                         561 GGGTGTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCNGGAGCG-AGGAACCTCCC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
             61 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAA-CTAAAATATGTCCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACCTGCAGTCAACCTATCGGAGATTCAGAACATTAAAAGTGAACTGAAGTATGTCCCCC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTCCTCCCACCTCGGATGAGGAGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGCTGAACAGTTGTTGGAAGAAAAA 382
                                                                                                   GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60
                                                                                                                                                   139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.4%;
                                                                                                                                               75.7%; Score 112.8; DB 1 92.7%; Pred. No. 7.7e-26; tive 0; Mismatches 9
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Pred. No. 2.2e-30;
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US-09-790-988-1
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Patent No. US20020127687A1
GENERAL INFORMATION:
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LENGTH: 1875
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Best Local Similarity
                                                             SOFTWARE:
SEQ ID NO 1
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24
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APPLICANT: Kreps, Joel
                                                                                                                   APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATAWABE, HIDEMI
APPLICANT: WATAWABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US/09/790,988
EVERNOR APPLICATION NUMBER: JP2000-107160
PRIOR PILING DATE: 2000-04-07
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                                                                                                        NUMBER OF SEQ ID NOS:
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                  TYPE: DNA
ORGANISM: Buchnera
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                                        ENGTH: 640681
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FILE REFERENCE: 30296
CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 15
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 2780
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CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEO ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 9726
                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09841786 Patent No. US20020054883A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.3%;
Best Local Similarity 56.1%;
Matches 60; Conservative
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                                                                                                                                                                            APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.
APPLICANT: CHENGAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NĀGĀRĀJĀ, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJERV K.
APPLICANT: CHENGAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
                                                                                                                                                                        FILE REFERENCE: 30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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58.0%;
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Pred. No. 12
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APPLICANT: COSCAPIANT CONSERVATION
APPLICANT: Obleen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
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APPLICANT: CHENGAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
FILE REFERENCE: 30296
CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                  Sequence 6627, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 15
LENGTH: 11130
TYPE: DNA
ORGANISM: Fusobacterium necrophorum
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Patent No. US20020054883A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver.
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Local Similarity 56.1%;
les 60; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAAAAAAGAAACTTATTGGAAATGCAGCAGTTTTTTATGGAAACTATAAAAATAATGC 3174
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PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23

APPLICATION NUMBER: 60/207,727

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US-09-764-887-338
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US-09-764-887-338
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 338, Application US/09764887
Patent No. US20020042096A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE PAL13
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 658
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SOFTWARE: FastSEQ for
SEQ ID NO 6627
                                                                                                                                                                                                                                         Query Match 20.0%;
Best Local Similarity 52.9%;
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SEQ ID NO 338
LENGTH: 32190
TYPE: DNA
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PRIOR APPLICATION NUMBER: 60/253,625
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                                                                         13242 GGCCTGCAGTATATTTTTAAAAATTTCTTAAAACTĀAĀTAACAĀCĀĀCĀĀAAAACCCTAĀ. 13301
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LOCATION: (1)
13302 A 13302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                    122 A 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 CTANAATATGTCCCCAAAGCTGAACAGTAGTAGG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 GCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAA 105
                                                                                                            62 GACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/257,931
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Pred. No. 6.9;
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Pred. No. 32
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RESULT 11

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Patent No. US20020115085A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVENTION: Sets
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SEQ ID NO 278
LENGTH: 329
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Best Local Similarity
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
                               CURRENT APPLICATION NUMBER: US/09/803, CURRENT FILING DATE: 2001-03-09 PRIOR APPLICATION NUMBER: 60/188,609 PRIOR FILING DATE: 2000-03-09 NUMBER OF SEQ ID NOS: 2396 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                  APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcia, Pablo Dominiguez
Sudduth-Klinger, Julie
Reinhard, Christoph
                                                                                                                                                                                                                                                                                                                                                                         Randazzo, Fire
Tonnedy, Giulia C.
                                                                                                                                                                                                                                                                                                                                                                                                                      Giese, Klaus
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Innis, Michael A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09803719
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                                                                                                                                                                                                                                                                                     Dickson,
                                                                                                                                                                                                                    Leshkowitz, Dena
Kita, David
                                                                                                                                                                                                                                                    Labat, Ivan
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                                                                                                                                                                                                                                                                                                      rkvenjakov, Radomir
                                                                                                                                                                                                                                                                                                                      rmanac, Radoje
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                                                                                                                                                                                                                                                                                                                                                                      David
                                     for Windows Version 4.0
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                                                                                                                                                                                                                                                                     Snezana
                                                                                                                                                                                                                                                                                       Mark
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Pred. No. 7;
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RESULT 14
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US-10-087-464-45
Sequence 45, Application US/10087464
Publication No. US20030059436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-10-087-464-45
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US-09-803-719-278
                                                                                                                                                                               Sequence 14091, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 69; Conser
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 45
LENGTH: 2232
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Iiu, David
APPLICANT: Goel, Vikas
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chishti, Athar APPLICANT: Oh, Steven APPLICANT: Liu, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1939 ACGGAĞGAAĞAAATĞGAAAAACAAĞTTGAAĞCAATCACCAAĞCAAATAGAAĞÇTĞAAĞTĞ 1998
                                                                                                                                                                                                                                                                                                                                             2059 GAANAAGAAGAAAAA 2073
                                                                                                                                                                                                                                                                                                                                                                                                          133 ТАСТАССААСАЛАЛА 147
                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 ACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 ACCAGAGAGTGGAAAGGTACTTTGACAACAATGTTGAAAGGTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AGGCAACTCCATCCGGGAAGATAGTTGTAGGTCCAATAAGCAAAACCCTCTCAAAGACATT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            АТАТТАЛЛАСТСАЛАСТАЛЛАТАТСТСССАЛАССТСАЛСАСТА 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 19.7%;
l Similarity 55.3%;
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
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US-09-978-295A-617
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                                               Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
   APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO ACOLL193.1
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN BT474
OTHER INFORMATION: EXPRESSED IN ADULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                  122
                                                                                                                                                             193 GTTAGCCACATAACTAGGAGTATGAAGACACAAAAATGGATTGAGCAAATAATGGAAATG 134
73 ATACAGAAAGTTGGAGGGAAAAAAAA 48
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
                                                                                                                                                                                                     2 GIGITCCTCCCACCTCGGATGAGGAGAAGAAGCCCAATTCCAGGAGCGAAGAAACTTCCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                   AAGCTGAACAGTAGTAGGAAGAAAA 147
                                                                           GAAATGTATCAAAGATAATGGAAGTCAAGTCACTCAATGTTGAAGAAGCTTCTATAAAAA
                                                                                                                   GACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                       19.6%;
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IN BT474, SIGNAL = 4.9
IN ADULT LIVER, SIGNAL = 0.99
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                                                                                                                                                                                                                                                                     Score 29.2; DI
Pred. No. 9.7;
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Baker Kevin P. Botstein, David

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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR PRIOR DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Polypeptides and Nuc
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                                                                                                             OR FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079689
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079663
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/064249 FILING DATE: 1997-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/918585 FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
APPLICATION 1998-03-20
APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/078939
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FILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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APPLICATION 1
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                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillan, Kenneth Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Goddard, Audrey
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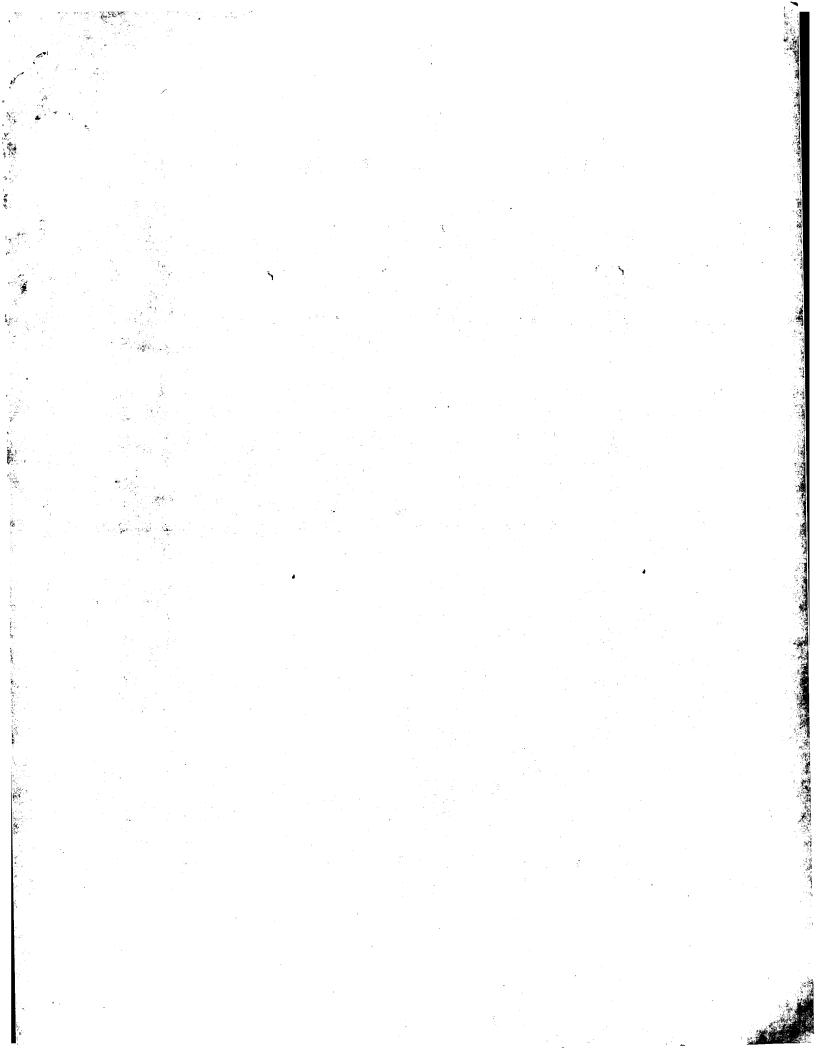
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APPLICATION NUMBER: 60/081838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                he number of results predicted by chance to have a
than or equal to the score of the result being printed,
by analysis of the total score distribution.
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65
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887
587
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778
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      AAD27226
AAD27216
AAX90904
ABK64187
ABL64590
AAX90903
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AAX90903
AAX9021483
ABN58272
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           Human 66214 cDNA c
Human 66214 EST cl
cDNA encoding huma
Human benign prost
Stomach cancer rel
cDNA encoding muri
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Mouse spliced tran
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Bunk D, Reuner B, Beck J, Henkel T;	(MBD1-) MBD1GENB AG.	(MEDI-) MEDICENE 10	30-MAY-2000; 2000US-207400P.	30 KW 2000		30-MAY-2001; 2001WO-EPOK165		06-DEC-2001.		WO200192567-A2		Homo sapiens.		CIOIR 66214; 88.	Simplify and the control of the cont	congenital heart disease. con the contract disease in the congenital heart disease.	pulmonary heart disease; valvular heart disease; perion disease;	Bystemic arterial hypertension; pulmonary hypertension; endocard;	- coronary neart disease	heart muscle disease: conduction disorder construction disorder conduction disorder co	hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhuth di

ALIGNMENTS

Pancreas cancer

Human

angiogenesis osteoblast d

AAF22303 AAC21058 ABL32350 ABL33270 AAK89112

ABK31243

AAS66690 AAS75823 AAS52990 ABL70198 AAS61156

Buchnera sp. genom Borrelia burgdorfe Drosophila melanog Human prostate exp Human prostate exp Human prostate exp Human prostate exp P. necrophorum tru P. necrophorum leu P. necrophorum leu Porcine muscular s Human secreted pro Human secreted pro Human prosophila melanog Human immune syste Human polynucleoti DNA encoding novel DNA encoding novel Enterococcus faeca Chemically treated Human gene regulat Signal transductio Arabidopsis thalia Human immune syste Human liver associ Human liver associ Human liver associ

5236 5474 32190 32190 32190 32190 40324 121724

ABQ67149 ABN90217 AAS31862 ABL49321
ABL3268
ABA92787
AAX20248
ABL28294
ABV34906
ABV43755
AAX167642
ABV167647
AAX62053
AAX167647
AAX62053
AAX62053
AAX62053
AAX6206392
AAX633588
ABL333188

11049 11049 140681 10715 10715 10715 10716 615 796 810 2780 2780 2780 2780 11130 111

AAD27226 standard; cDNA; 290 Human 66214 cDNA clone. 09-APR-2002 (first entry) AAD27226; BP.

Human; congestive heart failure; dilative cardiomyopathy; sudden ease; al; itis; death; sorder;

O

a a

WPI; 2002-122073/16

Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue

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Example

10; Fig

9a;

154pp;

English

The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to comethods for assessing the expression level of these genes. The method comethods for assessing the predisposition of mammals and preferably humans comeful to treat disease or for an acute state of such a disease. It is also considered that the cardiomyopathy, and the heart such as congestive heart failure, conjustive cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, componently, specific heart muscle disease, rhythm and conduction disorders, component for mention pulmonary heart disease, systemic arterial competension, pulmonary heart disease, valvular conducations, congenital heart disease, pericardial disease and conductions. Sequences of the invention are also used in gene therapy. Care useful for the development for medicaments for the treatments of cheart diseases. The present sequence is a cDNA from 66214 clone. This sequence used in the exemplification of the invention.

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RESULT 2
AAD27216
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                                                                                                                                Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone 66214; ds.
                                                                                                                                                                                                                                       Human 66214 EST clone DNA.
                                                                                                                                                                                                                                                                                                                AAD27216 standard; DNA; 886
polyA_signal
                                                                             CDS
                                     mise_feature
                                                                                                                Homo
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                                                                                                                sapiens
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                                       /*tag= a
/product=
298..588
   /*tag= b
/note= "66214 cDNA
857..862
                                                                           Location/Qualifiers
                                                     "Human
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                                                     66214 protein"
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RESULT 3

AAX90904 standard; cDNA;

ВP

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436 121

AAAGCTGAACAGTAGTAGGAAGAAAAAAG AAAGCTGAACAGTAGTAGGAAGAAAAAAG

464 149 376

GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCC

375

0

17-JAN-2000 AAX90904;

(first

entry)

cDNA encoding

human chisel (Csl)

gene.

Chisel gene; Csl; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; regulat Xq21.3-q22; adaptive process; muscle homeostasis; skeletal myopathy

g pathway; regulation; skeletal myopathy;

멍 δ 밁 8

79 19 19

GGACCTGCAGTCAATCTATCGGAAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC

120 78 60

GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCC

GCTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA

GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA

Query Best L

Local

Similarity

100.0%;

Score 149; DB 24; Pred. No. 1.1e-36; ; Mismatches 0;

Indels Length

Gaps

0;

290; <u>,</u>

Sequence

290

B₽;

103

P

50 C; 69 G;

68 T; 0 other;

Matches

149;

Conservative

0,

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tissues and their corresponding proteins. The invention also relates to comethods for assessing the expression level of these genes. The method comethods for assessing the expression level of these genes. The method comethods for testing the predisposition of mammals and preferably humans cometing the treat disease or for an acute state of such a disease. It is also constitute cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, precific heart muscle disease, rhythm and conduction disorders, comporathy, perferably heart disease, systemic arterial comporathy, pulmonary heart disease, systemic arterial comporation, pulmonary hypertension, pulmonary heart disease, valvular conductations. Sequences of the invention are also used in gene therapy. Comporated for the development for medicaments for the treatments of the invention composition the sequences of the invention composition in the sequence is expressed sequence tag composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a subject at risk for a heart disease e.g. (failure, dilative cardiomyopathy, heart muscle disease, the polypeptide expressed by genes abnormally expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bunk D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000US-207400P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2a; Fig 9b; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-122073/16.
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                                                                                                                                                                                         Sequence 886
                                             316
       61
                                                                          1 GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60
GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAAATATGTCCCC 120
                                           GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA
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                                                                                                                                       Similarity
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                                                                                                                     Conservative
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Pred. No. 1.5e-36;
                                                                                                                         Mismatches
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The present sequence is the cDNA encoding the human chisel gene (Cs1) that is mapped to the human chromosome Xq21.3-q22. It comprises 5 exons. It is a member of the EF-Hand protein super family and is involved in signalling pathways. It is predominantly expressed in heart and skeletal functions in regulation aspects of differentiation of cells. Cs1 functions in regulation aspects of differentiation or adaptive processes that maintain muscle homeostasis. This sequence can be used in the detection, diagnosis, prophylactic and therapeutic treatment of diseases such as those involving aberrant muscle cell development and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, skeletal myopathies such as Duchenne muscular dystrophy, heart failure, cardiac hypertrophy,
                                                                                                                                                              Claim 8; Page 149-150; 157pp;
                                                                                                                                                                                                                                                  WPI; 1999-610852/52
                                                                                                                                                                                                                 Isolated
                                                                                                                                                                                                                                                                          Harvey
                                                                                                                                                                                                                                                                                                           (CHAN-)
                                                                                                                                                                                                                                                                                                                                               27-MAR-1998;
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                                                                                                                                                                                                                                                                      RP, Musaro A,
                                                                                                                                                                                                                                                                                                CHANG CARDIAC RES INST VICTOR GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER &
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                                                                                                                                                                                     myopathies -
                                                                                                                                                                                                                                                                                            INST MEDICAL RES WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                     99WO-AU00220
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Exon_5
/note= "Corresponds to residues 4101-3680
human cosmid clone Ul12E8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466..887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human cosmid clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Exon_2
/note= "Corresponds
human cosmid clone t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317..465
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note= "Corresponds to residues
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U228D4"
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U228D4"
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RESULT 4
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XX ABK641
XX IN-
DT 18-JUN
XX Human;
XX Human;
XX Human;
XX Homo s
XX Homo s
XX Homo s
XX IN-
PH 07-AUG
PF 07-AUG
PF 07-AUG
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XX Identi
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Best Local
The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) fo or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolate from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profiles.

(I) is useful for diagnosing the onset or progression of BPH. (II) is
                                                                                                                                                                                                                                                                                                                                                                                       Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from parient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munger WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2000;
05-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACCTGCAGTCAATCTATCGGAAATCCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGCTGAACAGTAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAACTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGCTGAACAGTAGTAGGAAGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE LOGIC INC.
JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                     Page 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kulkarni P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-223323P.
2001US-0873319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostatic hyperplasia; BPH; prostate cancer; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , etc. The C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 149; DB 20;
Pred. No. 1.5e-36;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n Cel
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transgenic animals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto
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                                                              sion profile
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n of BPH.
n isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the level of expression of gene in the database, and displaying the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful treating BPH or prostate cancer. ABK64106-ABK64860 represent human benign prostatic hyperplasia gene sequences of the invention.
18-SEP-2000;

18-SEP-2000;

20-SEP-2000;

20-SEP-2000;

20-SEP-2000;

22-SEP-2000;

22-SEP-2000;

25-SEP-2000;

25-SEP-2000;

25-SEP-2000;

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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stomach cancer related gene sequence SEQ ID NO:2927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL64590 standard; DNA; 587
                                                                                                                                                                                                                                                                                               05-JUN-2000;
                                                                                                                                                                                                                                                                                                                             30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                      WO200194629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGCTGAACAGTAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGNCCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACCTAAAATATGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGCTGACCAGTAGTAGGAAGAAAAAAG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
2000US-23313P.
2000US-23467P.
2000US-23409P.
2000US-234034P.
2000US-23450P.
2000US-23450P.
2000US-23450P.
2000US-234923P.
2000US-235924P.
2000US-235924P.
2000US-23563P.
2000US-23563P.
2000US-235711P.
2000US-235840P.
2000US-235711P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
2000US-235840P.
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2000US-209531P.
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92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 112.8; DB 2
Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443
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                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
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28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young F
Soppet
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ
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                                      CAAAGCTGAACAGTAGTAGGAAGAAAAAAG
                                                                                                                                            GGACCTGCAGTCAATCTATCGGAAAATCCAGAATATTAAAAGTGAA-CTAAAATATGTCCC 119
                                                                                                                                                                                                  CANAGCTGACCAGTAGTAGGAAGAAAAAAG
                                                                                                                                                                                                                                                                                                     139;
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Augustus M, Weaver Z;
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2000US-237278P.

2000US-237294P.

2000US-237295P.

2000US-237316P.

2000US-237318P.

2000US-237425P.

2000US-237598P.
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2000US-237606P.
2000US-237608P.
2000US-244867P.
2000US-245084P.
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2000US-236032P.
2000US-236033P.
2000US-236034P.
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2000US-237172P.
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2000US-236111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID 2927; 44pp; English.
                                                                                                                                                                                                                                                                                                                             75.7%;
92.7%;
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                                                                                                                                                                                                                                                                                                   Ebner
          413
                                                      149
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                                                                                                                                                                                                                                                                                                                                                       Length 587;
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                                                                                                                                        The present sequence is the cDNA encoding the murine chisel gene (Cs1) CC that is mapped to the mouse X chromosome. It is a member of the EF-Hand protein super family and is involved in signalling pathways. It is correctly expressed in heart and skeletal muscles and is activated CC after the differentiation of cells. Csl functions in regulation aspects of differentiation or adaptive processes that maintain muscle corphylactic and therapeutic treatment of diseases such as those CC prophylactic and therapeutic treatment of diseases such as those CC is also used in the treatment of muscular and functional activity. It is also used in the treatment of muscular and myotonic dystrophies, cC myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, CC myotonic dystrophy, heart failure, cardiac hypertrophy, myocarditis, cc myofiber atrophy, etc. The Csl gene sequence can also be used in gene therapy, for the production of transgenic animals and for drug screening.
                                                                 Query Match
Best Local S
Matches 113
                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids encoding chisel, used to develop products treating cardiomyopathy, cardiac hypertrophy, heart failure and muscular myopathies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHAN-)
(GEHO)
(HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chisel gene; C81; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; thera; Becker's myotonic dystrophy; heart failure; cardiac hypertrophy;
          329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harvey RP, Musaro A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation; gene therapy; transgenic animal; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                  Local Sim
hes 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 0909xaa
                                      8
CTCCTACCACCTCAGAGGAAAAGAAGCCAATTCCTGGAATGAAGAAATTTCCAGGACCTG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              đB.
                    CTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGGAAGAAACTTCCAGGACCTG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-610852/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding murine chisel
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHANG CARDIAC RES INST VICTOR.
GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28650
                                                                                                                          778
                                                                 Conservative
                                                                                                                          B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98AU-0002634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-AU00220.
                                                                                                                  231 A; 166 C; 179 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "Chisel (CSL) protein"
/note= "Expressed especially in!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                            64.6%;
80.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palmer SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   778
                                                          Score 96.2; DE
Pred. No. 3.7e-
0; Mismatches
                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Cs1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal NA;
                                                                        .7e-20;
                                                                                          DB
                                                                                        20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heart
                                                                                      Length
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening; ss
                                                                                      778;
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                                                                                                                                              screening
                                                         Gaps
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RESULT 7
AACO14433
ID AACO14433
ID AACO14433
ID O6-0
XX AACO
DX Huma
XX Huma
XX Huma
XX Homo
PN EP10
XX EP10
XX EP10
XX EP10
XX ID E
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                                                                                                                   Matches
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene thorapy and chromosome mapping procedures. They are used to obtain vaccines
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 1481; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAG01477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC01483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC01483 standard; cDNA; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389
                                                               щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                      GGTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGA 49
GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCCAGGAGCGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAAACTGAAATTTGTCCCCAAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGTAGTCGAAAGGACACA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAGTAGTAGGAAGAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTCAATCTATCGGAAATACCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTG
                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' EST;
                                                                                                                                                                                                                   428
                                                                                                             Conservative
                                                                                                                                                                                                                   ₿₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; expressed
chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0122487
                                                                                                                                                                                                                   123
                                                                                                                                   32.9%;
                                                                                                                                                                                                             A; 111 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tag;
mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST,
                                                                                                          0
                                                                                                                                Score 49;
Pred. No.
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                                                                                                                                                                                                                104
                                                                                                        red. No. 1.4
Mismatches
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                                                                                                                                                                                                             90
                                                                                                                                                            DB 21;
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                                                                                                                              1.4e-05;
                                                                                                                                                                                                             T; 0 other;
                                                                                                          0
                                                                                                                                                      Length 428
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                                                                                                        Indels
                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                            full length
                                                                                                     Gaps
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RESULT 8 ABN58272

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The present invention describes oligonucleotide libraries for detecting CC messenger RNAs that populate a (sub-)transcriptome, where the CC (sub-)transcriptome comprises messenger RNAs transcribted from multiple CC (sub-)transcriptome units that populate a genome. The library comprises CC several oligonucleotides, each capable of hybridising selectively to a SC (set of messenger RNAs transcribed from a given transcription unit of CC the genome, which encodes one or more messenger RNAs splice variants. CC The oligonucleotide libraries are useful for detecting mRNAs from a CC biological sample, in expression profiling studies, in qualitatively or CC quantitatively characterising the corresponding transcriptome, and in CC transcriptomes. The libraries may also be used as specialised mini CC transcriptomes. The libraries may also be used as specialised mini CC particular biological or pathology specific genes such as those genes CC only expressed in specific tissue under a specific pathological CC condition; to detect developmental specific genes such as those genes CC transcripts and splice variants of a transcriptome of a patient suffering CC condition; to detect developmental specific genes; and to detect RNA CC transcripts and splice variants of a transcriptome of a patient suffering CC oligonucleotide sequences from ratt, humans and mice, which are used in CC the exemplification of the present invention
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                                                                         맑
        뭐
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                                                                                                                                           Query Match
Best Local S
Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-257383/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2001; 2001WO-IB01903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN58272 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID 31020; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental-specific genes
                                          108
          61
                                                                                                           48
                                                                            ч
                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                              exemplification of the present invention.

The sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from WIPO
GAAAT 65
                                                                            GAAGAAATTTCCAGGACCTGTTGTCAACTTGTCTGAGATCCAAAATGTTAAAAGTGAACT
                                                                                                             GAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACT 107
                                         AAAAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse; rat; splice transcript; detection;
variant; transcriptome; oligonucleotide 1
                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wasserman
                                                                                                                                                                                                             B₽;
                                                                                                                                               Conservative
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                                                                                                                                                                                                                 24
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                                                                                                                                                             31.8%;
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                                                                                                                                                                                                                 13
                                                                                                                                             0;
                                                                                                                                                               Score 47.4;
Pred. No. 2.
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                                                                                                                                                Mismatches
                                                                                                                                                                                                                 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mintz
                                                                                                                                                               .5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ
                                                                                                                                                                               DB 24;
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                                                                                                                                                Indels
                                                                                                                                                                               Length
                                                                                                                                                                                  65
                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unit of
                                                                                                                                               Gaps
                                                                                60
                                                                                                                                                0
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S

26 AGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAA 85

Matches Query Match Best Local

1 Similarity 67; Conserv

22.4%;

Score 33.4; Di Pred. No. 2.6; 0; Mismatches

ВB

0

56; 24;

Indels Length 11049;

0;

Gaps

0,

Sequence

11049

BP; 3032 A; 198 C; 2438 G; 5381 T; 0 other;

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RESULT 9
ABL92218/c
ID ABL922
XX DAL ABL922
XX DAL ABL922
XX DAL ABL922
XX DAL ABL922
XX Uniden
XX Uniden
XX Uniden
XX Uniden
XX O6-APR
XX O6-APR
XX O6-APR
XX O6-APR
XX O1-SEP
A (EPIG-
XX OLE A
XX WPI; 2
XX WPI; 2
XX WPI; 2
XX Claim
XX
                                                                                                                                                           cc acids comprising at least 18 base pairs of the chemically pretreated DNA co f genes associated with DNA repair selected from PMS2L1, PMS2L12, PMS2L13, PMS2L13, PMS2L5, PMS2L5, PMS2L5, PMS2L5, PMS2L5, PMS2L6, MGMT, MSB2, NUDT1, TDG, INPPL1, CC PMS2L23, PMS2L5, PMS2L5, PMS2L6, MGMT, MSB2, NUDT1, TDG, INPPL1, CC PMS2L13, PMS2L6, Nucleic acids of the invention and related coligomers, are useful for diagnosis of diseases associated with gene corpair, specifically ataxia telangiectasia, aging, Bloom's syndrome, CC Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, CC cockayne syndrome, trichthiodystrophy, Fanconi's anaemia, solid tumours candidated the particularly by determining status of cytosine methylation of candor by deterting single-nucleotide polymorphisms. Determination of CC and/or by detecting single-nucleotide polymorphisms. Determination of cherapies. The sequences given in records ABL92132-Ral92335 represent CC therapairs. The sequences given in records ABL92132-Ral92335 represent CC repair, and their complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMS2L1, PMS2L12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemically treated DNA repair gene fragment#14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-EP03972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 27; 25pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid derived from for diagnosis, e.g. of ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-034446/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek A,
                                                                                                     Note: The sequence data for specification, but is based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG
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                                                                           Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine
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                                                                           Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin
                                                                                                            this patent on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes associated with DNA repair, useful telangiectasia, by determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMS2L1;
                                                                                                        is not represented in the information supplied by t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
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CC The invention relates to nucleic acid sequences comprising at least 18 CC bases of a chemically pretreated gene associated with gene regulation, CS selected from 94 genes (ABL49301-ABL49394) and/or complementary sequences CC associated with DNA replication, CENUB, DNA21, ATR, CHDIL, ERCG3, SNRPA1, CC unmethylated at the 5-position to uracil or another base with DNA replication and the converts cytosine bases (CC hybridisation behaviour dissimilar to cytosine, to enable analysis of CC cytosine methylations. The DNA sequences and method are useful in the CC cytosine methylations of such diseases and method are useful in the CC replication and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes. They are especially useful of diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's Note: The sequence data for this patent did not form part of the printed specification and was supposed to be available directly from WIPO at the correspond to that referred to in the specification. The present data of taken from EPO data for the patent.
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ABL49321/c
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        Sequence 11049
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences from chemically modified genes associated with DNA replication, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. Ataxia telangiectasia
                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21; 23pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytostatic; neuroprotective; nootropic; immunostimulant; gene therapy; gene regulation; DNA replication; CEMPB; DNAZL; ATR; CHDIL ERCC3; SNRPA1; RAD50; LIG3; cytosine methylation; Ataxia telangiectasia; ATR-X; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001WO-EP03971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide associated with DNA replication SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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        BP; 3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
A; 198 C; 2438 G; 5381 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
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                                                                                                                                                                                                                                                          ' sequences
3, SNRPA1,
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Query Match

Score 33.4;

DB 24;

Length 11049;

Query Match Best Local Similarity

Sequence 11049

BP;

3032 A; 22.4%;

198 C;

2438 G;

5381 24; 56;

Η,

0 other;

Matches

Conservative

; Score 33.4; D; Pred. No. 2.6; 0; Mismatches

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Length 11049; Indels

<u>,,</u>

Gaps

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ABL32668/c
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The present invention provides a number of the final sequences which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, s disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                  Nucleic acid comprising fractor diagnosis and treatment cytosine methylation -
                                                                                                                                             Claim 1;
                                                                                                                                                                                                                         WPI; 2002-130909/17
                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                               (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                  WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5651
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acure myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL32668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32668 standard; DNA; 11049
                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurofibromatosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA 5649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ТСААЛАЙТАТТТАССАТАААЛАААААТАЛАТАЛАТАЛАСАТАССАЛТАЛАЛАСТАСААА 5652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds.
                                                                                                                                                                                                                                                                            EPIGENOMICS
                                                                                                                                   SEQ ID NO 641; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                            invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                     2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.5%;
                                                                                                                                                                           fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                Berlin
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene SEQ ID NO:
                                                                                                                                                                                                                                                <u>.</u>~
                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis; bowel dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
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                                                                                                                                                                           gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease;
                                                                                          sequences
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RESULT 12
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XX PR 07-A
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a gene (I) derived from Buchnera sp. CC containing the DNA (a) or (b), (a) has a fully defined base pair CC containing the DNA (a) or (b), (a) has a fully defined base pair CC sequence selected from a table of sequences found in the Buchnera sp. CC genomic DNA of ABA92787 given in the specification or is a DNA selected CC from complementary DNA sequences, and (b) is a DNA which hybridises with CC the DNA (a) and encodes a protein. Also described are: (1) a recombinant CC to CC (3) a genomic DNA of Buchnera sp. containing the sequence given in CC (3) a genomic DNA of Buchnera sp. containing the sequence given in CC (d), (c) is a DNA containing a fully defined sequence given in ABA92788 (C) (d), (c) is a DNA containing a fully defined sequence given in ABA92788 (C) is a DNA containing a fully defined sequence given in ABA92788 (C) the expression protein of the objective protein is collected from the CC resultant culture. The DNA is useful for developing agricultural CC chemicals for exterminating cockroaches. The present sequence, from the present invention.
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                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera; cockroach-symbiotic bacterium;
circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA92787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001292771-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A genomic DNA of cockroach-symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-126043/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000; 2000JP-0107160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-2000; 2000JP-0107160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 16-230; 237pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
               109
                                                                                                                                  49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARARARAACARACORACOCOCCOCCTCATCACCCGATTCCGCARTCRACCTRCCACGAR 5712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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AAATATGTCCCCAAAGCTGAACAGTAGTAGGAAGAAAAAA 148
                                                                      AATAAGATACAGAACGTGATTGTTTTTATCAGCAAACCAGTCTATTAAATATGGACTA 520494
                                                                                                                               AAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5649
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                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                  640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                  вP;
                                                                                                                                                                                                                                                                                                                     237522 A; 83822 C; 84757 G; 234580 T; 0 other
                                                                                                                                                                                                                         22.0%;
58.0%;
                                                                                                                                                                                               0;
                                                                                                                                                                                                                               Score 32.8;
Pred. No. 14;
                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                            DB 24; Length 640681;
                                                                                                                                                                                                      42;
                                                                                                                                                                                                      Indels
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RESULT 13
AAX20248/c
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                            Db 706680
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                                                                                   Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX20248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX20248 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1999
                                                                                                                                                                                          AAX20248 to AAX20402 represent polynuclectide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. to a family of motile, spiral-shaped bacteria called Spirochetes of prochetes are pathogenic in humans and Borrelia causes epidemic and spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                          New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-)
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayton R,
                                                                                                                                           Sequence 910715 BP;
                                                                                                                                                                                      endemic relapsing
 141 AGA 143
                                                         18
                                                      ддаалтссадаататтаааадтдаастаааататдтссссааадстдаасадтастадда 140
                            ĠĠĀĀĀTTĊĀĠĀĀTĀĀĀĀTĪĢĀĀĀCĀĀTĀĀCTTTTATĊĀĀĀTĊTĀĀĀĀĀĠTĀĠTGACĀ 706621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN GENOME SCI INC MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Dougherty BA,
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0057483.
                                                                                                                                                                                       fever, and Lyme borreliosis, more commonly
                                                                                                                                              327171 A; 129646 C; 130753 G;
                                                                                                  21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910715
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser
                                                                                        ٥,
                                                                                                     Score 32.6;
Pred. No. 1
                                                                                         Mismatches
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                                                                                                                      В
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                                                                                           19;
                                                                                                                    20;
                                                                                                                    Length 910715;
                                                                                            Indels
                                                                                                                                                 323091
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith
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                                                                                                                                                   T; 54 other;
                                                                                                                                                                                                                                                                                                                                                                   prevention
                                                                                            0,
                                                                                            Gaps
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RESULT 14 ABL28294 ID ABL28

ABL28294 standard; DNA; 10589

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706620

AA

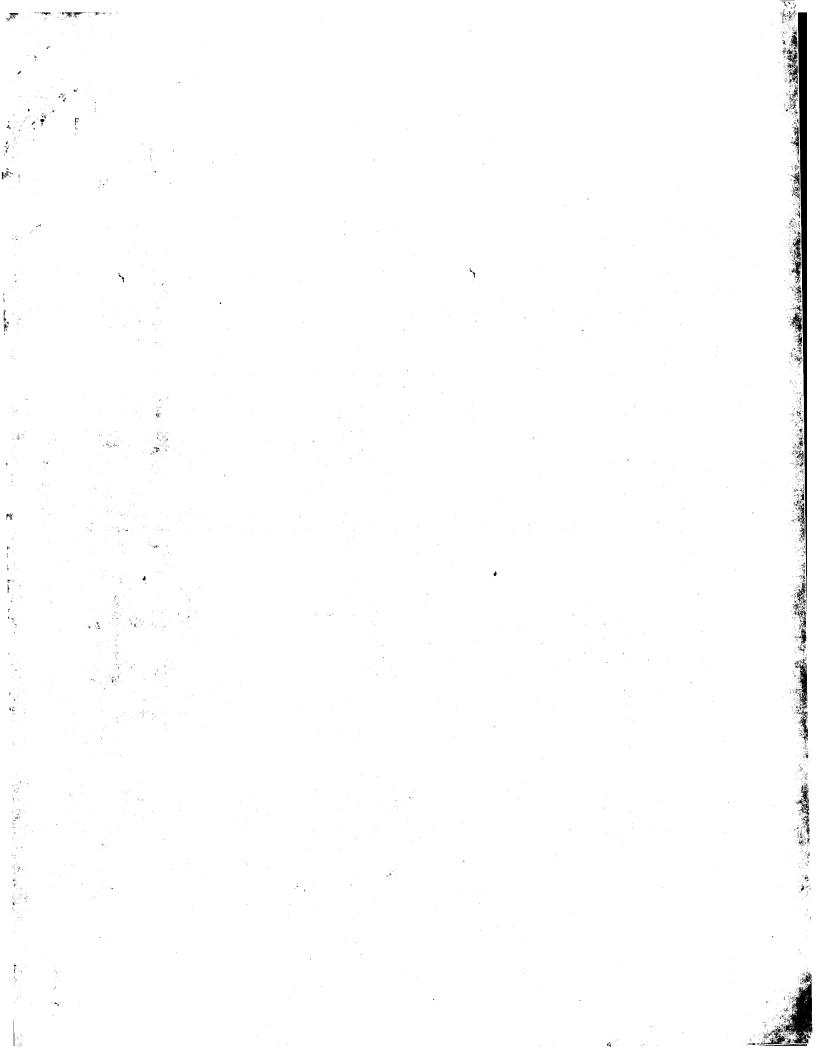
706618

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                                                                                                                                           RESULT 15
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Best Local
                                                                                                                                                                                                                                                                        Matches
   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic pharmacogenomic marker; gene; ss.
                                                                                                                                                                              1804
                                                                                                                                                                                                                          1744
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                         Human prostate expression marker cDNA 34897.
                                                                     16-SEP-2002
                                                                                            ABV34906;
                                                                                                               ABV34906 standard; cDNA; 615
                                                                                                                                                                                                                                                                                                            Sequence 10589 BP; 3083 A; 2231 C; 2183 G; 3092 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 36355; 21pp + Sequence Listing; English
                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI, 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 36355.
                                                                                                                                                                                                                                                                                                                                                                             ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL28294;
                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                      TAAGTTGTTCAACAAAAACTGACAAGTA 1831
                                                                                                                                                                                             таралтатетесесарастерасаста 134
                                                                                                                                                                                                                CGAAGAAACTTCCAGGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAAC 106
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                     Conservative
                                                                 (first entry)
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                                                                                                                                                                                                                                                                                21.5%;
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a and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                 Score 32; DB 2
Pred. No. 7.1;
0; Mismatches
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                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                       Length 10589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell-cell
                                                                                                                                                                                                                                                                Gaps
                marker;
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                                                                                         Search completed: April 15, Job time : 415.761 secs
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                                                                                                                                                                           Query Match
Best Local S
Matches 75
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                           in a patient;
(e) selecting
(f) assessing
(g) determinin
(h) assessing
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                               cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7298; 11750pp; English.
    468
                                122
                                                              408
                                                                                                                      348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                       62
                                                                                                                                                 N
                                                                                                                                                                                                                                                                                  selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                      is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                 GGCCTCTTATACAATAAAGAGATTTTTTTAAAAAAAAGATATAAAATTCACACATATGAGGA
                                                                            GACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCCA 121
                                                                                                         GTGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGCGAGCCACCATACCC 407
AAACTGGAGAGGAAAAGATAGCAACAA
                           AAGCTGAACAGTAGTAGGAAGAAAAA 148
                                                                                                                                   GTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCCAATTCCAGGAGCGAAGAAACTTCCAG
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                    615 BP;
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endege
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                                                                                                                                                                                                                            208 A; 131 C; 140 G; 136 T; 0 other;
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                                                                                                                                                                                      21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan JE;
                                                                                                                                                                        ٥.
                                                                                                                                                                                      Score 31.8;
Pred. No. 3.
                                                                                                                                                                        Mismatches
494
                                                                                                                                                                                                  DB 23;
                                                                                                                                                                       72;
                                                                                                                                                                     Indels
                                                                                                                                                                                               Length
                                                                                                                                                                                               615;
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                                                                                                                                                                 Gaps
                                                  467
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2003,

19:04:58



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Title:
Perfect score:
Sequence:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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Pred. No. is the number of results predicted by chance to have

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
R. M.
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Mammalia; Eutheria;
1 (bases 1 to 835)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Submitted (02-APR-2001) National Institutes of Health, Mammalian Submitted (02-APR-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                /clone="MGC:14584 IMAGE:4246501"
/tissue type="Skeletal Muscle"
/clone Tib="NIH MGC_81"
/lab host="DH10B"
                                                                                                                             /db_xref="LocusID:23676"
/db_xref="taxon:9606"
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                                    /note="Vector:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885)

Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Eastwood, M., Sassoon, D.A. and Coulton, G.R.

Identification of a novel stretch-responsive skeletal muscle gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA for stretch protein (Srmx gene).
                                                                                                                                                                                                                                                                                                                                     Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial College of Science Technology and Medicine, SAF Bldg, Level 2, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Related sequences:AJ245772, U73508 to U73509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Srmx gene; stretch responsive muscle (X-chromosome)
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                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                   gene="Srmx"
                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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Pred. No. 8.8e-33;
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                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        1 (bases 1 to 886)
Patzak,D., Zhuchenko,O.,
Identification, mapping,
                                                                  Homo sapiens
                                                                                                                  Homo sapiens
AF129505
                                                                                                                                      AF129505
                                                                                                    AF129505.1 GI:6625646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bunk, D., Reuner, B., Beck, J. and Henkel, T. Novel target genes for diseases of the he Patent: WO 0192567-A 18 06-DEC-2001;
                                                                              Homo sapiens.
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Sequence 18 from Patent
AX322774
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Pred. No. 8.8e-33;
       Lee, C.C. and Wehnert, M. and genomic structure of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 36503)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998) K
99063792
9847074
                                                                                                                                         Bequence.
U73508
                                                                                           Homo sapiens.
Homo sapiens
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cosmid clone U112E8
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DNA linear from Xp22.1-22.2,

complete

PRI 27-APR-1999

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316 GÓTGTTCCTCCCACCTCGGATGAGGAGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCA 375
                    AAAGCTGAACAGTAGTAGGAAGAAAAAAG
                                                                                       GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCC 120
                                                                 GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAAGTGAACTAAAATATGTCCCC
                                                                                                                                                          GGTGTTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAAGTTCCAGGAGCGAAGAAACTTCCA
 AAAGCTGAACAGTAGTAGGAAGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-JAN-1999) Molecular Human Genetics, Institut Human Genetics, Fleischmannstr. 42/44, D-17487 Greifswald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 886)
Patzak,D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-chromosomal human gene (SMPX) encoding a small muscular protein Hum. Genet. 105 (5), 506-512 (1999)
                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                   /gene="SMPX"
857. .862
/gene="SMPX"
a 172 c
                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mamskqpvsnvraiqaninipmgafrpgagqpprrkectpevee
gvpprsdeekkpipgakklpgpavnlseiqnikselkyvpkaeq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="Xq22.1-22.2"
<1. .>886
                                                                                                                                                                                                                                                                                                                                                                                           /gene="SMPX"
/note="alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not experimental
/product="small muscular p
/protein_id="AAF19343.1"
/db_xref="GI:6625647"
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/db_xref="taxon:9606"
/chromosome="X"
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Pred. No. 8.8e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-OCT-1996)
4 (bases 1 to 36503)
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                                                                                                                                                                                                                                                                                                                                                         This clone is from a chromosome X-specific cosmid library LLOXNCC01 'U'. The source of the chromosomes was a human/hamster hybrid, GM07297-F, from Robert Nussbaum at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livermore National Laboratory at http://www-bio.llnl.gov/genome to obtain the clone. VECTOR: Lawrist16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer/because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Department of Genetics
Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University, 44 SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 36503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. V., and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomics 44:227-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-APR-1999)
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                                                                                                                                    /rpt_family="L2" 3690. .4103
                                                                   /note="match to EST ÁA214031 (NID:g1812669) complement(3980. .4103)
                                                                                                                                                                         /rpt_family="L2"
1980: .2046
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/clone="U112E8"
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                                                                                                                    note="match to EST AA211443 (NID:g1810130)
                                                                                                                                                                                                                      'clone_lib="LL0XNCC01-U"
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'chromosome="X"
                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                     note="match to EST AA211521 (NID:gl810175) zn55b01.rl"
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4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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                     _family="L1"
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12453. .12505
                          /rpt_fami
29526. .2
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14107. .14274
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1732. .4953
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28660. .2
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23777. .23857
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24736. .24842
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24315. .24471
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20820. .21010
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7746. .180="
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RESULT 7
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Matches 149; Conserva
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Chemistry: Dye-terminator; 99% of reads
(Chemistry: Dye-terminator ET-amersham; 0% of reads Consensus
quality: 149793 bases at least Q40
(Consensus quality: 149914 bases at least Q30
(Consensus quality: 150006 bases at least Q20
Insert size: 150219; sum-of-contigs
Insert size: 152259; 2.5% error; agarose-fp
Quality coverage: 17.18x in Q20 bases; sum-of-contigs Quality
coverage: 17.58x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204612.
                                                                                                                                                                                                 Center project name: bA184B10
------ Summary Statistics
ABsembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                   Center code: SC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome X clone RP11-184B10,
PROGRESS ***, 2 unordered pieces.
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/note="match to EST AA211443 (NID:g1810130) zn55b01.g1"
/note="match to EST AA211521 (NID:g1810175) zn55b01.r1"
/note="match to EST AA21521 (NID:g1810175) zn55b01.r1"
/note="match to EST AA389647 (NID:g2042633)"
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/rpt_family="Retroviral"
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SEQUENCING IN
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Matches 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149;
                                                                  Patent: WO 0194629-A 2927 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                  Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using s
                                                                                                           Patent: W
                                                                                                                                                                                                                                                                                                                          Sequence 2927 from Patent AX332418
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47436
         177
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4860 4959: gap of 100 bp
4960 150319: contig of 145360 bp in length.
Location/Qualifiers
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/db_xref="taxon:9606"
122 c 103 g
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                                     organism="Homo sapiens"
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29741 c 29722 g
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fragment_chain:1
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/clone_lib="RPCI-11.1"
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db_xref="taxon:9606"
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Pred. No. 8.6e-33;
; Mismatches 0;
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WO0194629.
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Query Match

75.7%;

Score 112.8;

DB 6

Length 587;

Local

Conservative

Indels

2;

Gaps

2

92.7%;

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RESULT 9
AY026524
LOCUS
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AUTHORS
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                                                                                                                                   BASE COUNT
ORIGIN
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Matches
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MEDLINE
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                                                                   Matches
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGTCCTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCNGGAGCG-AGGAACCTCCC 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAAGCTGAACAGTAGTAGGAAGAAAAAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCTGCAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAA-CTAAAATATGTCCC 119
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al Similarity
139; Conserv
                                CTCCCACCTCGGATGAGGAGGAAGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mohun, T. and Harvey, R.P.
The small muscle-specific protein Csl modifies cell shape and promotes myocyte fusion in an insulin-like growth factor 1-dependent manner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus muscle-specific AY026524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-FEB-2001) Developmental Biology, Victor Chang Cardiac Research Institute, 384 Victoria St, Darlinghurst, Sydney, New South Wales 2010, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 787)
Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Mohun,T. and Harvey,R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                 Similarity
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                                                                Conservative
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                                                                                                                                                /translation="MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
167 c 185 g 202 t
                                                                                                                                                                                                   /codon_start=1/product="muscle-specific protein CSL"/product="muscle-specific protein CSL"/protein id="AAK07682.1"
/db_xref="GI:14575062"
                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                         'gene="Csl"
                                                                                                                                                                                                                                                                                                                       gene="Csl"
                                                                                                                                                                                                                                                                       note="ortholog of Homo sapiens SMPX"
                                                                                                                                                                                                                                                                                                                                                           chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
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                                                                                 64.6%;
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0; Mismatches
                                                                 0;
                                                                 Score 96.2; DB 10;
Pred. No. 1.7e-17;
0; Mismatches 28;
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protein CSL (Csl) mRNA, complete cds.
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9;
                                                                                                Length
                                                                                                     787;
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Koentgen, F.,
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                                                                   Gaps
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AF364070
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ACCESSION
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                Pocus
                                                                                                                                                                                                                                                            Matches 113;
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Best Local
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                                                                                     449
                                                                                                                                                                       68 САСТСААТСТАТССЕСААЛАТССАСААТАТТАЛАЛАСТСААСТАЛАТАТСТССССАЛАССТС 127
                                                                                                                                                                                                                              8 CTCCCACCTCGGATGAGGAGAAGGAAGCCAATTCCAGGAGCGAAGAAACTTCCAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTCAATCTATCGGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAGTAGTAGGAAGAAAAA 148
                                                                                                                                                                                                     CTCCTACCACCTCAGAGGAAAAGAAGCCAATTCCTGGAATGAAGAAATTTCCAGGACCTG
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                                                                                                                                            TTĠŢĊĄĀCŢŢĠŢĊŢĠĀĠĀŢĊĊĄĄĀĀŢĠŢŢĀĀĀĀĠŢĠĀĀĀĊŢĠĀĀĀŢŢĠŢĊĊĊĊĄĀĀĠĠŢĠ
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AF364070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular protein
Hum. Genet. 105 (5), 506-512 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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MMU245772 943 Mus musculus mRNA for stretch
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Direct Submission
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
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                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAK50398.1"
/db_xref="GI:13940508"
/translation="MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKFPGPVVNLSEIQNVKSELKFVPKGEQ"
906...911
                                                                                                                                                                                                                                                                                                                                /gene="Smpx"
/evidence=experimental
187 c 203 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="SMPX protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="Smpx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene≃"Smpx"
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                                                                                                                                                                                                                                                            0;
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Pred. No. 1.7e-17;
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1 (Smpx) mRNA,
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bp mRNA
responsive
                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                                                                               28;
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                                                                                                                                                                                                                                                                                           Length 936;
                linear
                                                                                                                                                                                                                                                                 Indels
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                  ROD 12-APR-2001
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                                                                                                                                                                                                                                                               Gaps
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DEFINITION

muscle

(X-chromosome)

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BASE COUNT
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AUTHORS
TITLE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
      Query Match
Best Local Similarity 80.
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, SAF Building, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; (bases 1 to 943)

Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Eastwood, M., Sassoon, D.A. and Coulton, G.R.
Identification of a novel stretch-responsive skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AJ245772
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                                                                                                                                                                                                                                                                                                      /gene="8rmx"
/function="mRNA c
740. .744
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/function="mRNA (
658. .662
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943
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535. .539
                                                                                                                                                                gene="Srmx"
[function="mRNA destabilising motif"
                                                                                                                                                                                                                                                                                                                                                                   gene="Srmx"
function="mRNA
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pttsbekkpipgmkkfpgpvvnlsbiqnvksblkfvdkgbq"
                                                                                                                                                                                                                    function="mRNA
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79. .785
                                                                                                                                                                                                                                                                                        gene-"Srmx"
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/db_xref="GI:10178963"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="Srmx"
function="mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="stretch responsive muscle (X-chromosome)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/10"
/db_xref="taxon:10090"
/tissue_type="skeletal muscle"
1. .943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Srmx"
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 64.6%; Score 96.2; DB 10; 80.1%; Pred. No. 1.7e-17; tive 0; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 226691 bases at least Q40
Consensus quality: 226148 bases at least Q30
Consensus quality: 226956 bases at least Q20
Insert size: 227331; sum-of-contigs
Insert size: 194478; 8.5% error; agarose-fp
Quality coverage: 6.42x in Q20 bases; sum-of-cont
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                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Direct Submission

Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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1 5544: contig of 5544 bp in length
5545 5644: gap of 100 bp
5645 1121: contig of 5477 bp in length
11122 11221: gap of 100 bp
11222 23110: contig of 11889 bp in length
23111 23210: gap of 100 bp
23211 42246: contig of 18936 bp in length
42147 42246: gap of 100 bp
42247 74225: contig of 32679 bp in length
74926 75025: gap of 100 bp
153829 153928: contig of 78803 bp in length
153829 172635: contig of 18707 bp in length
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                                                                                                                                                                                            Rattus norvegicus SMPX protein
AF364071
AF364071.1 GI:13940509
                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa;
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                                        Patzak,D., Zhuchenko,O., Lee,C.C. ai
Identification, mapping, and genomio
X-chromosomal human gene (SMPX) enco
Hum. Genet. 105 (5), 506-512 (1999)
                                                                                                                        Mammalia; Eutheria;
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172736 228031; contig of 55296 l
Location/Qualifiers
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(bases 1 to 892)
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fragment_chain:1"
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fragment_chain:2"
172736. _228031
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75026...153828
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/db_xref="taxon:10090"
/chromosome="X"
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fragment_chain:2"
42522 c 42780 g 70814 t
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fragment_chain:1"
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fragment_chain:I"
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fragment_chain:1"
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Rodentia; Sciurognathi; Muridae;
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Pred. No. 1.7e-17;
0; Mismafiches 28;
                                                       Lee, C.C. and Wehnert, M. and genomic structure of a novel (SMPX) encoding a small muscular
                                                                                                                                                                                                                                      892 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AF343894
                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
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TITLE
JOURNAL
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q.
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Direct Submission
Submitted (26-MAR-2001) E.M.-Arndt-Uni, Inst. f. Humang.,
Submitted (26-MAR-2001) B.M.-Arndt-Uni, Inst. f. Humang.,
Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99;
                                                                                                                                          Xenopodinae; Xenopus.

1 (bases 1 to 923)

palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,C.-C., palmer,S., Groves,N., Schindeler,A., Copeland,N.G., Koentgen,F., Mohun,T.J. and Harvey,R.P.

Mohun,T.J. and Harvey,R.P.

The small muscle-specific protein Csl modifies cell shape and promotes myocyte fusion in an insulin-like growth factor 1-dependent manner
                                                                                                                                                                                                                                                                                                                                                                              923 bp
Xenopus laevis Chisel (Csl) mRNA,
AF343894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
Cardiac
2010, Au
       2 (bases 1 to 923)
Sparrow,D.B., Wohun,T.J. and Harvey,R.P.
Direct Submission
Submitted (30-JAN-2001) Developmental Biology Unit, Victor Chang
Cardiac Research Institute, 384 Victoria St, Darlinghurst, NSW
                                                                                                                                                                                                                                                                                                                                                                    AF343894.1 GI:14599748
                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                    Xenopus laevis
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                                                                                                                                 Cell Biol.
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Australia
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/evidence=experimental
862. .867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1. .892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAK50399.1"
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/translation="MKKQPISNVRSIQANINIPMGAFRPGAGQPPRRKESTPGTAEGA
PATPEEKKPVPGMKKFPGPVVNLSEIQNVKSELKYVPKGEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
183 c 193 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Smpx"
/note="alternate"
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                                                                                                                                   (5), 985-998
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pred. No. 1.8e-14
0; Mismatches 2
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                                                                                                                                      (2001)
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JOURNAL REFERENCE
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AUTHORS
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ORGANISM
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VERSION
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ATL73G19
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ORIGIN
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TITLE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAATCCAGAATATTAAAAGTGAACTAAAATATGTCCCCAAAGCTGAACAGTAGTAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAĀĀTCCĀGĀĀTGTAĀĀĀĀĠTGTĀĊTTĀĀĀTTTGTACCAĀĀĀĞCĀGĀGGĀACĀĀTĀĞ
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                                                                                                                                                                                                                                                                                      2 (bases 1 to 42446)
EU Arabidopsis sequencing, project.
Direct Submission
Submitted (27-MAR-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopterspitz 18a, D-82152 Martinsried, FRG, E-mail:
schuelle@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
Arabidopsis thaliana
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; Pudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42446)
Bevan, M., Pohl, T., Weizenegger, T., Bancroft, I., Mewes, H.W.,
Mayer, K.F.X. and Schueller, C.
                                                                                                                                                                                                                                         annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                               Information on performance of analysis and a more detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          project).
AL050400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                               /notes overlap to BAC M7J2; please refer to EMBL
join(4971. .4989,5232. .5572,5666. .5761,5846. .5923,
6011. .6187,6602. .6670,6755. .6937)
/gene="L73G19.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                            Organisme"Arabidopsis thaliana"
/variety="Columbia"
/db_xrefe="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Ocdon_etart=1
/product="Chisel"
/product="Chisel"
/product="Chisel"
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PTPPESEKSEEKKPIPGAVKLPGPAFNLSEIQNVKSVLKFVPKAEEQ"
187 g 240 t
                                                      gene="L73G19.10"
                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Xenopus laevis"/db_xref="taxon:8355/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:4914454
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76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73.2; DB 5;
Pred. No. 7.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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cosmid clone L73G19 (ESSA
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/codon_start=1
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AYGAGQVNMLGVYMQRSWIILFVSCFFLLFIYIFATPVLRLLGQAEBIAVPAGQFTLL
                                                                                                                                                                                                 complement(join(7909..8120,8207.
8670..9295,9431..9697))
/gene="L73G19.20"
                                                                                                                                           contains EST gb:N65344"
                                                                                                                                                                gb:AB010463
                                                                                                                                                                                                                                                     complement(join(7909. .8120,8207. .8445,8522.
8670. .9295,9431. .9697))
/gene="L73G19.20"
                                                                                                                                                                      note="similarity to Norm, Vibrio parahaemolyticus,
                                                                                                                                                                                                                                                                                                                                     /product="tRNA-Leu"
/note="codon recognized: CAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6671. .6754
                                                                                                                                                                                                                                                                                                          'gene="L73G19.20"
                                                                                                                                                                                                                                                                                                                                                                                                                  gene="L73G19.10"
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/gene="L73G19.10"
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gene="L73G19.10"
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gene="L73G19.10"
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contains EST 9b:N38537, N38536, Z17495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="L73G19.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="fibrillarin-like protein"
/protein_id="CAB43694.1"
/db_xref="G1:4914455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number=
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Picea mariana, AF051216
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AFNITNWGTAIAQIVYVIGWCNEGWTGLSWLAFKEIWAFVRLSIASAVMLCLEIWYMM
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SVYVTVPQSLLIGLVFMVAIIIARDHFALIFTSSKVLQRAVSKLAYLLGITMVLNSVQ
PVVSGVAVGGGWQGLVAYINLGCYYIFGLPFGYLLGYIANFGVMVREFRKWHELSQLM
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complement(join(11753. .12008,12083. .12273,12367. .12555,

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/gene="L73G19.20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="Meaalaacalpslrilnikprercsfsnpslpispnslitrkss 
/translation="Meaalaacalpslrilnikprercsfsnpslpispnslitrkss 
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Rettavssppssppssppskokkydgcperlabelsgridwgrlwcspc 
Kymgidlvywwdrnekwekympdicphrlabelsgridwgrlwcydcydeiiw 
Wenspphryknitetnkppyipeledbeftklwgrdipygyllaftsgolcylliae 
Kidreggkpleinvyklddnkgpfskoewgysnfiapcyyrsstdplebgeheyapab 
Kidreggkpleinvyklddnkgpfskoewgysnfiapcyyrsstdplebgeheyapab 
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Sikalaskrelslificipvsgorskliwifpraveudkivsgarkudwrgkedpp 
Dlhllhveerkiiergpenwokacfipyksdanvytferrwenkksbarvudwrgkedpp
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SNVARIAVLVAAVLSFAASKWLSHFIYKTFHYHDYNHAVV"
complement (11753. . . 12008)
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/gene="L73G19.30"
/number=2
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/gene="L73G19.30"
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/gene="L73G19.30"
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complement (12556.
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Search completed: April 15, 2003, 20:59:14 Job time : 446.585 secs
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/gene="L73G19.30"
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/gene="L73G19.30"
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ORGANISM
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BM717052
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                                                      TITLE
                 JOURNAL
 MEDLINE
                             l (bases 1 to 541)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                              541 bp mRNA linear EST 28.
UI-E-EJO-ahk-c-03-0-UI.r2 UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahk-c-03-0-UI 5', mRNA sequence.
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
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Matches 422;
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CAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTT
                                 CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTT 360
                                                                                             GATATGATTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                                                                             GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                                                                                                                                                                                       CACCTCACAGAACAATTAGCCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                            TAITTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                              TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 156
                                                                                                                                                                                              CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTTGAGGAGG
                                                                                                                                                                                                                                                                                           TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG
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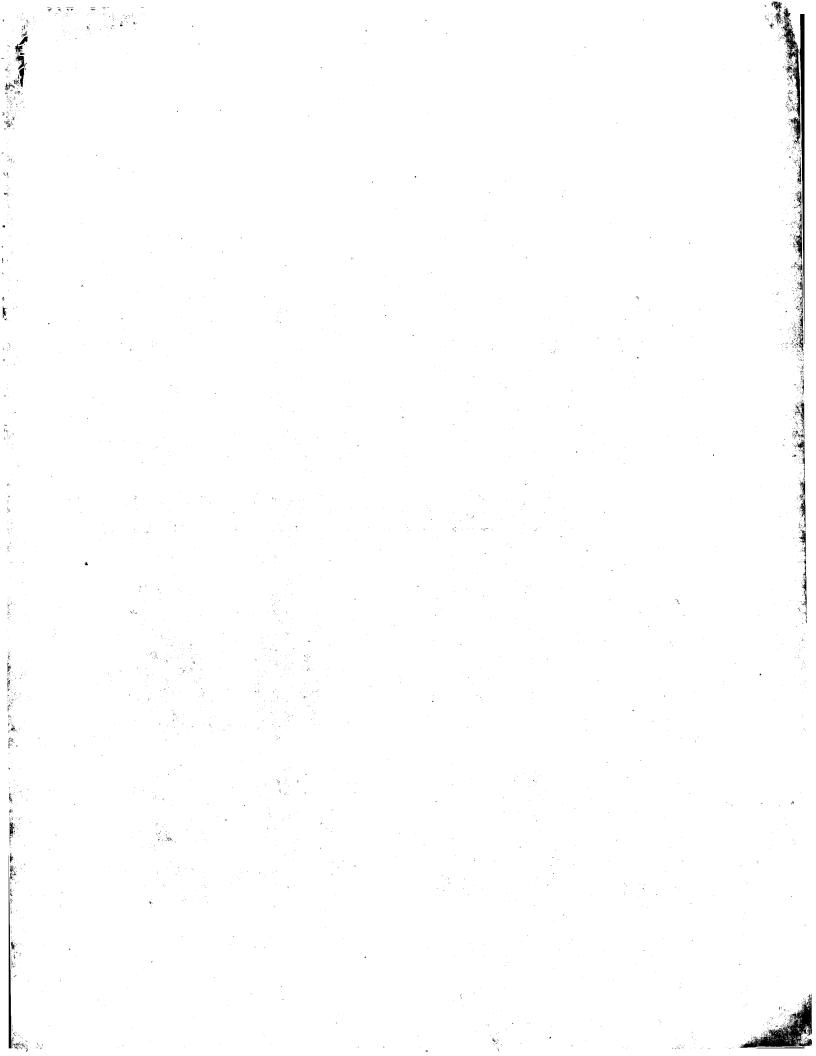
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse.
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Tissue Procurement: Dr. Gregg Hage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_bost="MING" (Life Technologies) (Tl phage resistant) "
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Rot I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAAGCG; eye anterior segment, AATGCGCCAT;
optic nerve, CCATTAAGTG; retina, CGGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Bye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="fetal eyes, lens, eye anterior segment,\optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-E-EJO-ahk-c-03-0-UI"
/clone_lib="UI-E-EJO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 422; DB 14; 100.0%; Pred. No. 3.6e-83;
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KEYWORDS SOURCE

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AUTHORS TITLE

COMMENT

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RESULT 3 BM674432/c LOCUS

DEFINITION

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Gaps

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Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arzayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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1 (bases 1 to 544)
Bonaldo, M.F., Lennon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-E-EJO-ahk-c-03-0-UI.81 UI-E-EJO Homo sapiens cDNA clone EM674432
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                  /dev_stages"fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//note="Organ: eye; Vector: pT777-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJO is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
e:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I; and cloned directionally into pT773-Pac
rector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
sequence tags for the Not I site and the (dT) ls tail The
sequence tags for this library are: fetal eyes, AGAATCAAGA
optic nerve, CCATTAAGGTG; retina, CCGGG; Retina Foveal and
Accular, GTCC; RPE and Choroid, ACCTA. This library was
System, supported by National Eye Institute (NEI).

TAG_TISUTE_BYOKE]

TAG_TISUTE_BYOKE]
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319 335 9565
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/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye
optic nerve, retina, Retina Foveal a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                  TISSUE-Poveal and Macular Retina
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and Macular, RPE a
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                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llni.gov) for further information. Seq primer: -40Up from Gibco
High quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                      Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 683)
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                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
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note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                  /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                      /clone="IMAGE: 3300004"
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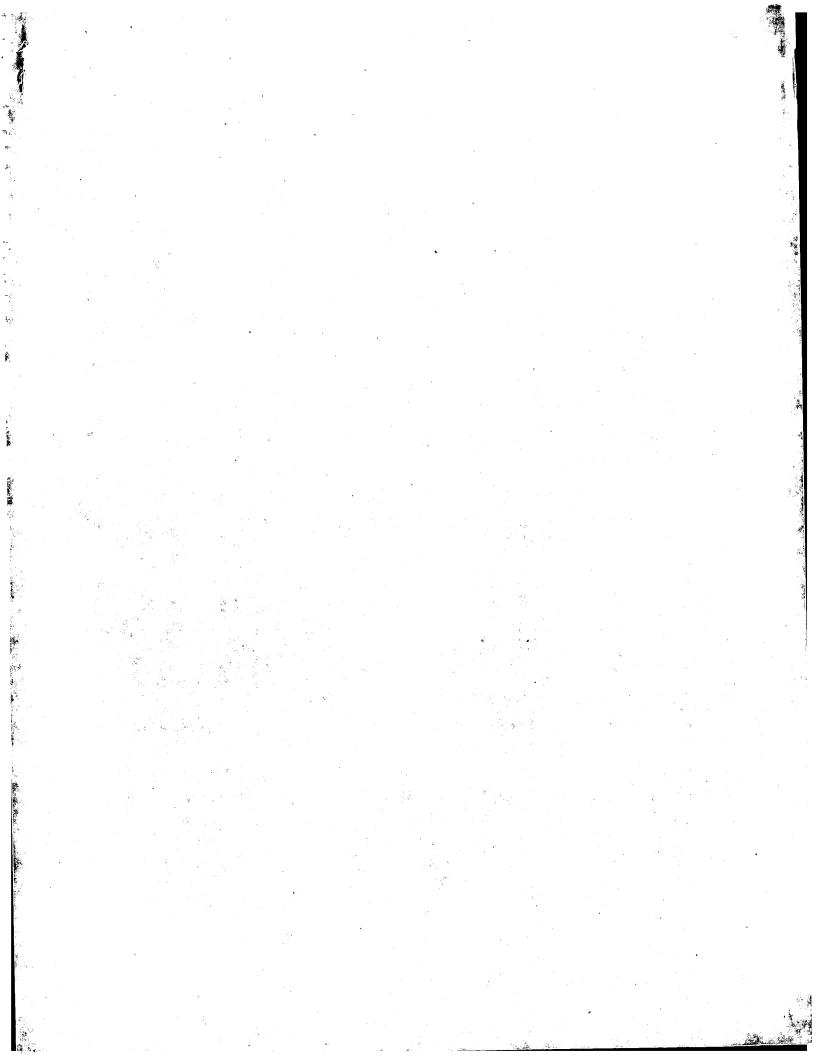
260

420 80 360

FEATURES

POLYA=Yes.

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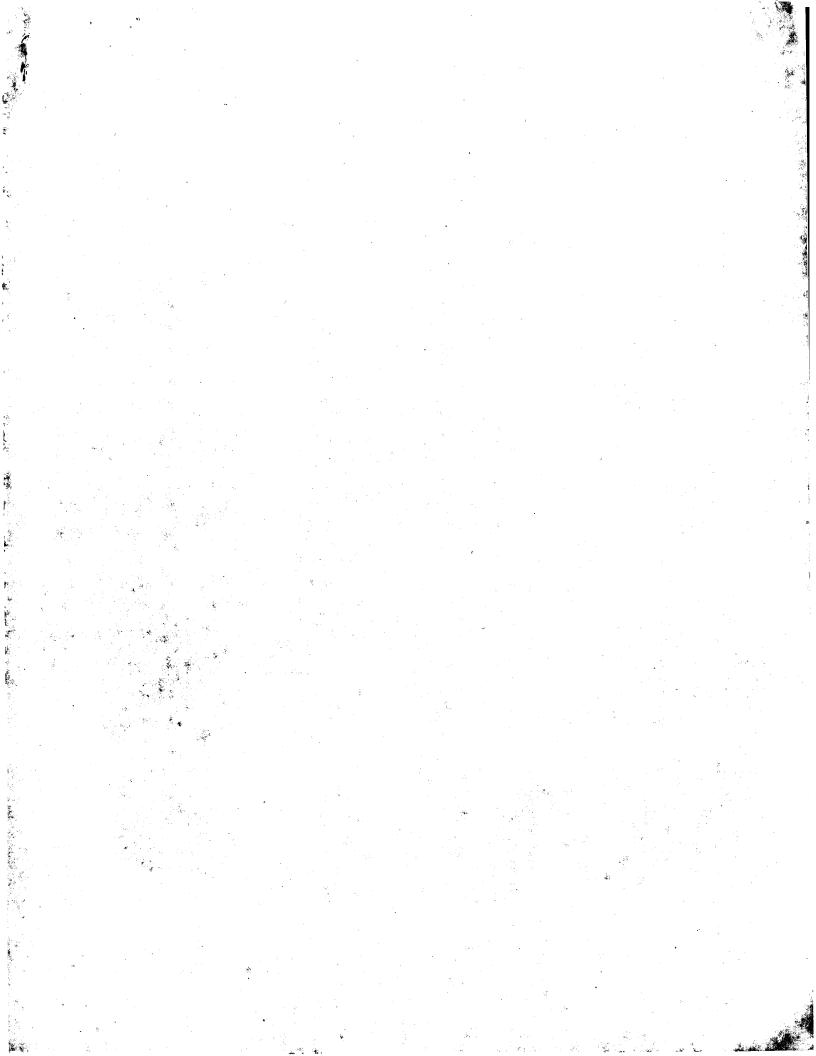
587 bp mRNA linear EST 31-JAN-1997 zn55b01.81 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562057 3', mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 265.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:562057"
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tissue_type="muscle"
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FEATURES source	•	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AI355676/c LOCUS
High quality sequence stop: 438. Location/Qualifiers 1. 455 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1952006"	Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 854	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D.	Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 455) NCI-CGAP http://www.nchi.nlm.nih.com/colory	HL19W Homo sapiens cD	AI355676 455 bp mRNA linear RST 15-FFR-1000

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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin_resistant)"
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Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Program for Rat Gene Discovery and Mapping
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/clone="UI-E-EJO-ahk-c-03-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iov
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com). //
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of lows
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Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              /dev_stage="fetal and adult"
//dev_stage="fetal and adult"
//dev_stage="fetal and adult"
//dev_stage="Phi08 (Life Technologies) (Ti phage resistant)"
//not="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-RJO is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand CDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded CDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
ptic nerve, CCATTAAGTG; rettina, CCGCG; Rettina Foveal and
Macular, GTCC, RPE and Choroid, ACCTA. This library was
System, supported by National Eye Institute (NEI).
TAG_ILB-UI-E-EJO

TAG_ILB-UI-E-EJO

National Accuration of the contains of the contains
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Choroid"
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optic nerve, retina, Retina Foveal and Macular, RPE and
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/clone_lib="UI-E-EJ0"
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                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 683)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                   Tumor Gene Index 
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                BE856875

683 bp mRNA linear EST 29-SEP-
7f70C03.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone
IMAGE:3300004 3' Similar to TR:Q9UHP9 Q9UHP9 SMALL MUSCULAR
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/clone="IMAGE:330004"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: pooled; Vite_1: Not I; Site_2: Eco RI;
                                                                                     organism="Homo sapiens"

db_xref="taxon:9606"
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AI090520.1
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                                                                                                                                                                                                                                                                                                                                                                                                               qa70d01.x1 Soares fetal heart NbHH19W Homo IMAGE:1692097 3', mRNA sequence.
Seq I
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                numan
                                                                                                                          Contact: Robert Strausberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHF pool 1: 1309384-310919, 323208-325895 Soares NbHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbHFPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 733720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
     quality sequence stop: 457.
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qd50d01.x1 Soares fetal heart
IMAGE:1732897 3', mRNA sequenc
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (Dases 1 to 452)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 3.5e-81;
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heart_NbHH19W Homo sapiens
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IMAGE:562057 3', mRNA 8
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High quality sequence stop: 423.
Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 855 Std Error: 0.00
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="Soares_fetal_heart_NbHH19W"
/sex=""Description"
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/db_xref="taxon:9606"
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Query Match
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                        CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTTAGTTCTTCACCTTT
                                                                                                        GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 265.
Location/Qualifiers
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/db_xref="GDB:4595347"
/db_xref="taxon:9606"
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  GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAAGTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Gene (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

IMAGE Tanoth: 851 Std Error: 0.00
               GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                      CACCTCACAGAACAAATTAGCCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG 240
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
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CACCTCACÁGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTTGAGGAGG
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xj35g08.x1 Soares_NFL_T_GBC_S1 Homo
IMAGE:2659262 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metrazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 494)
1 (Dases 1 to 494)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW170011.1 GI:6401536
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                               165
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2659262"
/clone lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 9.6e-81;
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                                                                                                      Local Similarity
                         1 GATTGATGTGAAGAAATAAAGAGGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60
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                                                                                     402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP111459 683 bp mRNA linear EST 20-OCT-2000 7134h12.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:3523462 3' Similar to TR-QOUHP9 QOUHP9 SMALL MUSCULAR PROTEIN: , mRNA sequence.

BF111459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 683)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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h quality sequence stop: 470
Location/Qualifiers
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                                                                                                                                                                               /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 322208-325895 Soares NbHSF pool 1: 150407, 151176-152327 Soares NbHSF pool 1: 758280-760583, 772104-774407 Soares NbHSP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. FactmaryBonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:3523462"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW
http://grup.bio.unipd.it.
Location/Qualifiers
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1 (bases 1 to 368)

Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A. Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
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ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected streptavidin coated magnetic beads ligated to non-palindromic BetXI adapters, NotI digested and directionally cloned into BetXI-NotI cut pcDNAII vect a 60 c 74 g 118 t
                                                                                                                                                                                            /tissue_type="pectoral muscle (after mastectomy)", 
/note="Vector: pc0NAII (Invitrogen); Site 1: BstXI; 
Site_2: Not1; The library was constructed by G. 
Lanfranchi. This library is not subtracted nor normalized. 
The first strand cDNA was primed with a biotinylated 
Click for the construction.
                                                                                                                                                oligo-dT-NotI primer
(5'-blotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTTTT-3').
                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="8H5-000020-0/B05"
                                                                                                                                                                                                                                                                                                                               /sex="female"
                                                                                                                                                                                                                                                                                                                                                         clone_lib="HM3"
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                              pcDNAII vector."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI824667
wc48c01.x1 NCI_CGAP_Pr28
mRNA sequence.
AI824667
                                                                                                                                                                                                                                                                                                  Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates;
1 (bases 1 to 321)
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EST.
                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization
                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2321856"
                                                                                                                                            /clone_lib="NCI_CGAP_Pr28"
/sex="male"
                                                                                                     /lab_host="DH10B"
                                                                                                                       dev_stage="adult"
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Pred. No. 7.7e-60;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATGAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTT
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1 (bases 1 to 313)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A. Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                               Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information are http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                     University of Padua
                                                                                                                                                                                                                                                                                         CRIBI Biotechnology Centre
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              /tissue_type="pectoral muscle (after mastectomy)", note="Vector: pcDNAII (Invitrogen); Site1: BstXI; Site 2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized.
                                                                                         /sex="female"
                                                                                                         /clone="84000062D03"
/clone_lib="HM3"
                                                                                                                                           organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                        I (bases 1 to 302)

I (bases 1 to 302)

Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavici Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization

Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                  CRIBI Biotechnology Centre University of Padua Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSPD22104 HM3
F31142
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/tissue_type="pectoral muscle (after mastectomy)" /note="Vector: pcDNAII (Invitrogen); Site 1: BstXI; Site 2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="84000109D09"
/clone_lib="HM3"
                                                                                           sex="female"
                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:4816768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 bp mRNA linear EST 13-MAY-1999
sapiens CDNA clone s4000109D09, mRNA sequence.
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Pred. No. 6.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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TITLE
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SOURCE
ORGANISM
                                                                          FEATURES
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BM697544
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hes 292;
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                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 355 8250
Fax: 319 335 9256
Email: msoares@blue.weag.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                            Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9),
                                                                                                                                                                                                                                                                                                                                                                                                            human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM697544 719 bp mRNA linear E
UI-E-DXO-agn-1-12-0-UI.rl UI-E-DXO Homo sapiens cDNA
UI-E-DXO-agn-1-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction:
                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 719)
Bonaldo, M.F., Lennon, G. and
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                     primer: M13 Reverse.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DXO-agn-i-12-0-UI"
/clone_11b="UI-E-DXO"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:19010802
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99.7%;
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Pred. No. 2.3e-54;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                     approaches
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BASE COUNT
ORIGIN
Search completed: April 15, 2003, 22:02:37 Job time : 877.253 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                481 TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                             181 CACCTCACAGAACAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG 240
                                                                                                                                                                                                                                                                                                                                             541 TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DXO is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGANTCAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.9%; Score 290.6; DB 14; Length 719; 98.0%; Pred. No. 3e-54; tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                        is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseg/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseg/geneseqn-emb1/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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AAX90904
ABK64187
ABL64590
AAX90903
AAD27226
ABN49389
ABL33800
ABL33420
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                             cDNA encoding muri
Human 66214 cDNA c
Human spliced tran
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Stomach cancer rel
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cDNA encoding huma
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                                                                                                                                                                                                        Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone 66214; ds.
              WO200192567-A2
                                                      polyA_signal
                                                                                                misc_feature
                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   Human 66214 EST clone DNA.
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/note= "66214 cDNA fragment"
857.862
                                                                                                /product= "Human 66214 protein"
298..588
                                                                                                                          Location/Qualifiers
184..450
/*tag= a
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ABN91584
ABL05122
AAT58840
ABL33824
ABQ67091
ABL33821
ABC67091
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ABC67091
ABL33331
ABC67097
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AAF88379
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ABL32850
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ABL33402
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AAA70230
AAV21209
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Human immune syste
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Human immune syste
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Drosophila melanog
AmEPV genome fragm
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Title: Perfect score:

US-09-647-019-10 422 1 gattgatgtgaaga

OM nucleic -

Database

N_Geneseq_101002:*
1: /SIDS2/gcgdata/
2: /SIDS2/gcgdata/

Result

Score

Match

Length

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a a

422 422 412 412 412 146.8

100.0 100.0 97.6 97.6 34.8 29.1 14.2 10.2

06-DEC-2001

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tissues and their corresponding proteins. The invention also relates to cerebrods for assessing the expression level of these genes. The method cerebrods for assessing the expression level of these genes. The method cerebrods is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also cerebrody to treat diseases of the heart such as congestive heart failure, cerebrody, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial cerebrody, pulmonary hypertension, pulmonary heart disease, systemic arterial cerebrody, pulmonary hypertension, pulmonary heart disease, are therapy. Cerebrody and sudden death heart disease, pericardial disease and cerebrody congenital heart disease, pericardial disease and cerebrody conduction conclumnan mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of the invention of the treatments of the streatments of the stre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a subject at risk for a heart disease e.g. congestive heart
failure, dilative cardiomyopathy, heart muscle disease, by quantifying
the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 886 BP; 278 A; 172 C; 191 G; 245 T; 0 other;
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                                                                                                                                                                                                                                                          GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTTCC
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                                                            CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCCTTCACCTTT
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Pred. No. 1.7e-98;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
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(GEHO )
(HALL-)
Isolated nucleic acids encoding chisel, used to develop products for treating cardiomyopathy, cardiac hypertrophy, heart failure and
                                                                 WPI; 1999-610852/52.
P-PSDB; AAY28651.
                                                                                                                                                                                                                                                                27-MAR-1998;
                                                                                                                                   Harvey
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                                                                                                                                                                        CHANG CARDIAC RES INST VICTOR.
GEN HOSPITAL CORP.
HALL INST MEDICAL RES WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466..887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Exon_3
/note= "Corresponds
human cosmid clone U
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'label= Exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Exon_5
/note= "Corresponds to residues
human cosmid clone Ull2E8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Exon_4
/note= "Corresponds
numan cosmid clone (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85..451
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                                                                                                                                        SJ,
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Ull2E8"
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U228D4"
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U228D4"
                                                                                                                                          Rosenthal NA;
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muscular myopathies

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RESULT 3
ABK64187/c
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XX DE Human |
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C that is mapped to the human chromosome Xq21.3-q22. It comprises 5 exons.
C It is a member of the EF-Hand protein super family and is involved in comparison of the EF-Hand protein super family and is involved in comparison of the EF-Hand protein super family and skeletal comparison of the matter the differentiation of cells. Call comparison of the maintain muscle homeostasis. This sequence can be used in the comparison of the maintain muscle homeostasis. This sequence can be used in the comparison of the compari
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Best Local Simi
Matches 422;
                                                                                               Human, benign
                                Homo sapiens
                                                                                                                                                                 Human benign
                                                                                                                                                                                                                                          18-JUN-2002
                                                                                                                                                                                                                                                                                                                   ABK64187
                                                                                                                                                                                                                                                                                                                                                                          ABK64187 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGCTACTACAGTATTTTGGTCAATATTTGGAATGCGTTTTTAGTTCTTCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCTACTTCCTACAGTATTTTTGGTCAATATTTTGGAATGCGTTTTTAGTTCTTCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATATGATTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTTGAGGAGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCTCACAGAACAATTAGCCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTTGTATGATGATGATGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 149-150; 157pp; English
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                                                                                                                                                         prostatic hyperplasia gene #82.
                                                                                                                                                                                                                                   (first entry)
                                                                                prostatic hyperplasia; BPH; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 1.7e-98;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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301

CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTTAGTTCTTCACCTTT

360

GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG

300 113

173 240 233 180 293 120 353

GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC

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181 292 121 352 Matches Query Match Best Local

412;

Conservative

100.0%;

97.6%; Score 412; DB 24; 100.0%; Pred. No. 5.4e-96; 0;

Length 587; Indels

٥,

Gaps

0

Local Similarity

587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;

412 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA

TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG

TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT TATTTGTATGATGATGATGGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT

CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGGTTTTGAGGAGG TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG 1 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA

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The invention relates to a method of diagnosing (I) the onset or CC progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate (CC prompared to normal prostate tissue. (I) comprises (CC detecting the expression levels of one or more genes in prostate cells (II) comprises preparing a first gene expression profile (CC prostate cells. (II) comprises preparing a first gene expression profile (CC agent, preparing a second gene expression profile of the agent exposed (I) is useful for diagnosing the first and second gene expression profiles. (CC cells, and comparing the first and second gene expression profiles. (CC is useful for diagnosing the onset or progression for BPH. The methods are useful to precent information identifying (CC level of genes given in the specification in the tissue or cells to the compared to the expression of gene in the database, and displaying the cell is compared to the expression level in a tissue or cells as the compared to the expression level in bPH. Agents using (II) are useful for compared to the expression level in BPH. Agents using (II) are useful for benign prostatic cancer. ABK64106-ABK64860 represent human than the intention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from parient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 104; 444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Munger WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2000; 2000US-223323P
05-JUN-2001; 2001US-0873319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2001; 2001WO-US24708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kulkarni P, Getzenberg RH,
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RESULT 4 4
RABL645
AC ABL645
XX ABL645
XX IS-MAY
XX IS-MAY
XX IS-MAY
XX Human;
XW Stomac
XX IS-MAY
XX IS-MAY
XX IS-MAY
XX IS-SEE
PR 18-SEE
PR 20-SEE
PR 20-SEE
PR 27-SEE
PR 27-S
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25-SEP-2000;

25-SEP-2000;

25-SEP-2000;

26-SEP-2000;

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27-SEP-2000;

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29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

02-OCT-2000;

02-OCT-2000;

03-OCT-2000;

03-OCT-2000;
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20-SEP-2000;
22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2002
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25-SEP-2000;
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                           2000US-209473P.
2000US-209531P.
2000US-233139P.
2000US-234009P.
2000US-234509P.
2000US-234569P.
2000US-234569P.
2000US-234569P.
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2000US-234569P.
2000US-23567P.
2000US-23567P.
2000US-23563P.
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2000US-23563P.
2000US-23603P.
2000US-23703P.
2000US-23703P.
2000US-237173P.
2000US-23773P.
2000US-23775P.
2000US-237
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Length

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The present invention describes a method (MI) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC expression is indicative of anti-neoplastic activity and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC is the data collected with respect to the anti-neoplastic agent as a CC result of MI, and the data is sufficient to convey the chemical CC expensions of cancer such as colon, breast, stomach, lung, thyroid, CC caccorona, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soppet
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 2927; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-188264/24.
Sequence 587 BP; 177 A; 122 C; 103 G; 183 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ਨ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horrigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bet
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8 밁 Ş **,** B S 멼 Ś 밁 S 밁 Ś 밁 밁 Ś Matches Query Match Best Local 9 412 GATTGATGTGAAGAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 181 292 121 352 112 301 172 241 232 361 61 52 1 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60 TGTACATTTATATCTTCCTTCCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120 CAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTT GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTTCC GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTTGAGGAGG rgracarriararcrerrecrieciagriegeriarricriacritarerrecarrireg CAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTT TAAATTATGTCACTAAACTTTGTATGAGTTCAAATAATATTTGACTAAATG 412; Similarity Conservative 97.6%; but 100.0%; Pr Score 412; DB 24; pred. No. 5.4e-96; Mismatches <u>.</u> Indels 412 0 Gaps 353 180 293 300 240 233 53 360 113 173 0

RESULT 5
AAX90903
ID AAX9
XX
AC AAX9
XX AAX90903 standard; cDNA; ВP

AAX90903;

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                                                                                                                                                                                                                            CC The present sequence is the cDNA encoding the murine chisel gene (Cs1)
CC that is mapped to the mouse X chromosome. It is a member of the EF-Hand
CC protein super family and is involved in signalling pathways. It is
CC predominantly expressed in heart and skeletal muscles and is activated
CC of differentiation of cells. CS1 functions in regulation aspects
CC of differentiation or adaptive processes that maintain muscle
CC prophylactic and therapeutic treatment of diseases such as those
CC prophylactic and therapeutic treatment of diseases such as those
CC is also used in the treatment of muscular and functional activity. It
CC skeletal myopathies such as Duchenne muscular dystrophy and Becker's
CC myotonic dystrophy, heart failure, cardiac hypertrophy and Becker's
CC myotonic dystrophy, etc. The Cs1 gene sequence can also be used in gene
CC therapy, for the production of transgenic animals and for drug screening.
                                                                                                                                                     Best Local Sig
Matches 175;
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating muscular
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chisel gene; CB1; EF-Hand protein super family; muscle development; heart/skeletal muscle cell development; signalling pathway; murine; X chromosome; regulation; adaptive process; muscle homeostasis; detection; diagnosis; prophylaxis; treatment; skeletal myopathy; muscular and myotonic dystrophy; Duchenne muscular dystrophy; heart failure; cardiac hypertrophy; secker's myotonic dystrophy; heart failure; cardiac hypertrophy; differentiation; gene therapy; transgenic animal; drug screening; ss.
                                        611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvey RP,
                                                                                               551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO)
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                                                                  95
                                                                                                                           35
                             CAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTTGC
ATTTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCCATAAATTCAAC
                                               ATTCAATAGCTCACTAAAATTTTTATATATTTTGTATGATGATTGTTGAACCTCCTGAATGCC 94
                                                                                    ATAPÁCPACTTCCTGAÁCATTTTÁTÁCATTTGTÁTGATGÁTGATCACPAÁCCTCCTGÁÁTGCC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHANG CARDIAC RES INST VICTOR. GEN HOSPITAL CORP.
                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids encoding chisel, used to develop products cardiomyopathy, cardiac hypertrophy, heart failure and myopathies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Musaro
                                                                                                                                                   Conservative
                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product "Chisel
/note= "Expressed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98AU-0002634
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                                                                                                                                                              34.8%;
                                                                                                                                                                                                        A; 166 C; 179 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chisel (Csl) gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palmer
                                                                                                                                                   0
                                                                                                                                             Score 146.8; DB 2
Pred. No. 4.3e-28;
0; Mismatches 47
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                                                                                                                                                                         DB 20; Length
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                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                    screening.
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 214
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GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60

Query Match Best Local S Matches 123

Similarity

29.1%;

Score 123; DB 24; Pred. No. 4.2e-22;

Length

Indels

<u>,</u>

0

4.2e-22;

Conservative

0

Mismatches

290

BP;

103 A; 50 C; 69 G;

68 T; 0 other,

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The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method of is used for testing the predisposition of mammals and preferably humans of our analysis of the heart such a congestive heart failure, of useful to treat disease of the heart such a congestive heart failure, or dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiocomyopathy, specific heart muscle disease, rhythm and conduction disporders, typertransion, pulmonary heart disease, systemic arterial for hypertransion, pulmonary heart disease, valvular of endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of the art disease. The present sequence is a cDNA from 66214 clone. This sequence used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD27226
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                                                                                                                                                                                                                                                                                                                                                                                              Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertrophic cardiomyopathy; schaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal;
                                                                                                                                                                                                                                                                                                                                               Example 10; Fig 9a; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-122073/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000; 2000US-207400P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD27226 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIGENE AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290
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                                                                            (gub-) transcriptome comprises messenger RNAs transcribed from multiple transcriptom units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or detecting RNA transcripts and splice variants of human or animal CC detecting RNA transcripts and splice variants of human or animal CC transcriptomes. The libraries may also be used as specialised minic CC detection of tissue- and pathological state, and so allowing the CC detection of tissue- and pathology-specific genes such as those genes conly expressed in specific tissue under a specific pathological CC condition; to detect developmental specific genes such as those genes CC condition; to detect developmental specific genes; and to detect RNA CC transcripts and splice variants of a transcriptome of a patient suffering CC condition; to detect developmental specific genes; and to detect RNA CC cranscripts and splice variants of a transcriptome of a patient suffering CC digonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human spliced transcript detection oligonucleotide SEQ ID NO:22137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN49389 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2002 (first entry)
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02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID 22137; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20~JUL-2001; 2001WO-IB01903
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N.B. The sequence data for this patent did not specification, but was obtained in electronic at ftp.wipo.int/pub/pub/ished not reserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COMP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUGEN INC
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2001US-287724P.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; noottopic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL33800 standard; DNA; 6115
  5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33800;
                                                                                                                                                                                          Sequence 6115 BP; 1623 A; 47
                                                                                                                                                                                                                                                              macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including the content of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                          diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGATGATGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGTACAT
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AGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTT
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                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                     eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                       The present sequence is a gene
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                                                                                                  Conservative
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                                                                                                                   10.2%;
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                                                                                                                        Score 43; I
Pred. No. 0.
                                                                                                                                                                                            C; 1519 G; 2926 T;
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3.8e-06;
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                                                                                                                                               Length 6115;
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bowel disease;
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abnormal
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                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and necular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid eukaemia, Alzheiner's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulccrative bowel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 393; 32pp + Sequence Listing; German.
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                       862
                                       119 TITGTACATTIATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTT 178
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                                                                                                                  Conservative
                                                                                                                                                                                                    BP; 1964 A; 94 C; 1241 G;
                                                                                                                                                                                                                                                    present sequence is a gene of the
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                                                                                                                                  . 76;
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RESULT 10
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                     The present invention describes a method of screening for genes which modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably prosophila, and toxic polyglutamine sequences include the human and (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful for identifying treatments for neurodegenerative and proliferative disorders, including Alzheimer's disease, Parkinson's disease, Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke, head trauma and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1999;
12-AUG-1999;
18-JAN-2000;
                                                                                                                                                                                                                                      Identifying genes or other compounds that modulate toxicity, useful for treating Alzheimer's disease, and Creutzfeldt-Jakob disease -
                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                      WPI; 2001-147537/15.
                                                                                                                                                                                                                                                                                                                                   Benzer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1; heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease; Parkinson's disease; CJD; BSE; Huntington's disease; head trauma;
                                                                                                                                                                                                                                                                                                                                                         (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000; 2000WO-US22496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila tetratricopeptide repeat protein 2 regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF75571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF75571 standard; DNA; 13015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 AAAAATGGTATGATAGAATAGTATTTATATATATTTGAAATG 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTGATTATTTTTAAAGATGGAATTGAATATGAATTTTAAAGATTTTAATTTTATAAT
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                                                                                                                                                                                                               Fig
                                                                                                                                                                                                                                                                                                                                Kazemi-Esfarjani
                                                                                                                                                                                                                                                                                                                                                                                        99US-0148934.
2000US-0177047.
2000US-0205720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0148933.
                                                                                                                                                                                                              17; 275pp;
                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВÞ
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                                                                                                                                                                                                                                                   polyglutamine
Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke;
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Query Match Best Local S Matches 83

l Similarity 83; Conser

9.7%;

Score 41; Pred. No.

DB

Length 13015;

Conservative

0,

Mismatches

Indels

0,

Gaps

0

Sequence 13015 BP; 3746 A;

2643 C; 2515 G;

4111 22; 70;

T; 0

other;

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RESULT 11
ABL08614
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                                               Query Match
Best Local S
Matches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical;
 14133
                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                            Sequence 21475 BP; 6025 A; 4524 C; 4394 G; 6532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                         ABB57737-ABB72072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTTGACAGCCCGAGGAGTTCGGTTGGTTCAG 1255
                                                                                                                                                                                                                                                                                                                                                    2001-656860/75.
 1; SEQ ID NO 20324; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                         ABB64511
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental biology; ce'll signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                           Adams M,
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss.
                                                                                                                                                                                                                                                                                                                   acid
                                                            9.7%;
54.2%;
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                                                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 for elucidating cell signalling and o
                                                Score 41; DB 23;
Pred. No. 1.2;
0; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                             Myers
                                                                                                                                                                                                                                                                                                                                                                               EE.
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                                                    70;
                                                                         Length 21475;
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                                                    Indels
                                                                                                   0 other;
                                                    0;
                                                                                                                                                                                                                                                                                                           or more
                                                    Gaps
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RESULT 12
ABL56202/c
ID ABL562
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14253
                                                                                                                                                                                                                                                              The invention relates to a recombinant entomopox virus (EPV) vector, comprising a polynucleotide encoding a protein operably linked with a heterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a human cell. The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in vitro or in vivo. The vector is useful for the delivery and expression of invivo. The vector is useful for the delivery and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AmBPV; gene therapy; viral vector; chromosome mapping; gene mapping; genetic deficiency disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AmEPV genome fragment#4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL56202;
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                                                    biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for engineering of vertebrate cells. Polymuclectides of the invention have applications in techniques such as polymucles insertion sites for foreign genes of interest, hybridisation their use as insertion sites for acapting, in PCR technologies, and in the production of sense or antisense nucleic acids. Vectors of the invention production of stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polymucleotide inserts which can be delivered in an infected or transformed cell and expressed in a stable fraction. The current sequence represents a fragment of the genome of the genus B entomopoxvirus from amsacta moorei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147
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14-SEP-2000; 2000US-0662254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2001; 2001WO-US25287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amsacta moorei entomopoxvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 201-226; 326pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-227161/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREGITTEGTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTTCCAACACTTTTCCECCTCTC 14252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTCAACACCTGGAGGGTGTGGTTTTGAGGAG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
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Query Match
Best Local Similarity
Matches 89; Conserv

Conservative

0;

0.8

0

Gaps

0

9.7%; 52.7%;

Score 41; DB 24; Pred. No. 1.4; Mismatches

Sequence 50000 BP;

20248 A; 4709 C; 4703 G;

20340 T; 0 other;

Length 50000; Indels

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cc by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

CC vaccines against P. falciparum infection comprising (I) or (II), and (2)

CC (I) and (II) are useful for the development of vaccines against P. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against CC (II) and (II) are useful for the development of vaccines against CC (II) and polyclomal antisers or a monoclonal CC useful in the detection of infection with P. falciparum. Furthermore, CC (II) (specially when they are rifins or secreted or membrane proteins)

CC infection, or they can be used to identify drug resistance in CC infection. Sequencing of the Plasmodium chromosome 2 and the CC complexity of the parasitic lifecycle, and provide new targets for CC complexity of the parasitic lifecycle, and provide new targets for CC complexity of the parasitic lifecycle, and provide new targets for CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC and protein sequences given in the present invention, but which are not CC specifically mentioned within the present invention, but which are not CC specifically mentioned within the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAA70230/c
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                                                                                                                                                                                                                                                                                                       The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

Yangalana and (1) mucleotide sequences (II) encoding (I); and (2)
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 550-551; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalaria); malaria; protozoacide; infection; insecticide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ТСАСТАЛАСТІТЕТАТЕЛЕТІСЛАЛІТАЛАТАТІТЕЛЕСТАЛАТЕТАЛАЛІ 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTGAĀGĀĀTTTAĀATGTTCGTTTCĀTĀTAGĀTGTĀGĀTĀĀTĀĀĀĀGTĀGCGĀĀGĀĀĀT 33042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCCAAGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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apecification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC
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sequence of the Methanococcus jannaschii circular chromosome. The CC genome sequence. The invention also describes a computer based system CC genome sequence. The invention also describes a computer based system CC for identifying fragments of the M. jannaschii genome that are CC homologous to target nucleotide sequences, comprising: (a) data storage means comprising the nucleotide sequence of the 1664976, 58407 or 1650 cc means comprising the nucleotide sequence of the 1664976, 58407 or 1650 cc sequence (see AAV21209, AAV21210 and AAV21211), or a nucleotide target sequence (see AAV21209) a AAV21210, or a nucleotide cc target sequence (see AAV21209) and (c) retrieval means for comparing a cc identify a homologous sequence, and (c) retrieval means for obtaining cc inhomologous sequence. The method, which is based on whole genome cc for which consists of 3 physically distinct elements, a large circular ctra-chromosoma lement (the 58407 by sequence given in AAV21210), and created the consists of 3 physically distinct elements in AAV21210), and created the consists of a sequence given in AAV21210), and created the consists of a sequence given in AAV21210), and consists of a consist of a sequence given in AAV21210), and consists of a consist of a sequence given in AAV21210), and consists of a consist of a sequence given in AAV21210), and consists of a consist of a c
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the complete 1.66-megabase pair genome sequence of the Methanococcus jannaschii circular chromosome. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 152-585; 614pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of methano-genic jannaschii - useful in identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) INST GENOMIC RES.
(UNII ) UNIV ILLINOIS FOUND.
(UYJO ) UNIV JOHNS HOPKINS (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09807830-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV21209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV21209 standard; DNA; 1664976 BP
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; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 GCCTGTTTGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
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01-SEP-2000; 2000DE-1043826
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-)
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Pred. No. 6.8;
0; Mismatches 122;
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es 96; Conserv
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

AX322774 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	AX322774 886 bp DNA linear PAT 07-JAN-2002 Sequence 18 from Patent WO0192567. AX322774 AX322774.1 GI:18093754
ACCESSION VERSION	AX322774 AX322774.1 GI:18093754
KEYWORDS	
SOURCE	unidentified.
ORGANISM	unidentified
	unclassified.
REFERENCE	1
AUTHORS	Bunk, D., Reuner, B., Beck, J. and Henkel, T.
JOURNAL	Novel target genes for diseases of the heart Patent: WO 0192567-A 18 06-DEC-2001;
	Medigene AG (DE)

Pred. ŏ.

is the number of results predicted by chance to have

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Homo sapiens small muscular protein (SMPX) mRNA, c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Craniata; Hominidae;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 886)
1 (bases 1 to 886)
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                                                             Submitted (18-JAN-1999) Molecular Human Genetics, Institut
Human Genetics, Fleischmannstr. 42/44, D-17487 Greifswald,
Location/Qualifiers
                                                                                                   2 (bases 1 to 886)
Patzak,D.
Direct Submission
                                                                                                                                                                   1 (bases 1 to 886)
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Patzak,D., Zhuchenko,O., Lee,C.C. and Wehnert,M.
Identification, mapping, and genomic structure of a novel
X-chromosomal human gene (SMPX) encoding a small muscular
Hum. Genet. 105 (5), 506-512 (1999)
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/db_xref="taxon:32644"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xq22.1-22.2"
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                                                                             sequence.
U73508
U73508.1
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 36503)
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                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SMPX"
/codon_start=1
/evidence=not_experimental
/product="small muscular pr
/protein_id="AAF19343.1"
/db_xref="d1:6625647"
/db_xref="d1:6625647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SMPX"
857. .862
/gene="SMPX"
a 172 c
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451. .>886
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gvpptsdeekkpipgakklpgpavnlseiqnikselkyvpkaeq"
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184. .450
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<1. .183
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cosmid clone Ull
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100.0%; Pred. No. 9.6e-79;
tive 0; Mismatches 0;
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                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                       This clone is from a chromosome x-specific cosmid library LLOXNCC01 'U'. The source of the chromosomes was a human/hamster hybrid, GM07297-F, from Robert Nussbadm at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livermore National Laboratory at http://www-bio.llnl.gov/genome to obtain the clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomic 44:227-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Submitted (27-APR-1999)
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Submitted (20-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 36503)
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Submitted (04-OCT-1996)
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Department of Genetics
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Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University
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                                                              /rpt_family="L2"
3690. .410
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3711. .3929
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1980. .2046
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/chromosome="X"
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                                                                                                                                                          clone_lib="LLOXNCC01-U"
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4444 Forst Park Avenue, St. Louis, Missouri 63108, USA
Y: WUGSC
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27011. .27234
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8529, .85cc
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11095. .11460
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/note="match to EST AA211521 (NID:g1810175) zn55b01.r1"
4141. .4364
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|5512..15625
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1640. .11719
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|0938. .11032
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1874. .8264
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4638. .14751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 4042
                                                                                                                                                                                                                                                                                                                                                          CAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTT 360
                                                                                                                                                                                                                                                                                                                                                                                                     GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                     GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG 3862
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                                                                                                                                                                                                                                                                                                                                          CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTACATTTATATCTCCTTCCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG 3922
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     AL772392
Human DNA sequence
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AL772392
                                                                           AL772392.4
                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MIR"
34281. .34328
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30427. .30777
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29526. .29750
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28660. .29064
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7354 c 7510 g 10866 t
                                                                              GI:21912756
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT, Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at thitp://www.sanger.ac.uk/Projects/C_legans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP11-450P7 is from the library RPCI-11.2 constructed by the group of Pister de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60
                                                                                                                                                                                                                                                                                                                                                                  TATTIGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120
  GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC
                               GATATGATTTTATGGAGAAIGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTTCC
                                                                                                                                              CACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTTGAGGAGG
                                                                                                                                                                                                                       TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG 100470
                                                                                                                                                                                                                                                                                                                                  GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 100590
                                                                                                                                                                                                                                                                              TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG
                                                                                                           CACCTCACAGAACAATTAGCCCATAAATTCAACACCTGGAGGGTGTGGTTTTGAGGAGG
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 19, 2002 this sequence version replaced gi:21614755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
Center code: SC
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Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chapman, J
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
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/db_xref="taxon:9606"
/chromosome="X"
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/clone_lib="RPCI-11.2"
24595 c 23947 g 38
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     13
                                                                                                 Local Similarity
TATTIGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120
                                            GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTT
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                           GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-NOV-1999) Kemp T.J., Molecular pathology, Imperial College of Science Technology and Medicine, SAF Bldg, Level 2, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM Related sequences:AJ245772, U73508 to U73509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kemp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kemp, T.J., Sadusky, T.J., Simon, M., Brown, R., Sassoon, D.A. and Coulton, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AJ250584
AJ250584.1 GI:10178976
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                                                                                  99.8%;
llarity 100.0%;
Conservative
                                                                                                                                                                                  /gene="Srmx"
857. .862
                                                                                                                                                                                                                   /translation="mmmskopvsnvraioaninipmgaprpgagopprrkectpevee
gvpptsdeekkpipgakklpgpavnlseionikselkyvpkaeo"
                                                                                                                                                                 /gene="Srmx"
                                                                                                                                                                                                                                                 /product="stretch responsive muscle
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                                                                                                                                                                                                                                                                                         /gene="Srmx"
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                                                                                                                                                                                                                                                                                                                                  'gene="Srmx"
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                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="skeletal
|. .885
                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                              Score 421; DB 9; ...
;; Pred. No. 1.6e-78;
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IMAGE:4246501,
BC005948
                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6625646
                                                                                                                                                                                                                                                                                               cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human (Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Mammalia; Eutheria;
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/clone="MGC:14584 IMAGE:4246501"
/tissue_type="Skeletal Muscle"
/clone_Tib="NIH_MGC_81"
                                                                               organism="Homo sapiens"
/db_xref="LocusID:23676"
                                                            /db_xref="taxon:9606"
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Primates; Catarrhini; Hominidae;
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, X-linked, clone MGC:14584
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Sequence
AX332418
                                                                                                                                                       Young, P.E., Augustus, M., Carter, K.C., Ebne Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pharmaceuticals (US)
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                                                                                                         Location/Qualifiers
                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 2.4e-77;
D; Mismatches 1
 Score 412; DB 6; : Pred. No. 1.3e-76; 0; Mismatches 0;
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                                                                                                                   Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 99% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 224691 bases at least Q40
Consensus quality: 226148 bases at least Q30
Consensus quality: 226956 bases at least Q20
Insert size: 227331; sum-of-contigs
Insert size: 227331; sum-of-contigs
Quality coverage: 6.42x in Q20 bases; sum-of-contigs
Coverage: 8.63x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute Center code: SC
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heath, P.
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NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Sciurognathi; Muridae;
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*** SEQUENCING IN
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; Murinae; Mus
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DD 187521 ATTICTCACITTAGCTACATTITTGGCACCTTGTAGAGCAAATCAGCACACGAATTTACA 187580
                                                                                                                                                                                                    Db 187461 CAAGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTTGC 187520
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                                                                                                                                                 155 ATTTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAAC 214
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274 GC--CTAACGATTTTGATGAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTGGTCAATA 331
                                                                                                                                                                                                                               ACCTGGAGGGTGGGTTTTGAGGAGGGATATGA-TTTTATGGAGAATGATATGGCAATGT 273
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5645 5644: gap of
110 bp
11122 11221: gap of
110 bp
1122 23110: contig of 11889 bp in length
23111 23120: gap of
23111 23210: gap of
23111 42146: contig of 18936 bp in length
42147 42246: gap of
42247 74925: contig of 32679 bp in length
74926 75025: gap of
100 bp
75026 153828: contig of 78803 bp in length
153829 153928: gap of
172636 172735: gap of
172636 172735: gap of
172636 172735: gap of
172636 23031: contig of 55296 bp in length
172736 228031: contig of 55296 bp in length
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fragment_chain:I"
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(db_xref="taxon:10090"
(chromosome="X"
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Dest local Similarity 78.2%; Pred. No. 5.5-36; Hest Local Similarity 78.2%; Pred. No. 5.5-36; Matches 302; Conservative 0; Mismatches 75; Indels 9; Gaps 3; Qy 35 ATTCAATAGCTCACTAAAATTTTATATATATTTGTATGATGATGATGTGAACCTCCTGAATGCC 94
Best Local Similarity 78.2%; Pred. No. 5.5e-36; Matches 302; Conservative 0; Mismatches 75; Indels 9; Gaps 35 ATTCAATAGCTCACATAATTTTATATATTTGTATGATGTGTAACCTCCTGAATGCC 94
Best Local Similarity 78.2%; Pred. No. 5.5e-36; Best Local Similarity 78.2%; Pred. No. 5.5e-36; Matches 302; Conservative 0; Mismatches 75; Indels 9; Gaps 35 ATTCAATAGCTCACTAAAATTTTATATATTTGTATGATTGTGAACCTCCTGAATGCC 94
es 302; Conservative 0; Mismatches 75; Indels 9; Gaps
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CDS 199456
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AUTHORS Patzak, D. TITLE Direct Submission
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(5), 506
0,0., Lee,C.C. and Wehnert,M. ling, and genomic structure of a novel
18. Motavoa. Obordata. Osaadata. Valtigram
DEFINITION MUS musculus SMPX protein (Smpx) mRNA, complete cds. ACCESSION AF364070
070
Db 187755 AATAAATATTTGAGTAAATGTAACATATGA 187785
TGTGA 422
QY 332 TTTGGAATGCGTTTTAGTTCTCACCTTTTAAATTATGTCACTAAACTTTGTATGAGTTC 391
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-AUG-1999) Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, SAF Building, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 943)
Kemp, T.J., Sadusky, T.J., Simor
Sassoon, D.A. and Coulton, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMU245772 943 | 943 | Mus musculus mRNA for stretch
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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Rattus norvegicus clone CH230-20D15,
***, 60 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plasmid;
Chemistry: Dye-terminator' Big Dye: 100% of reads
Chemistry: Dye-terminator' Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 142614 bases at least Qa0
Consensus quality: 149653 bases at least Qa0
Consensus quality: 149656 bases at least Qa0
       1104: contig of 1104 b

1204: gap of unknown

2491: contig of 1287 b

2591: gap of unknown l

3744: contig of 1153 b

3844: gap of unknown l

5424: contig of 1580 b

5524: gap of unknown l

6848: contig of 1324 b
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COMMENT

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KEYWORDS
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              AP364071 892 bp
Rattus norvegicus SMPX protein
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AF364071.1 GI:13940509
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                  TCAAATAAATATTTGACTAAATGTAAAA 417
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Submitted (26-MAR-2001) E.M.-Arndt-Uni, Inst. f. Humang.,
Fleischmannstr. 42-44, D-17487 Greifswald, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patzak,D., Zhuchenko,O., Lee,C.C., and Wehnert,M. Identification, mapping, and genomic structure of a novel X-chromosomal human gene (SMFX) encoding a small muscular Hum. Genet. 105 (5), 506-512 (1999)
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/note="alternate"
/evidence=experimental
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/db_xref="taxon:10116"
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/product="SMPX_Protein"
/protein_id="AAK50399.1"
/protein_id="AK50399.1"
/db_xref="GI:13940510"
/translation="MSKQPISNVRSIQANINIPMGAFRPGAGQPPRRKESTPGTAEGA
PATPEEKKPVPGMKKFPGPVVNLSEIQNVKSELKYVPKGEQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 210.4; DB 10; pred. No. 2.2e-34; 0; Mismatches 66;
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Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                    Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                              Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 82586)
                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 82586)
Worley, K.C.
Direct Submission
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Eukaryota, Metazoa,
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Rattus norvegicus clone CH230-29I1,
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, *** SEQUENCING IN PROGRESS ***,
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length
    (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 46 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GEGR
Center clone name: CH230-2911
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of ref
Assembly program: Phrap; version 0, 990329
Consensus quality: 35907 bases at least Q40
Consensus quality: 40324 bases at least Q30
Consensus quality: 44113 bases at least Q20
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Best Local Similarity
Matches 175; Conserv
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Palmer,S., Groves,N., S
Sparrow,D.B., Barnett,L
Mohun,T. and Harvey,R.P
                                                                       CANGACTCTAGCAAAAATATCCTGTTTGTACATTTATATTTCTTCCTTTTACTTGGTTGC 677
                          ATTTCTTACTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAAC 214
                                                                                                  ATTCAATAGCTCACTAAAATTTTATATATTTTGTATGATGATTGTGAACCTCCTGAATGCC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 787)
Palmer,S., Groves,N., Schindeler,A., Yeoh,T., Biben,C., Wang,C
Sparrow,D.B., Barnett,L., Jenkins,N.A., Copeland,N.G., Koentge
Wohun,T. and Harvey,R.P.
Wohun,T. and Harvey,R.P.
The small muscle-specific protein Csl modifies cell shape and
promotes myocyte fusion in an insulin-like growth factor
1-dependent manner
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Mus musculus muscle-specific protein CSL (Csl) mRNA,
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ilarity 78.8%;
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    Groves, N., Schindeler, A., Yeoh, T., Biben, C., Wang, C.-C.,
D.B., Barnett, L., Jenkins, N.A., Copeland, N.G., Koentgen, F.,
and Harvey, R.P.

                                                                                                                                                                                                                                                                                                                /note="ortholog of Homo sapiens SMPX"
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/tranblation="MSKQPISNVRAIQANINIPMGAFRPGAGQPPRRKESTPETEEGA
PTTSEEKKPIPGMKKEPGPVVMLSEIQNVKSELKFVPKGEQ"
167 c 185 g 202 t
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/strain="C57BL/6"
/db_xref="taxon:10090"
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Pred. No. 4.8e-21;
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Search completed: April 15, 2003, 21:03:31 Job time: 1213.11 secs
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                                            288 TGT 290
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                                                                               215 ACCTGGAGGTGTGGTTTTGAGGAGGGATATGATTTTATGGA 256
                                                                                                                                                                                                                                                                                                                                             unidentified.
unidentified
unclassified.
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Location/Qualifiers
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Sequence 27 from Patent W00192567.
AX322783.1 GI:18093762
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/db_xref="taxon:32644"
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Perfect score:
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Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 7373, Ap	Sequence 5273, Ap		Sequence 438, App	Sequence 26, Appl	Sequence 206, App		Sequence 7472, Ap	Sequence 10280, A	Sequence 4, Appli	Sequence 3, Appli	Sequence 735, App	Sequence 2816, Ap	Sequence 89, Appl		Sequence 9307, Ap	Sequence 394, App	Sequence 4, Appli	Sequence 468, App	Description

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7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8		7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.9	7.9	1.9
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Sequence 4824, Ap Sequence 1, Appli			Sequence 2, Appli	Sequence 130, App	Sequence 4, Appli	Sequence 4210, Ap	Sequence 3670, Ap	Sequence 13, Appl	Sequence 34, Appl	Sequence 4535, Ap	ž	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 122, App	Sequence 3883, Ap	Sequence 1017, Ag	Sequence 1543, Ap		Sequence 3008, Ap	295,	Sequence 30, Appl	sequence 30, Appl

ALIGNMENTS

RESULT 1 US-09-962-436-468/c

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Sequence 468, Application US/09962436

| Sequence 468, Application US/09962436
| Patent No. US20020081301A1
| GENERAL IMPORMATION:
| APPLICANT: Soppet, Daniel
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing Office of INVENTION: Sets
| FILLE REFERENCE: 689290-75
| CURRENT APPLICATION NUMBER: US/09/962,436
| CURRENT FILING DATE: 2001-09-25
| PRIOR APPLICATION NUMBER: US/60/235,082
| PRIOR APPLICATION NUMBER: US/60/235,082
| PRIOR APPLICATION NUMBER: US/60/235,082
| PRIOR FILING DATE: 2000-09-25
| PRIOR APPLICATION NUMBER: US/60/234,924
| PRIOR FILING DATE: 2000-09-25
| NUMBER OF SEQ ID NOS: 568
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 468
| LENGTH: 587
| TYPE: DNA ORGANISM: Homo sapiens PEATURE: MANE/KEY: misc feature OTHER INFORMATION: n=a,t,g or c
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Matches 412; Conservative
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                                      TGTACATTTATATCTCCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTTGG 180
                                                                                                                           TATTIGTATGATGATIGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT 120
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TGTACATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCATTTTTGG
                                                                                                 TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
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100.0%; Pred. No. 2.2e-95;
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CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09880192
Patent No. US20020077470A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.3%; Score 326; DB 10; Best Local Similarity 100.0%; Pred. No. 1.8e-73; Matches 326; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020077470A1 3601719CB1
-09-880-192-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 GATTGATGTGAAGAAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATA 558
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                                                                                                                                           CAAGCTACTTCCTACAGTATTTTGGT 326
                                                                                                                                                                                                               GATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTGTATGATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTT
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                                                                                                     CAAGCTACTTCCTACAGTATTTTGGT 824
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GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
APPLICANT: Patrick J. Dillon
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 394
SEQUENCE CHARACTERISTICS:
                                          4283
                                                                                                                             4343 TGCGATTGTGCTAAAACAACTGAACGCAATGGTGCAAATTCACTTTCAACATGCATTTTT 4284
                                                                                    325
385
                                                                                                                                                                     265 TGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                  GTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTAAACTTTGTA 384
TGAGTTCAAATAATATTTGACTAAATGTAAAATGT 420
                                        TTCATTATTTGACCTCACTTTTATCTGGTTACCTTCATTATAACAGAGATAAAATTTTTA 4224
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14141 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                               Score 37.6; Di
Pred. No. 14;
0; Mismatches
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                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                     Length 14141;
                                                                                                                                                                                                               0; Gaps
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US-09-815-242-9307/c; Sequence 9307, Application US/09815242; Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.

RESULT 4

Carr, Grant J. Yamamoto, Robe Xu, H. Howard

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RESULT 5
US-10-044-090-123
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                                                      US-10-044-090-123
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 123, Application US/10044090 Patent No. US20020137081A1
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SEQ ID NO 9307
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 123
SEQ ID NO 123
SEQ ID NO 123
                                                                                                                                                                                                                                                 APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR FILING DATE: 2000-05-23
                                                        FEATURE: MAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 892168.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 22
TYPE: DNA
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                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                              TYPE: DNA
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                                                                                                                                                             ENGTH: 3633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT 218
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53.1%;
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 Score 36.6;
Pred. No. 1:
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                DB 12;
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              Length 3633;
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US-09-070-927A-89
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                                                                                                               Best Local Similarity Matches 99; Conserv
                                                                                                                                                   Query Match
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                                INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 20072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3241 AAGCCTAGAATTTCTCTTTAGGTATAT 3267
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265 TGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCCCAAGCTACTTCCTACAGTATTTTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION INDEX: 60/046,655
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
PILING DATE: 1997-11-14
ATTORNEY,AGENT INFRMATION:
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OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scie:
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTAAAAAAAAAAAAGACTATGACCAAAATGGCTTAAGATAAAGTATTTTTAAGGAAG 3180
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                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kenley K. Hoover REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Maryland
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                                                                                                               Conservative
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                                                                                                                              8.7%;
48.8%;
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                                                                                                           Score 36.6; DE Pred. No. 29; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00669
PRIOR PPLICATION NUMBER: PCT/USO1/00665
PRIOR PPLICATION NUMBER: PCT/USO1/00666
PRIOR PPLICATION NUMBER: PCT/USO1/00668
PRIOR PPLICATION NUMBER: PCT/USO1/00668
PRIOR PPLICATION NUMBER: PCT/USO1/00663
PRIOR PPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PRILING DATE: 2001-01-30
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                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 2816
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/608,408,
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      OTHER INFORMATION: MAP TO AL033539.17
OTHER INFORMATION: EXPRESSED IN BONE I
OTHER TUPORMATION: EXPRESSED IN FETAL
OTHER INFORMATION: EXPRESSED IN FETAL
                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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BONE MARROW, SIGNAL
HEART, SIGNAL = 1.4
FETAL LIVER, SIGNAL
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; FEATURE:
, NAME/KEY: SITE
; LOCATION: (1841)
; OTHER INFORMATION: n equals a,t,g, or
US-09-764-864-735
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US-09-764-864-735
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                                                                                                                                                                   US-10-014-799A-3
                                                                                                                                                                                    RESULT 9
                                                                                                          GENERAL INFORMATION:
                                                                                                                            Sequence 3, Application US/10014799A Publication No. US20030055219A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 735
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Best Local
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                APPLICANT: Myriad Genetics,
APPLICANT: Cimbora, Daniel
APPLICANT: Heichman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
             APPLICANT: Bartel, Paul L. TITLE OF INVENTION: Protein-Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
FILE REFERENCE: 2318-272-II
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           1434
                                                                                                                                                                                                                                                                                                                   1374
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                                                                                                                                                                                                                                                                              134
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                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                              14 AAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATATATTTGTATGATG
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                                                                                                                                                                                                                                           CTAGAATTTCTCTTTAGGTATAT 1456
                                                                                                                                                                                                                                                                              CTCTTCCTTCTAGTTGGCTGTAT 156
                                                                                                                                                                                                                                                                                                                                                    ATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGTACATTTATAT 133
                                                                                                                                                                                                                                                                                                                                                                                           ÁBÁBAÁAÁAAAAAGÁCTÁTGACCABÁÁTGGCTTÁAGATABAGTATTTTTTAAGGAAGBAAG 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
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llarity 57.5%;
Conservative
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Pred. No. 16
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Pred. No. 6.3;
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US-09-754-853A-4/c
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LOCATION: 551
OTHER INFORMATION: Xaa
US-10-014-799A-3
                                                                                                                                            US-09-754-853A-4
                                                                                    Query Match
Best Local /
                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 513509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09754853A Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810) B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILLING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR PILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
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CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/255,152
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
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                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (111805)..(113968),(114684)..(115204)
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LOCATION: (1)..(2271)
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                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2552 AMAMAMAMAMAGACTATGACCAMMATGGCTTAAGATAAAGTATTTTTAAGGAAGAAAG 2611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2672 CTAGAATTTCTCTTTAGGTATAT 2694
242 ATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTGATGAAAAGTTTCCC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 CTCTTCCTTCTAGTTGGCTGTAT 156
                                                              Match 8.5%;
Local Similarity 50.3%;
tee 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGTACATTTATAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATATATTTTGTATGATG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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53.1%;
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                                                          Score 35.8; DB 9;
Pred. No. 1.8e+02;
0; Mismatches 87;
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Pred. No. 20;
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                                                                                                Length 513509;
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                                                          0; Gaps
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GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

ITILE OF INVENTION: Methods For Monitoring Multiple Gene

ITILE OF INVENTION: Expression

FILE REFERENCE: 10005.500-US

CURRENT APPLICATION UNMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/60,598

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR APPLICATION NUMBER: 60/279,526

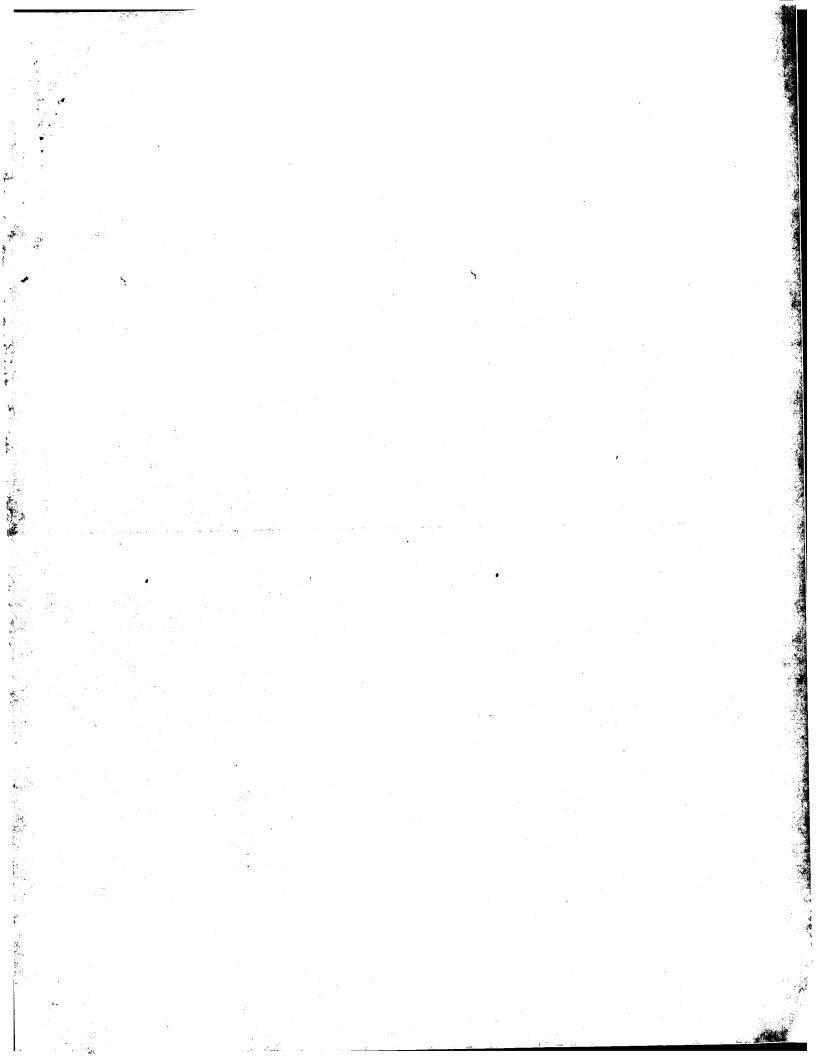
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-974-300-7472/c
; Sequence 7472, Application US/09974300
; Patent No. US20020146721A1
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US-09-974-300-7472
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                                                       NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7472
LENGTH: 411
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LENGTH: 345
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Best Local S
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
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SOFTWARE: FastSEQ for Windows Version
             ORGANISM: Bacillus clausii
                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 GTTTCCCAAGCTACTTCCTACAGTATTTTGGTAATATTTGGAATGCGTTTTAGTTCTTC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 AAATGTGA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 AAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTT 361
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54.7%;
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Pred. No. 11;
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US-09-867-701-4700/c
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4700
LENGTH: 439
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Best Local
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                                                                         NUMBER OF SEQ ID NOS: 275
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                  Sequence 206, Application US/09920455 Patent No. US20020168647A1
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN
FILE REFERENCE: 210121.497
                                                                                                                                                                                     APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF HEAD AND NECK CANCER
                                                                                                                                    FILE REFERENCE: 210121.540
CURRENT APPLICATION NUMBER: US/09/920,455
CURRENT FILING DATE: 2001-08-01
ORGANISM: Homo sapiens
                                   LENGTH: 461
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 AAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTTAGTTTCTTCACCTTTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 CGTGTCGGTCGATTCCACCCCTACGTCCCCAGAATCTTTAATATAAATGAGCTCTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 GATGCGGATÄATTAAÄGCCATGGCAGCTTGGATGGCTACTTGTTTACCAATCGCTGCTTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                            113 A 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 GAAGTATCTTCCTATGCTTGTGATGACTGTATGAGAAAACTAGGCTAATAGTGTAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AAATTATGTCACTAAACTTTGTATGAGTTCAAATAATATTTTGACTAAATGTAAAATGTG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AAACTATTTGGTATTTGAATTAAATGAATATTAATGATGCACCTTGGTTTTTTTGGTTTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 CATTTATATCTCTTCCTTCTAGTTGGCTGTATTTCTTACTTTATCTTCA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 8.2%;
Local Similarity 50.3%;
hes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 55.4 tes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 AACTIGGATCTCTTTCTTTACCTGCGCTGCATCTTGCTCTATATCGCCA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 TGTATGATTGTGAACCTCCTGAATGCCTGAGACTCTAGCAGAAATGGCCTGTTTGTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GATGTGAAGAATAAAGAGGCAGAAGATGGATTCAATAGCTCACTAAAATTTTATATATT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A 422
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Pred. No. 17;
0; Mismatches
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; LOCATION: (182)...(1349)
; OTHER INFORMATION: K+Hnov42
US-10-121-746-26
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Best Local Similarity
Matches 67; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3204
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
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APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. US20030036648A1el Human
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LOCATION: 453 _
OTHER INFORMATION: n = A,T,C
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Local Similarity 49.2%;
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                                                               AAATTATGTCACTAAACTTTGTATGAGTTCAAATAAATATTTGACTAAATGTAAAATGTG 421
                                                                                                                              AAACTATTTGGTATTTGAATTAAATGAATATTAATGATGCACCTTGGTTTTTTTGGTTTT
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Pred. No. 41;
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Pred. No. 17;
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APPLICATION NUMBER: PCT/US99/03826
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Search completed: April 16, 2003, 01:19:58 Job time : 187.167 secs 2157 Å 2157 422 A 422



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2: /cgn2_6/ptodata/1/

3: /cgn2_6/ptodata/1/

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/cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
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      US-09-484-970B-111
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US-08-961-527-48
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US-08-961-527-48
US-08-971-395-1
US-08-971-335-455
US-09-071-035-455
US-09-071-035-453
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US-09-071-035-453
US-08-998-416-287
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US-08-9154-344-1
US-08-30-188-1
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US-08-31-080-1
US-08-31-080-1
Sequence 111, App Sequence 1047, App Sequence 1047, App Sequence 1, Appli Sequence 26, Appli Sequence 26, Appli Sequence 455, App Sequence 455, App Sequence 453, App Sequence 453, App Sequence 287, App Sequence 1, Appli Sequence 105, Appli Sequence 105, Appli Sequence 105, Appli Sequence 105, Appli Sequence 1, Appli
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US-09-484-970B-111

Sequence 111, Application US/09484970B

Patent No. 6426186

GENERAL INFORMATION:

APPLICANT: Jones, Karen A.

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONB REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL Program

LENGTH: 909

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

NAMEKEY: misc feature

OTHER INFORMATION: Incyte ID No. 6426186 0216
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      CAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTTAGTTCTTCACCTTT
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ilarity 100.0%; Pred. No. 1.5e-100;
Conservative 0; Mismatches 0;
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US-07-618-312A-1
US-08-110-786A-7
US-08-180-228-1
US-08-909-965C-8
US-08-909-965C-8
US-08-68-381A-6
US-08-68-392-46-3-14
US-09-385-982-72
US-09-385-982-72
US-09-385-982-72
US-09-385-982-73
US-09-385-982-73
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US-09-385-982-73
US-09-385-982-73
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US-08-441-803-36
US-08-445-265A-36
US-08-455-265A-36
US-08-455-265A-36
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US-08-961-527-111/c
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Sequence 1047, Application US/09134001C
Patent No. 6380370
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9110
CITY: Rockville
CTATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION: Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 AAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTTT 361
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OPERATING SYSTEM:
SOFTWARE: ASCII T
                                                                                                                                                                                                                                                                                                                                                    442
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5. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATAACATTCTAGACGAATACGAATCGTCCTTGAAATTCGTGTCAATTATGTATCTATT
                                                                                                                                                                                                                                                                                                                                                AGCTATAGGTACTAATGATTGTATTACATACAATAATGCTGTTACAAAAAATAAAAT 386
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; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1047
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SEQ ID NO 1047
LENGTH: 1755
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Charles
TITLE OF INVENTION:
              ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1373 AAACAGTTGTATGTTTTGTAGGAGATGGCGGTTTTCAAATGACGAACCAAGAAATGGCTT 1432
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MEDIUM TYPE: Diskett
COMPUTER: HP Vectra
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                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 TCCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAAT 339
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                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                        FILING DATE:
TELEFAX:
                                                                                                                                                                                                                            APPLICATION NUMBER:
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(301) 309-8512
                                                                                                                                                                                                                                                                  ASCII Text
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46.1%;
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                                                                                                                                                                                                                                                                                                          3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                      version
                                                        PB340P1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
TYPE: nucleic double
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                                              Query Match 8.4%;
Best Local Similarity 48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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                                                                                                        TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
APPLICANT: Gan, Sueheng
TITLE OF INVENTION: Transgenic I
TITLE OF INVENTION: Senescence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8192 AGACTTCTGCGGTTTTAGCTTGCAAGTCCAGTAATTTCTCCACAGCTTGGGACGTATTTT
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                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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1 South Pinckney Street
                                  Conservative
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                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic Plants with Altered Senescence Characteristics
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                                              Score 35.4; DB 4;
Pred. No. 1.3;
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                             ed. No. 1.3;
Mismatches 106;
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                                                        Length 3182;
                               Indels
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                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                             TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                   163 CTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAG 222
                                                                                                                                                                                                                                                    TELEPHONE: 608-251-5000
223 GGTGTGGTTTTGAGGAGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGA 282
                                                                                                                        CURRENT APPLICATION DATA:
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APPLICANT: Gan, Sushang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
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                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 GGTGTGGTTTTGAGGAGGGTATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 CTTTATCTTCATTTTTGGCACCTCACAGAACAAATTAGCCCATAAATTCAACACCTGGAG 222
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STATE: WI
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                                       TAGCTAATATAGCATGATTCTAAATTTGTTTTTTGACACCCTTTTTTTCTCTCTTTGGTG 256
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Pred. No. 1.3;
0; Mismatches 106;
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US-09-071-035-455/c
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SOFTWARE: FastSEQ for
SEQ ID NO 26
LENGTH: 3204
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                                                                                                                                                                                                                          Sequence 455, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
TITLE OF INVENTION: No. 639761el Human Potassium Channels
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                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gil H. Choi
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NAME/KEY: CDS
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OTHER INFORMATION: K+Hnov42
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2277
                                                                                                                                                                                                                                                                                                                                   2157 A 2157
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                                                                                                                                  APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ent
NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTTT 361
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                    362 АДАТТАТСТСАСТАЛАСТТТСТАТСАСТСАЛАТАДАТАТТТСАСТАЛАТСТАЛАДСТС
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                                                                                                                         ADDRESSEE:
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                                                                                  T: 9410 Key West Avenue
Rockville
                                    20850
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Hu, Ping
Rutter, Marc
                                                                   Maryland
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                                                                                                                         Human Genome Sciences, "Inc.
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Pred. No. 2.
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RESULT 9
US-09-071-035-449/c
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Best Local Similarity 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 449, Application Patent No. 6448043
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APPLICANT: Gil H. Choi
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ODERATING SYSTEM: MSDOS Vei
SOFTWARE, ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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STREET: 9410
CITY: Rockville
CTATE: Maryland
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                        OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                      CLASSIFICATION:
                NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
REFERENCE/DOCKET NUMBER:
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HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1924;
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US-09-071-035-453
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                                                                                               TELECOMOUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 453:
SEQUENCE CHARACTERISTICS:
LENGTH: 3953 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-071-035-449
                         Best Local
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6448043
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 3963 base pairs
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDO:
SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2582 AAAGCTTGNATATCCGCGTACTTCTCTTTAATTTCCTTAATCACTGCTTCTACTTCTGGA 2523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 TCATTTTTGGCACCTCACAGAACAAATT 198
                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y Match
Local Similarity 51.4%; Pred. No. 4.8;
hes 76; Conservative 0; Mismatches 72; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AAATTTTATATATATTATGATGATGATGTGAACCTCCTGAATGCCTGAGACCTCTAGCAGAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGGGTCTTTAAATGTCACCTTCTCTACGTTTTTTCGGGTGTTTTCGTTGCTGTTTCT 2463
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o. 6448043
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maryland
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9410 Key West Avenue ,
           Conservative
                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            ם: שופאפtte, 3.50 inch, 1.4Mb etorage
HP Vectra 486/33
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                    7.9%;
51.4%;
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     Score 33.4; DB Pred. No. 4.8; 0; Mismatches
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                                  DB 4; Length 3963;
      72,
     Indels
   <u>,</u>
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Gaps
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US-08-998-416-287
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                                                                         Query Match 7.9%;
Best Local Similarity 48.4%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: CH 0016/97
EILING DATE: 31-DEC-1996
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Patent No. 62
                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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APPLICANT:
534 TTTTAAAATGTTTTATGTTTAAATAGATAATAACAATTAAATAATAAAATTAAGATGCC 593
                      230 TTTTGAGGAGGGATATGATTTTATGGAGAATGATATGGCAATGTGCCTAACGATTTTTGAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wendiand, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                       LENGTH: 860 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27709
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T: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                    PAG1240UP
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Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                      single
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                                                                       Pred. No. 3.5;
0; Mismatches
                                                                                          Score 33.2;
Pred. No. 3.
                                                                                                       DB 4;
                                                                         95;
                                                                                                         Length 860;
                                                                       Indels
                                                                     0,
                                                                   Gaps
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FILING DATE:

14-DEC-1995

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US-09-502-600-30
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US-08-557-146-1/c
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CURRENT PILLING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 30
LENGTH: 969
TYPE- NUMBER: 069
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: full length cDNA of SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               654 TTTTATCCTTCTATCTTATGTNTTTTACCTAAGAATTTAANAATATATACCTCCTAAATAT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714 ATAT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 GAAAAGTTTCCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTTGGAATGCGTTTTAGT 349
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377
                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 GTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTAA 376
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 CAGGGCATGAGGTTTAAATATATCTTTGAGGAAAGGTAAAGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 57.8%; es 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                        STATE: New York COUNTRY: U.S.A. ZIP: 10036-2787
                                                                                                                                                                                                                   ADDRESSEE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ТСТТСАССТТТБААТТАТСТСАСТАААСТТТСТАТСАСТСАААТААТАТТТСАСТАА 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTTGTATGAGTTCAAATAATATTTGACTAAATGTAAAAT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTTGTGTTTTATTTGTTTTTGGTTTTAGGTCTTTACCAATTTGATTGGTTTATCAA 66
                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien, Timothy J.
                                                                                                                                                                                                  1155 Avenue of the Americas
                                                                                                                                                                                                                   White & Case,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions and Methods for the Early Diagnosis
                                                                                                                                                                                                                                                      Recombinant S
Enzyme (SCCE)
: 17
US/08/557,146
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                                                                                                                                                                                                                     Patent Department
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                          Stratum Corneum Chymotryptic
                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                      #1.25
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US-09-154-344-1/c
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Best Local Similarity
Matches 59; Conserva
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LOCATION:
US-08-557-146-1
                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09154344
Patent No. 5981256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 354-81
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CI
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                  APPLICANT: Egelrud,
APPLICANT: Hansson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 ACTTTGTATGAGTTCAAATAATATTTGACTAAATGTAAAAT 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                  CITY: New York
STATE: New York
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                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                               STREET:
                                       CLASSIFICATION:
                                                     FILING DATE:
                                                                    APPLICATION NUMBER:
                                                                                                                                                                                    COUNTRY: U.S.A.
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1155 Avenue of the Americas
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          US 08/557,146
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Matches
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08930188 Patent No. 6093397
                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Johnstone, Edward M.

APPLICANT: Little, Sheila P.

TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSE: Bli Lilly and Company

STREET: Lilly Corporate Center

CITY: Indianapolis

STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
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Local Same
59;
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REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           COUNTRY:
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Similarity 57.8%; Pred. No. 3.6;
59; Conservative 0; Mismatches
                                                                                                                                                                                                                    United States of America
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NO: 1:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-930-188-1
                                                                                                                                                            Query Match 7.9%;
Best Local Similarity 57.8%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                        317 GTATTTTGGTCAATATTTTGGAATGCGTTTTAGTTCTTCACCTTTTAAATTATGTCACTAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
                            377 ACTITGTATGAGTTCAAATAAATATTTGACTAAATGTAAAAT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
86 CAGGGCATGAGGTTTAAATATATCTTTGAGGAAAGGTAAAGT 127
                                                                       26 GTTTTGTGTTTCTTTATTTGTTTTTGGTTTTAGGTCTTTACCAATTTGATTGGTTTATCAA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9;
                                                                                                                                                                                                                                                                                                                                                                                                                      317-277-1090
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Pred. No. 3.8;
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Search completed: April 15, 2003, 22:53:50 Job time: 46.9694 secs

